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Peptide B2 major f OA-519 peptide E2 from a Peptide B2 from a Peptide 1. Promega peptide 7. Promega peptide 7. Phosphokinase subs Phosphokinase subs Protein kinase sub promega protein kinase sub promega protein kinase sub Labelled peptide s Protein kinase sub Shigella-like toxi Sequence of novel Phosphokinase subs Phosphokinase subs
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Synthetic sequence
Protein kinase A p
HiNOS immunogenic
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HLA-B2702 CTL modu
HLA-B2702.75-84(T)
HACroxymethylgluta
T-cell modulating
T-cell modulating
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Radiolabelled HiNO
C-terminally subst
                                                                                           February 8, 2000, 01:00:28; Search time 122.56 Seconds (without alignments) 1.933 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                  188963 seqs, 23686106 residues
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Listing first 45 summaries
                                                               - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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R31168
R73670
W12322
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17
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W12321 W23651 W23311 W33788 W73273 R8687 W35792 W35790 W35790	ALI	Ą.	OA-51 globi globi	•					activ with pecia	pp; E tide	cross-reactive with the haptoglobin related (hpr) 0A-519 can be used to raise antibodies reactive w found on the hpr gene product, but not on haptogic useful in cancer, especially breast cancer, prognagence 6 AA;	Score 9; DB 1; Pred. No. 1.5e+05 ; Mismatches			
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		1 886	JAN- JAN- Lide 119;	5658 SEP-	JAN-	- HE	P N	70) 1 da 7 97	enc rais	ays nple pre	cross-re OA-519 c found on useful i	altc		I KAAL	2 229; 229; 229; 229; 219 210 220; 230 230
00000000000000000000000000000000000000		JLT 386 W328	AC 16-72808; DI 16-7281998 (first entry) DE Peptide B2 major fragment of OA-519. KW OA-519; cross-reaction; haptoglobin related; hp. KW epitope; haptoglobin 1; haptoglobin 2; cancer; lx. KW promonsis assay: nentide R2 major	Home USS(24-7-1	26 - I	26-0	Kuha Kuha	to r	assa Exan The	cros OA-E four usef	Query Ma Best Loc Matches	, ,	•	RESULT 2 W57229 W57229 standard; peptide; 6 AA. AC W57229; DT 04-AUG-1998 (first entry) DE 0A-519 peptide fragment SEQ ID NEW Human; hpr gene; haptoglobin; screening; prognosis; prostatic OS Synthetic. OS Homo sapiens. PD 02-JUN-1998.
		RESU W326 ID	XXX DOT	OS PN PD	ዋ ዋ ዋ ዋ ສ	7 7 7 8 8 8 8	7 H	P P P	E L L L	F 8 5	888888	N M M	δo :	2	REST W572 ID AC DD DD KW KW KW COS OS

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ID R3
AC R3
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                                                                                                                                                                               The present sequence represents an OA-519 peptide fragment from an example 12; Column 39; 50pp; English.

The present sequence represents an OA-519 peptide fragment from an example of the present invention. The present invention describes a method and a kit for screening human samples to aid in determining the prognosis of breast carcinoma. The kit comprises in one or more containers: an antibody which specifically binds to one or more containers: an antibody which specifically binds to one or more set Asp Asp Arg Phe Pro Lys Pro Pro Glu Ile Ala Asn Gly Tyr Val Glu Lys Leu Phe Arg Tyr Glu Cys Dut not found on haptoglobin 1 or 2; and a histologic section from the tumour, and contracting the section with an antibody (as described above), and determining whether the antibody antibody collically binds to the section in cytoplasmic cellular regions, where the presence of the antibody binding correlates with a worsened the prognosis of the collicit where the presence of the social tumour. The method is useful for the prognosis of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                projectide comprising epitope of hpr gene product - useful for producing antibodies for cancer prognosis
Example 12; Column 25; 51pp; English and the present sequence represents a peptide derived from a protein that is immunologically cross-reactive with the haptoglobin related (hpr) gene product from breast cancer cells. The specification also describes a peptide that is immunologically cross-reactive with projectional antibodies that specifically bind the hpr gene product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide B2 from a protein cross-reactive with the hpr gene product. Haptoglobin related gene; hpr gene; haptoglobin 1; haptoglobin 2; antibody; breast carcinoma; diagnostic marker; human solid tumour. Synthetic.
                                                                                                                                          Prognosis of solid tumours e.g. breast carcinoma - based on detection of OA-519 protein or mRNA in histological sections and
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                                                                                                                                                                                                                                                                                                                                                                                                    solid tumours, especially breast carcinomas and prostatic adenocarcinomas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.9%; Score 9; DB 1; Le 50.0%; Pred. No. 1.5e+05; iive 0; Mismatches 2;
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26-JUL-1991; US-735522.
24-JUL-1993; US-97716.
26-JUL-1993; US-96908.
05-JUN-1995; US-469009.
(UXJO) UNIV JOHNS HOPKINS.
Kuhajda FP. Pasternack GR;
WPI: 99-131358/11
                                                                    21-JUL-1992; US-917716.
25-JUL-1993; US-096908.
(UVJO ) UNIV JOHNS HOPKINS.
Kuhajda FP, Pasternack GR;
WPI; 98-332128/29.
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26-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                         04-DEC-1990; US-622407
26-JUL-1991; US-735522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUN-1995; 469009
24-JAN-1994; US-188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                        biological fluids
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W84380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-APR-1999 (first entry)
Peptide fragment derived from protein OA-519.
Monoclonal antibody; OA-519; haptoglobin 1; Hg1; Hg2;
haptoglobin related protein; hpr; diagnostic marker; human solid tumour;
The peptide can be used to raise antibodies specific for a protein that is immunologically cross-reactive with the hpr gene product but not with haptoglobin 1 or haptoglobin 2. The peptide is found in the cytoplasm of breast carcinoma cells and is a useful diagnostic marker in human solid tumours for predicting the propensity for tumour invasion and early metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of clinical recurrence and overall worsened prognosis. The antibodies
                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            markers for human solid tumours, particularly breast cancers brample 12; Column 25; 51pp; English.

Peptides W96750-53 are derived from the OA-519 protein. The peptides whof specification describes monoclonal antibodies which specifically bind an epitope found on OA-519 but not on haptoglobin 1 (Hg1) or Hg2 or, optionally haptoglobin related protein (hpr) gene product. The antibodies can be used to detect OA-519 which is useful as a diagnostic marker in human solid tumours and for predicting the propensity for tumour invasion and early metastasis, particularly with breast cancers. They can detect aggressive tumour cells which result in decreased survival, increased mates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUN-1995; 469007.
24-JAN-1994; US-188426.
24-JAN-1999; US-297722.
04-DEC-1999; US-622407.
26-JUL-1991; US-735522.
24-JUL-1995; US-917716.
26-JUL-1995; US-906908.
05-JUN-1995; US-469007.
(UVJO ) UNIV JOHNS-HOPKINS.
Kuhajda FP, Pasternack GR;
WPI; 99-166717/14.
New anti-OA-519 antibodies - useful as diagnostic and prognostic
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                                                                                                                                                                                                                                                                 DB 1; Length 6;
1.5e+05;
ches 2; Indels
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Pred. No. 1.5e+05;
); Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tumour invasion; early metastasis; breast cancer
                                                                                                                                                                                                                                                                 Score 9; DB 1, Pred. No. 1.5e-0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W96753 standard; peptide; 6 AA. W96753;
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50.0%;
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Best Local Similarity 50.0
Matches 2; Conservative
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Best Local Similarity
Matches 2; Conserv
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US5872217-A.
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Gaps

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R= H or an amino protecting gp.; and -CO.X-NHR= a residue of a peptide of formula NHR-X-COOH capable of acting as substrate for a phosphokinase. Examples of such substrate peptides include the heptapeptide that has become known as Kempide having the sequence given in R38351 or related peptides given in R38352-63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-0cT-1993 (first entry)
Phosphokinase substrate peptide (2)
Tumour-binding protein; target; substrate; phosphokinase; Kemptide.
                                                                                                                                                                                                                                                    15-007-1993 (first entry)
Phosphokinase substrate peptide (1).
Tumour-binding protein; target; substrate; phosphokinase; Kemptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Creighton AM;
WPI; 93-199247/25.
WPI; 93-199247/25.

Structurally-modified tumour-binding proteins - used as targetting proteins, for treatment of tumours claim 5; Page 13; 20pp; English.

A protein that will bind to a tumour-associated structure has the amino gp. in at least one basic amino acid in the binding protein structurally modified to convert the amino gp., NH2, to the gp.-NH-CO-X-NHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Structurally-modified tumour-binding proteins - used as targetting proteins, for treatment of tumours Claim 5; Page 13; 20pp; English.
A protein that will bind to a tumour-associated structure has the amino gp. in at least one basic amino acid in the binding protein structurally modified to convert the amino gp., NH2, to the gp.
                                         2; Indels
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  Length 7;
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DB 1; Le
. 1.5e+05;
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. 1.5e+05;
Score 9; DB 1;
Pred. No. 1.5e4
0; Mismatches
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Pred. No. 1.5e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                        23 JUN-1993.
15-DEC-1992; 026144.
16-DEC-1991; GB-026650.
(BRTE-) BRITISH TECHNOLOGY GROUP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JUN-1993.
15-DEC-1992; 026144.
16-DEC-1991; GB-026650.
(BRTE-) BRITISH TECHNOLOGY GROUP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R38352 standard; peptide; 7 AA.
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                                                                                                                                                                                                                     R38351 standard; peptide; 7 AA.
52.9%;
50.0%;
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Query Match 52.9
Best Local Similarity 50.0
Matches 2; Conservative
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WPI; 93-199247/25.
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                                                                                                                                                                                                                                                                                                                                                Promega peptide 1 is tagged with dansyl at residue 1 and may be used in a novel non-radioactive method of quantitating the presence or activity of an enzyme. The method can be used for rapid, specific and highly sensitive detection of enzymes such as protein kinases, phosphatases and proteases. They can be used to study enzyme function in metabolism and in diagnosis of disease. They also see also R37427-36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 24; Page 27; 103pp; English.

Promega peptide 7 is tagged with dansyl at residue 1 and may be used in a novel non-radioactive method of quantitating the presence or activity of energyme. The method can be used for rapid, specific and highly sensitive detection of enzymes such as protein kinases, phosphatases and proteases. They can be used to study enzyme function in metabolism and in diagnosis of disease. They also allow quantitative determ. of the enzyme's activity.

See also R37426.36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
Modified peptide substrate; non-radioactive; detection; dansyl; sulphorhodamine 101; lissamine; rhodamine; enzymes; phosphatases; protein kinases; proteases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Promega peptide 7. Modified peptide substrate: non-radioactive; detection; dansyl; sulphorhodamine 101; lissamine; rhodamine; enzymes; phosphatases; protein kinases; proteases.
                                                                                                                                                                                                                                                                              Ouantitating presence or activity of enzyme – by incubating with modified peptide substrate and measuring the modified peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI: 93-182698/22.
Quantitating presence or activity of enzyme - by incubating with
modified peptide substrate and measuring the modified peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 9; DB 1; Length 7;
Pred. No. 1.5e+05;
Mismatches 2; Indels
                                                                                                                    /note= "detection tag= dansyl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                     prod.
Claim 24; Page 27; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R37432 standard; peptide; 7 AA.
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50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                       27-MAY-1993.
12-NOV-1992; U09595.
12-NOV-1991; US-791928.
(PROM-) PROMEGA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-MAY-1993
12-NOV-1992; U09595.
12-NOV-1991; US-791928.
(PROM-) PROMEGA CORP.
                                                                                                                                                                                                                                       White DH;
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Best Local Similarity
Matches 2; Conserv
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                                                                                                modified_site
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                                                           Synthetic.
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WO9523612-A1.
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R94549
ID R94549
AC R94549;
DT 19-JUN-
DE Proteir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goueli
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acting as substrate for a phosphokinase.

Examples of such substrate peptides include the heptapeptide that has become known as Kemptide having the sequence given in R38351 or related Sequence 7 AA;
                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                               Well: 94-20019474.

Wew fatty acyl-peptide conjugates for inhibiting cell
proliferation - more active than free peptide, partic. for
treating tumours, virus-infected cells, psoriasis, etc.
Disclosure: Fig. 1; 45pp; English.
The peptides given in R55718-48 can each be conjugated through an
amide linkage with a polyunsaturated fatty acid molety, such as
docosahexaenoic acid or elcosapentanoic acid, to improve
antiproliferative activity. The cAMP-dependent
protein-kinase inhibitor given in R55736 can be used to modulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein Kinase A phosphorylation site in Kemptide sequence. Peptide library: phosphorylation site; protein kinase; substrate; inhibitor; competitor; cellular response; cell cycle control; immune response; transcriptional activation; cell development.
                                                                                                                                                                                                                   16-NOV-1994 (first entry)
Protein-kinase inhibitor.
Protein-kinase inhibitor; fatty acyl-peptide; conjugate;
antiproliferative; tumor; pordasis; docosahexaenoic acid; DHA;
elcosapentaenoic acid; EPA; antitumor.
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                                                                                Score 9; DB 1; Length 7;
Pred. No. 1.5e+05;
0; Mismatches 2; Indels
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1.5e+05;
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                                                                                                                                                                                                                                                                                          09-JUN-1994.
29-NOV-1993. HU0065.
30-NOV-1993. US-984293.
(BIOS-) BIOSIGNAL KUTATO FEJLESZTO KFT.
(SYNT-) SYNWHEDIT C PEPPIDES INC.
BALOGH A. CACHIA BJ, HOGGES RS, HOTV
SZEGGETKENYİ F, Vadasz Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 9;
Pred. No.
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13-70L-1995.
06-JAN-1995; U00147.
07-JAN-1994; US-178570.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R79663 standard; peptide; 7 AA.
R79663;
                                                                                                                                                                                                R55736 standard; peptide; 7 AA.
                                                                               52.9%;
nilarity 50.0%;
Conservative 0
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Best Local Similarity
                                                                                Query Match
Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 AA;
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WO9518823-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                          The foliated peptides can be used to screen cpds. for effects on the protein kinase activity, generate antibodies to identify native kinase substrates, or modulate a variety of cellular responses in which protein kinases are involved eg. cell cycle control, immune response, transcriptional activation or cell development.
Determined and sequence of protein kinase phosphorylation site - by phosphorylation of peptide library and sequencing blosphosphorylation of peptide library and sequencing for modulating or detecting protein kinase Example 5: Page 32; 131pp; English.

An oriented degenerate peptide library of the amino acid formula R79661 was constructed to isolate the amino acid sequences at the phosphorylation sites of a protein kinase eg. protein kinase A, cyclin B/p33(cdc2), src family kinases, etc. Peptides which are phosphorylated are isolated and their amino acid sequences are compared to known substrate/inhibitor peptide sequences for that protein kinase. The peptides R79662-73 represent phosphorylation sites for protein kinase A. This peptide sequence is the phosphorylation site in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quantitating activity of a selected protein kinase on a peptide substrate - by conjugating the substrate to a binding cpd. Claim 15; page 33; 49pp; English.

The activity of a selected protein kinase (PK), pref. Ser-Thr or Tyr PK, is quantified by conjugating a binding cpd. to a peptide substrate, pref. one of the Promega peptides A.H (R83007.14), adding this to a PK contg. soln., incubating the soln. to form a modified beptide prod. and then measuring the activity of the PK.
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Promega protein kinase substrate peptide A.
Promega: peptide; substrate; A; protein kinase; activity; assay.
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J. 1.5e+05; 2; Indels
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Pred. No. 1.5e
0; Mismatches
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Pred. No.
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19-JUN-1996 (first entry)
Protein kinase substrate peptide.
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50.0%;
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Best Local Similarity 50.0
Matches 2; Conservative
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04-MAR-1994; US-208573.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                 Kemptide sequence
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20-MAY-1997 (first entry)
Labelled peptlade substrate used in enzyme activity assay.
Enzyme activity; assay; measurement; label; rhodamine; dansyl;
non-radioactive; electrophoretic separation; protein kinase; protease;
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Labelled peptide substrate used in enzyme activity assay.
Enzyme activity; assay; measurement; label; rhodamine; dansyl; non-radioactive; electrophoretic separation; protein kinase; protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         wooled a peptide substrate used in a non-radioactive assay for measuring enzyme activity. The assay comprises incubating the enzyme with the labelled peptide substrate to form a labelled peptide substrate to form a labelled peptide product from the substrate by agarose gel electrophoresis and measuring the amount of product by detecting the label by fluorescener chemiuminescence. The assay can be performed rapidly and with great sensitivity. This peptide is especially for determining cyclic AMP-dependent protein Kinase activity, e.g. to study its function in metabolism or to screen for potential inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shultz JW, White DH; WPI: 97-033568/03. WPS: 97-033568/03. Non:radioactive assay for measuring enzyme activity - involving electrophoretic sepn. of labelled cleavage prod. from labelled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "labelled with dansyl detection tag'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 7;
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1.5e+05;
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detection tag"
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Pred. No. 1.5e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide substrate
Claim 5; Column 37-38; 35pp; English.
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50.0%;
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12-NOV-1991; 791928.
12-NOV-1991; US-791928.
21-0AN-1994; US-185448.
(PROM-) PROMEGA CORP.
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03-DEC-1996.
12-NOV-1991; 791928.
12-NOV-1991; US-791928.
21-JAN-1994; US-185448.
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Shultz JW, White DH
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Best Local Similarity
Matches 2; Conserv
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3 RASL 6
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                                                         RASL
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1 RXXL
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                                                                                                                                                                                                                                W09649;
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W09655
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W09649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                         Phosphorus labelled antibodies for use in cancer therapy - comprise protein kinase peptide substrate sequence and specific targetting CDR, for radio-labelling diseased cells with a phosphorus isotope CDR, for radio-labelling diseased cells with a phosphorus isotope CDR in 5; Page 43; 62pp; English.

Peptide substrates (R94549-56) for protein kinases are incorporated into fusion proteins that also include an antibody complementarity determining region. The fusion protein is produced by recombinant DNA methods and can be expressed in prokaryotic or eukaryotic host cells. The peptide substrate moiety of the fusion protein can be radiolabelled by treatment with a protein kinase and a 32P- or 33P-labelled phosphate donor. The radiolabelled fusion protein is used for targetted radiotherapy of a patient suffering from a
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                              humanised antibody; complementarity determining region; CDR;
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Cancer; therapy; radiotherapy; radiolabelling; phosphorus;
humanised antibody; complementarity determining region; CDR;
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n. 1.5e+05;
2; Indels.
radiolabelling; phosphorus;
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1.5e+05;
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Pred. No. 1.5e
0; Mismatches
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Pred. No.
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                                                                                                                                                                                                                                                                  Leung S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tumour or an infectious lesion.
Sequence 7 AA;
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   therapy; radiotherapy;
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R94550;
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                                                      targetting; protein kinase
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WPI; 96-179897/18.
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18-SEP-1995; U11405.
16-SEP-1994; US-308103.
(IMMU-), IMMUNOMEDICS INC.
                                                                                                                                                                      18-SEP-1995; U11405.
16-SEP-1994; US-308103.
(IMMU-) IMMUNOMEDICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 52.9
Best Local Similarity 50.0
Matches 2; Conservative
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Best Local Similarity
Matches 2; Conserv
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WO9608506-Al.
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RESULT 13

R94550

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Gaps

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PT Non:radioactive assay for measuring enzyme activity - involving PT Non:radioactive assay for measuring enzyme activity - involving PT electrophoretic sepn. of labelled cleavage prod. from labelled PT peptide substrate used in a non-radioactive assay for measuring enzyme activity. The assay comprises incubating the enzyme activity. The assay comprises incubating the enzyme activity. The assay comprises incubating the enzyme of product; separating the product from the substrate by agarose gel conduct; separating the product from the substrate by agarose gel corrophoresis and measuring the amount of product by detecting the captorned rapidly and with great sensitivity. This peptide is especially for determining cyclic ANP-dependent procein kinase contential inhibitors.
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Query Match 52.9%; Score 9; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.5e+05;
Matches 2; Conservative 0; Mismatches 2; Indels 0;
Qy 1 RXXL 4

Db 3 RASL 6

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Gaps

Search completed: February 8, 2000, 01:29:33 Job time: 1745 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

February 7, 2000, 05:08:50; Search time 117.7 Seconds (without alignments) 4.008 Million cell updates/sec Run on:

US-08-653-294-1 17 1 RXXLXXXXXX 10 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

142080 seqs, 47169319 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

Database :

PIR_62:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	CF	pyruvate kinase (E	rotein -	ķe	ical	ᄗ	Ig kappa chain V-I	hain	_	pothetical p	pase	Ig kappa chain V-I		trp operon leader			P.	N	Ig kappa chain V r	rot	Ig kappa chain V-I	Ig kappa chain V-I	transposase - Lact	pro	otei	ribosomal protein	last	Ig kappa chain V-I		photosystem II pro	II
SUMMARIES	Ω	A11490	S54270		T01691		D30609				B44180	C30607	B61318	LFSEW	JQ0272	521816	S21815	138914	PH0882	D70144	F30608	D30608	S52346	S22304	42	260	137	090	F2RZL	F2WTL	F2SKL
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	, A	9	18	18	20	20	22	24	26	56	27	27	27	28	28	30	30	30	30	30	31	31	31	32	32	33	35	37	38	38	38
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38 2 TO7254 38 2 TO7254 38 2 SO4064 38 2 SO4064 38 2 SO508 38 2 SO508	photosystem II pro	1
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ALIGNMENTS

RESULT 1 A11490 pyruvate kinase (EC 2.7.1.40) - pig (fragment) pyruvate kinase (EC 2.7.1.40) - pig (fragment) C;Species: Sus scrofa domestica (domestic pig) C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 03-Mar-1995 C;Accession: A11490 R;Hjelmquist, G; Andersson, J; Edlund, B.: Engstrom, L. Biochem. Biophys. Res. Commun. 61, 559-563, 1974	A: Title: Amino acid sequence of a (32-P)phosphopeptide from pig liver pyruvate kinase A: Riterence number: Ali490; MUID:75127438 A: Accession: Ali490 A: Molecule type: protein A: Molecule type: protein A: Regidues: 1-6 (410E) A: Experimental source: Liver C: Keywords: glycolysis; phosphotransferase	Query Match 52.9%; Score 9; DB 2; Length 6; Best Local Similarity 50.0%; Pred. No. 1.4e+05; Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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1 RXXL 4 ò ద

3 RASL 6

RESULT 2
554270
GATA-2 protein - African clawed frog
GATA-2 protein - African clawed frog
C.Species: Xenopus laevis (African clawed frog)
C.Species: 27-oct-1995 #sequence_revision 03-Nov-1995 #text_change 03-Nov-1995
C.State: 27-oct-1995 #sequence_revision 03-Nov-1995 #text_change 03-Nov-1995
A.Feference number: 554270
A.Feference number: 554270
A.Feference number: 554270
A.Feference number: S4270
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Gaps .; 0 Query Match 52.9%; Score 9; DB 2; Length 18; Best Local Similarity 50.0%; Pred. No. 3.8e+02; Matches 2; Conservative 0; Mismatches 2; Indels

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12 RAAL 15 1 RXXL 4 ద ô

RESULT S58277

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C; Accession: D30609 R; McGinis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; S R; Gonl, F.R.; Chen, P.P.; McGinis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; S J R; Gonl, F.R.; Chen, P.; McGinis, D.; McGinis, D.; McGinis, D.; McGinis, D.; McGinis, D.; McGinis, D.; McGinis,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RiGoni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; S. J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoa A;Reference number: A30601; MUID:89215279
A;Accession: B30609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; S. J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoa A;Reference number: A30601; MUID:89215279
A;Accession: D30607
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                                                                                                                                                                                                                                                                                             Ig kappa chain V-III regions (Jon and Mit) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 30-May-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 30-May-1997
C;Accession: B30609
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D30607
Ig Kappa chain V-III region (Sal) - human (fragment)
Ig Kappa chain Sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 30-May-1997
C;Accession: D30607
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A; Molecule type: protein
A; Residues: 1-22 <GON>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
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A;Molecule type: protein
A;Residues: 1-24 GGON>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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Pred. No. 5e+02;
.0; Mismatches
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Pred. No. 4.6e+
0; Mismatches
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llarity 50.0%;
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A;Molecule type: protein
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Best Local Similarity
Matches 2; Conserv
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Best Local Similarity
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                                                      8
insulin-like growth factor receptor type II - human (fragment)
C;Species: Homo sapiens (man)
C;Oate: I3-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 10-Sep-1997
C;Caccession: S58277
R;Smrzka, O.W.; Stoger, R.; Kurzbauer, R.; Fae, I.; Fischer, G.F.; Barlow, D.P.
Submitted to the EMBL Data Library, January 1995
A;Description: Conservation of a methylation imprint and a putative imprinting box at the A;Reference number: S58277
A;Reference number: S58277
A;Accession: S58277
A;Accession: S58277
A;Accession: Je ype: DNA
A;Molecule type: DNA
A;Residues: 1-18 <SMR>
A;Coss references: EMBL:X83702; NID:g929644; PID:g929645
C;Keywords: growth factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
441717
P100 protein - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Species: Rattus norvegicus (Norway rat)
C:Species: Rattus norvegicus (Norway rat)
C:Species: 24-Jul-1992 #sequence_revision 24-Jul-1992 #text_change 23-Mar-1993
C:Accession: A4717
R:Traub, L.M.; Sagi-Eisenberg, R.
J. Biol. Chem. 266, 24642-24649, 1991
A:Title: Purification of p100, a protein antigenically related to the signal transducing A:Reference number: A4717; MUID:92105130
A:Accession: A47177
A:Accession: A4717
A:Accession: Preliminary
A:Molecule type: protein
A:Residues: 1-20 <TRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein - maize chloroplast (fragment)
C;Species: chloroplast Zea mays (maize)
C;Species: i9-reb-1999 #sequence_revision 19-reb-1999 #text_change 19-reb-1999
C;Accession: T01691
R;Werr, W.
Submitted to the EMBL Data Library, June 1982
A;Reference number: 214397
A;Residues: 1-20 <WER>
A;Residues: 1-20 <WER>
A;Residues: L-20 <WER>
A;Cross-references: EMBL:V01469; NID:g14307; PID:g388251
C;Genetics:
A;Genome: chloroplast
A;Note: Intron positions not resolved (incomplete sequence)
C;Keywords: chloroplast
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Pred. No. 4.2e+02;
0; Mismatches 2; Indels
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Pred. No. 4.2e+02;
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Pred. No. 3.8e+02;
0; Mismatches 2
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Best Local Similarity 50.0%;
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Best Local Similarity 50.0
Matches 2; Conservative
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momordin - balsam pear (fragment)
C.Species: Momordica charantia (balsam pear, bitter gourd)
C.Species: Momordica charantia (balsam pear, bitter gourd)
C.Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999
C.Accession: B61318
R.LJ. S.S.L.
Experientia 36, 524-527, 1980
A.Title: Purification and partial characterization of two lectins from Momordica char A; Reference number: A61318; MUID:80201763
A.Accession: B61318
A.Status: preliminary
A.Molecule type: protein
A; Residues: 1-27 < LIA>
C.Superfamily: rRNA N-01ycosidase; rRNA N-91ycosidase homology
C; Keywords: lectin: seed
                                                                                                                                                                                                 Rigoni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; S. J. Immunol. 142, 3158-3163, 1989
A; Title: Structural and idiotypic characterization of the L chains of human IgM autoa A; Reference number. A30601; MUID:89215279
A; Accession: C30607
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-27 <GGNS
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trp operon leader peptide - Serratia marcescens
C;Species: Serratia marcescens
C;Species: Serratia marcescens
C;Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 13-Nov-1998
C;Accession: A03591
R;Miozzari, G.F.; Yanofsky, C.
Nature 276, 684-689, 1978
Nature 276, 684-689, 1978
A;Title: The regulatory region of the trp operon of Serratia marcescens.
A;Title: The regulatory region of the trp operon of Serratia marcescens.
A;Accession: A03202; MUID:79093989
A;Accession: A03591
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-28 <MIO>
C;Genetics:
C;Function:
                                                                                              Ig kappa chain V-III regions (Ang, Cin, and Sar) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 01-Oct-1992 #text_change 30-May-1997
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Pred. No. 5.7e+02;
0; Mismatches 2; Indels
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llarity 50.0%;
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Best Local Similarity 50.0
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Best Local Similarity
Matches 2; Conserv
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A; Molecule type: protein
B; Residues: 1-27, PoOS>
B; Residues: 1-27, PoOS>
B; Residues: 1-27, Martin, B.M.; Yatani, A.; Mochca-Morales, J.; Zamudio, F.Z.; Gurrola, G Toxicon 30, 1343-1364, 1992
Toxicon 30, 1343-1364, 1992
Toxicon 30, 1343-1364, 1992
Toxicon 30, 1343-1360, Mulb:93134601
A; Reference number: A44180; Mulb:93134601
A; Accession: B44180
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Nucleic Acids Res. 18, 6458, 1990
Aritle: Sequence of gene E15 of bacteriophage D108 and comparison with phage Mu. A;Reference number: $12145; MUID:91057162
A;Accession: $12146
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                                                                                                                                                                                                                                                                                                                                             hypothetical protein E16 - phage D108 (fragment)
C;Species: phage D108
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Sep-1997
                                                                                                                                                            Gaps
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                                                                                              DB 2; Leng.
5.4e+02;
2; Indels
A;Residues: 1-26 <GON>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
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5.4e+02;
ches 2; Indels
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A:Note: sequence extracted from NCBI backbone (NCBIP:122481)
C:Superfamily: phospholipase A2
C:Keywords: carboxylic ester hydrolase; toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-26 <ABAT>
A:Cross-references: EMBL:X54298; NID:g14794; PID:g14796
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Pred. No. 5.4e+
0; Mismatches
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Pred. No. 5.4e
0; Mismatches
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50.0%;
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Best Local Similarity 50.0
Matches 2; Conservative
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Best Local Similarity 50.0
Matches 2; Conservative
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submitted to the EMBL Data Library, December 1990
A:Description: Two separate genes encode the catalytic 70kDa V-ATPase subunit in Psilotu
A:Reference number: S21814
A:Accession: S21816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Experimental source: cv. Nihonbare
R;Hiratsuka, J.; Shimada, H.; Whittier, R.; Ishibashi, T.; Sakamoto, M.; Mori, M.; Kondo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mol. Gen. Genet. 217, 185-194, 1989
A;Title: The complete sequence of the rice (Oryza sativa) chloroplast genome: intermoled
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A;Residues: 1-30 <STR>
A:Cross references: EMBL:X56985; NID:g20604; PIDN:CAA40303.1; PID:e35787; PID:g1345563
A;Genetics: GEN1
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A; Description: involved in control of tryptophan operon transcription by attenuation C; Superfamily: trp leader peptide
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A;Reference number: JQ0200
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                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical 3K protein (trnH-trnV intergenic region) - rice chloroplast C; Species: chloroplast Oryza sativa (fice) C; Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 20-Mar-1998 C; Accession: J00272; S05152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Psilotum nudum
C;Date: 25-Feb-1994 #sequence_revision 01-Mar-1996 #text_change 22-Jun-1999
                                                                                                                                                                 Gaps
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n. 5.9e+02;
2; Indels
                                                                                                      Score 9; DB 1; Length 28;
Pred. No. 5.9e+02;
0; Mismatches 2; Indels
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Pred. No. 5.9e4
0; Mismatches
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A; Accession: S05152
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Best Local Similarity 50.0%;
Matches 2; Conservative
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Best Local Similarity
Matches 2; Conserv
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C; Keywords: chloroplast
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A; Residues: 1-28 <SHI>
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A; Residues: 1-30 <STW>
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A; Gene: P1
A; Introns: 2/2
C; Genetics: <GEN2>
A; Introns: 2/2
A; Genetics: <GEN2>
A; Introns: 2/2
C; Superfamily: vacuolar H+-transporting ATPase 69K chain; H+-transporting ATP synthas
C; Superfamily: vacuolar H+-transporting ATPase 69K chain; H+-transporting ATP synthas
C; Superfamily: vacuolar H+-transporting ATPase 69K chain; H+-transporting ATP synthas
C; Superfamily: vacuolar H+-transporting ATPase 69K chain; H+-transporting ATP synthas
C; Superfamily: vacuolar H+-transporting ATPase 69K chain; H+-transporting ATP synthas
C; Superfamily: vacuolar H+-transporting ATPase 69K chain; H--transporting ATPase 69K chain; H+-transporting ATPase 6
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William.

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bacteriopha
serratia ma
shigella fl
psilotum nu
equisetum a
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borrella bu
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euglena gra
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pinus thunb
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                                                     7, 2000, 23:56:51; Search time 63.71 Seconds (without alignments) 4.688 Million cell updates/sec
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Gaps

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Score 9; DB 1; Length 24; Pred, No. 2.3e+02;); Mismatches 2; Indels

52.9%; Scor. 50.0%; Pred 0;

Query Match 52.9 Best Local Similarity 50.0 Matches 2; Conservative

ò g E16_BPD10 STANDARD; PRT; 26 AA. P24796; 01-MAR-1992 (Rel. 21, Created) 01-MAR-1992 (Rel. 21, Last sequence update) 01-MAR-1992 (Rel. 21, Last annotation update) PROTEIN E16 (FRAGMENT).

RESULT 2 E16_BPD10 ID E16B AC P247_9B DT 01-MA DT 01-MA DT 01-MA DF 01-MA DF E16. OS Bacte

E16. Bacteriophage D108.

P31534 lampetra pl P04139 pseudomonas P04337 shigalla fl P21306 saccharomyc P56268 klebsiella P39427 bacteriopha P39427 bacteriopha P39511 bacteriopha P48105 cyanophora P48105 bacteriopha		AA.) ite) is rrna methylase leader	PEFFILDE). SITEPTOMYCES fradiae. Bacteria: Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.	»F, an inducible resistance rase from Streptomyces	22 H	uced through a and the EM are no restr its content Isage by and	12;
THE COLUMN THE E	MENTS	24	update) on update DE (23S	Act	f ermSF,	ED IN INCOS	It is loinform; ute Tl as long removed ment (See	G. CRC.
HMEN_LAMPL MERC_PSEAE MERC_SHIFL ATPE_YEAST FLAW_KLEOX YOLH BPT4 Y01H BPT4 Y01H BPT4 Y16G_BPT4 PSBH_CYAPA	ALIGNMENTS	PRT;	ed) sequence annotatic DER PEPTI	lae. tes; Actinobacteria; Streptomycineae; Sti	SEQUENCE FROM N.A. MEDLINE; 88165508. KAMIMIYA S., WEISBLUM B.; "Translational attenuation control of ermSF, effectional encoding rRNA N-methyltransferase	170:1800-1811(1988). THIS PEPTIDE IS INVOLVED IN THE SIS OF THE MACROLIDE-LINCOSAMIDE PROTEIN. T IS UNCERTAIN WHETHER MET-1 OR	This SWISS-PROT entry is copyright. It is procedetived the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There wase by non-profit institutions as long as modified and this statement is not removed. It entities requires a license agreement (See httor send an email to licensee(15D-11D-11D).	er peptid 91CB30C
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		FRFR	1995 1995 1995 DMYCIN	i). Omyces La, Fi nyceta	E FRC 3; 881 7A S., Lation Inant	acteriol. FUNCTION: THE SYNTH RESISTANC	VISS-PR Topean One non- d and ed and es requ	419269 otic r SE 2
		SUL ER		DE FEFTIDE). OS Streptomyces fra OC Bacteria; Firmic Actinomycetales;		H C I	CC This SWISS-PROT entry is CC the European Bioinformatic CC use by non-profit inst CC modified and this stateme CC entities requires a licen CC or send an email to licen	EMB Ant SEQ
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RTSL 24

21

Viruses; dsDNA viruses, no RNA stage; Tailed phages; Myoviridae.

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Query Match 52.9
Best Local Similarity 50.0
Matches 2; Conservative
                                                   STANDARD;
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30 AA;
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                                                ENTF_SHIFL P29698;
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SEQUENCE
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                RESULT 4
ENTF_SHIFL
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                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED cutstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Nature 276:684-689(1978).
-!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
                                 PATO M.L., BANERJEE M., WAGONNER B.T.; "Sequence of gene E15 of bacteriophage D108 and comparison with phage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Pred, No. 2.5e+02;
0; Mismatches 2; Indels
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21-JUL-1986 (Rel. 01, Last sequence update)
01-MAY-1991 (Rel. 18, Last annotation update)
RPP OPERON LEADER PEPTIDE.
                                                                                                                                                                                                                                                                                                                       26 AA; 3102 MW; FCC4ED24 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tryptophan blosynthesis; Leader peptide.
SEQUENCE 28 AA: 3391 MW; 3C9CA0F6 CRC32;
                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                       Nucleic Acids Res. 18:6458-6458(1990).
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                                                                                                                                                                                                                                                                                                                                                                           52.9%;
50.0%;
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PIR; S12146; S12146.
NON_TER 26 26
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MIOZZARI G.F., YANOFSKY C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 52.9
Best Local Similarity 50.0
Matches 2; Conservative
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Best Local Similarity 50.0
Matches 2; Conservative
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P03055;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE STREET AND THE SHIP OF THE CARBOXYLATE GROUP OF L-SERINE VIA

1. Bacteriol. 173:816-825(1991).

1. Bacteriol. 173:816-825(1991).

2. - PUNCTION: ACTIVATION OF THE CARBOXYLATE GROUP OF L-SERINE VIA

ATP-DEPENDENT PPI EXCHANGE REACTIONS TO THE AMINO ACYLADENYLATE,

PREPARING THAT MOLECULE FOR THE FINAL STAGES OF ENTEROBACTIN

SYNTHESIS. BRYER MAY, IN THE PRESENCE OF 2,3-DIHYDROXYBENZOATE

ENTE, GENERALE THE AMIDE BOND LINRAGE PRESENT 3 TIMES IN THE

CYCLIC (2,3-DIHYDROXYBENZOYL)SERINE TRIMER ENTEROBACTIN.

- - OFFACTOR: COMPAINS I COVALENTLY BOUND PHOSPHOPANTETHEINE.

- - OFFACTOR: COMPAINS I COVALENTLY BOUND PHOSPHOPANTETHEINE.

- - PATHMAY: ENTEROBACTIN BIOSYNTHESIS. ENTEROBACTIN IS AN IRON-

CHELATING COMPOUND INVOLVED IN TRANSPORTING IRON FROM THE

BACTESIAL ENVIRONMENT INTO THE CELL CYTOPLASM.

- - SUBUNIT: PROTEINS ENTD, ENTE, ENTE, AND ENTG FORM A MULTIENZYME

COMPLEX CALLED ENTEROCHELIN SYNTHASE.

- - SIMILARITY: TO OTHER REZYMES WHICH ACT VIA AN ATP-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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004237;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1998 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
(FRAGMENT).
                                                                                                                                                                                                                                                                                       Shigella flexneri.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDINE; 91100373.
SCHMITT M.P., PAYNE S.M.;
"Genetic analysis of the enterobactin gene cluster in Shigella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterobactin biosynthesis; Iron transport; Phosphopantetheine;
                                                                                                       01-APR-1993 (Rel. 25, Last sequence update)
15-DEC-19998 (Rel. 37, Last annoctation update)
ENTEROBACTIN SYNTHEFASE COMPONENT F (ENTEROCHELIN SYNTHASE (SERINE ACTIVATING ENZYME) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 9; DB 1; Length 30;
Pred. No. 2.9e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COVALENT BINDING OF AMP TO THEIR SUBSTRATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M63304; -; NOT ANNOFATED CDS.
PROSITE; PSO0012; PHOSPHOPANTETHEINE; PARTIAL.
PROSITE; PSO0455; AMP_BINDING; PARTIAL.
30 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3398 MW; SFE5B79F CRC32;
                                                                    01-APR-1993 (Rel. 25, Created)
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VAA1_PSINU
ID VAA1_PV
DD 0404237
DT 01-0CT
DT 01-0CT
DT 15-0UL
DE VACUOLL
DE (FRAGM
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VAA2_PSINU
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Eukaryota: Viridiplantae: Streptophyta: Embryophyta; Tracheophyta;
euphyllophytes; Equisetophyta; Sphenopsida; Equisetales; Equisetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                      FUNCTION: CATALYTIC SUBUNIT OF THE PERIPHERAL VI COMPLEX OF VACUOLAR ATPASE IS RESPONSIBLE FOR ACIDIFYING A VARIETY OF INTRACELLULAR COMPARTMENTS IN EUKARYOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEBS Lett. 315:252-258(1993).
-!- FUNCTION: CATALYTIC SUBUNIT OF THE PERIPHERAL VI COMPLEX OF VACUOLAR ATPASE. VATPASE VACUOLAR ATPASE: VATPASE VACUOLAR ATPASE IS RESPONSIBLE FOR ACIDIFYING A VARIETY OF INTRACELLULAR COMPARTMENTS IN EUKARYOTIC
                                                                                                                                                                                                                                                                                                         SUBUNT: V-ATPASE IS AN HETEROMULTIMERIC ENZYME COMPOSED OF A PERIPHERAL CATALYTIC VI COMPLEX (MAIN COMPONENTS: SUBUNITS A, B, B, C, D, E, AND F) ATTACHED TO AN INTEGRAL MEMBRANE VO PROTON PORE COMPLEX (MAIN COMPONENT: THE PROTEOLIPID PROTEIN).

MISCELLANEOUS: TWO SEPARATE GENES ENCODE THE CATALYTIC 70KDA V-ATPASE SUBUNT IN PSILOTOWM AND EQUISETUM.

SIMILARITY: TO THE BETA CHAINS OF ATP SYNTHASES AND TO A LESSER EXTENT TO THE ALPHA CHAINS.
Psilotum nudum (Whisk fern).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Psilotophyta; Psilotales; Psilotaceae; Psilotum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, ISOFORM 2 (EC 3.6.1.34)
                                                                                                            MEDLINE; 93138084.
STARKE T., GOGARTEN J.P.;
"A conserved intron in the V-ATPase A subunit genes of plants and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
SIJSOBA.
STARKE T., GOGRAFIEN J.P.;
A conserved intron in the V-ATPase A subunit genes of plants and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00152; ATPASE_ALPHA_BETA; PARTIAL.
ATP Synthesis; Hydrogen ion transport; Hydrolase; ATP-binding; Multigene family.
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2.9e+0
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Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 9;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last seq
15-JUL-1998 (Rel. 36, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52.9%;
50.0%;
                                                                                                                                                                            algae.";
FEBS Lett. 315:252-258(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3380 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X56985; CAA40303.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 AA;
                                                                                         SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 RTTL 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RXXL 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VAA2_EQUAR
Q04238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
NON_TER
SEQUENCE
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SUBUNIT: V-ATPASE IS AN HETEROMULTIMERIC ENZYME COMPOSED OF A PERIPHERAL CATALYTIC VI COMPLEX (MAIN COMPONENTS: SUBUNITS A, B, C, D, E, AND F) ATTACHED TO AN INTEGRAL MEMBRANE VO PROTON PORE COMPLEX (MAIN COMPONENT: THE PROTECLIPID PROTEIN).

MISCELLARDONE: TWO SEPRARE GENES ENCODE THE CATALYTIC 70KDA V-ATPASE SUBUNIT IN PSILOTUM AND EQUISECTUM.
SIMILARITY: TO THE BETA CHAINS OF ATP SYNTHASES AND TO A LESSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACIDIFYING A VARIETY OF INTRACELLULAR COMPARTMENTS IN EUKARYOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: V-ATPASE IS AN HETEROMULTIMERIC ENZYME COMPOSED OF A PERIPHERAL CATALITIC V1 COMPLEX (MAIN COMPONENTS: SUBUNITS A, B, C, D, E, AND F) ATTACHED TO AN INTEGRAL MEMBRANE VO PROTON PORE COMPLEX (MAIN COMPONENT: THE PROTEOLIPID PROTEIN).
SIMILARITY: TO THE BETA CHAINS OF ATP SYNTHASES AND TO A LESSER EXTENT TO THE ALPHA CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, ISOFORM 2 (EC 3.6.1.34)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Psilotophyta; Psilotales; Psilotaceae; Psilotum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 93138084.
STARKE T., GOGARTEN J.P.;
"A conserved intron in the V-ATPase A subunit genes of plants and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEES LELT. 315:252-258(1993).
-!- FUNCTION: CATALYTIC SUBUNIT OF THE PERIPHERAL VI COMPLEX OF
VACUOLAR ATPASE. V-ATPASE VACUOLAR ATPASE IS RESPONSIBLE FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00152; ATPASE_ALPHA_BETA; PARTIAL.
ATP synthesis; Hydrogen ion transport; Hydrolase; ATP-binding;
Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Le
2.9e+02;
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3372 MW; BD406FF0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 9; DB 1
Pred. No. 2.9e-
0; Mismatches
                                                                                                                                                                                                                                           EXTENT TO THE ALPHA CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 34, Created)
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50.0%;
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Best Local Similarity
---- 2; Conserv?
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01-0CT-1996
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Q04239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: NOT KNOWN. POSSIBLY A PERIPHERAL COMPONENT OF CYTOCHROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KUDLA J., IGLOI G.L., METZLAFF M., HAGENMANN H., KOESSEL H.;
"RNA editing in tobacco chloroplasts leads to the formation of a
translatable psbL mRNA by a C to U substitution within the initiation
codon.",
EMBO J. 11:1099-1103(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chloroplast.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Lamiales; Scrophulariaceae;
                                                                                                                                                                                                              MEDLINE; 92253404.

LORENI F., FRANCESCONI A., JAPPELLI R., AMALDI F.;

"Analysis of mRNAs under translational control during Xenopus
"Analysis of mRNAs under wibosomal protein clones.";

Buryogenesis: isolation of new ribosomal protein clones.";

Nucleic Acids Res. 20:1859-1863(1992).

-i - SIMILARITY: BELONGS TO THE L28E FAMILY OF RIBOSOMAL PROTEINS.
                                                                                     Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-1992 (Rel. 24, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PHOTOSYSTEM II REACTION CENTER L PROTEIN (PSII 5 KD PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 9; DB 1; Length 33;
Pred. No. 3.2e+02;
); Mismatches 2; Indels
  01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
60S RIBOSOMAL PROTEIN L28 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01329266 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -! - SIMILARITY: BELONGS TO THE PSBL FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antirrhinum majus (Garden snapdragon).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-CV. SIPPE 50; TISSUE-LEAF;
MEDLINE; 92191997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.9%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 33
AA; 3907 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X64209; CAB56812.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE; 92253404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ribosomal protein.
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15-DEC-1998 (
15-DEC-1998 (
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                       Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
PSBL_ANTMA
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    à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-ATCC 35210 / B31;
MEDLINE; 98065943.

MEDLINE; 98065943.

FRASER C.M., CASJENS S., HUANG W.M., SUTTON G.G., CLAYTON R.A.,
LATHIGRA R., WHITE O., KETCHUM K.A., DODSON R., HICKEY E.K., GWINN M.,
DOUGHERTY B., TOMB J.-F., FLEISCHMANN R.D., RICHARDSON D.,
PETERSON J., KERLAVAGE A.R., QUACKENBUSH J., SALZBERG S., HANSON M.,
VAN VUGT R., PALMER N., ADAMS M.D., GOCANNE J.D., WEIDMAN J.,
UTTERBACK T., WATTHEY L., MCDONALD L., ARTIACH P., BOMMAN C.,
GARLAND S., FUJII C., COTTON M.D., HORST K., ROBERTS K., HATCH B.,
SMITH H.O., VENTER J.C.,
                                                                                                                                                                                                                                    Gaps
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EMBL; X56986; CAA40304.1; -.
PROSTIE; PS00152; ATPASE_ALPHA_BETA; PARTIAL.
ATP Synthesis; Hydrogen ion transport; Hydrolase; ATP-binding;
Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 30;
2.9e+02;
ches 2; Indels
                                                                                                                                                                                             Length 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Borrelia burgdorferi (Lyme disease spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
                                                                                                                                                                                           Score 9; DB 1; Leng
Pred. No. 2.9e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
HYPOTHETICAL PROTEIN BB0357.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l protein.
30 AA; 3495 MW; E2EF5F42 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                           30 AA.
                                                                                                                             55C24CFA CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 9;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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P46780;
01-NOV-1995 (Rel. 32, Created)
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                                                                                   1 1
30 30
30 AA; 3380 MW;
                                                                                                                                                                                           52.9%;
ilarity 50.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.9%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 390:580-586(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 52.9
Best Local Similarity 50.0
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical
SEQUENCE 30
                                                                                                                                                                                                                                                                                                                    25 RTTL 28
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ID Y357_BORBU
AC O51332;
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SEQUENCE
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37 AA.

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EDITING OF INITIATOR CODON.
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MEDLINE; 92191997.
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             SPECIES-N.TABACUM;
MEDLINE; 97076156.
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   modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                         Gaps
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SHINDZAKI K., OHME M., TANAKA M., WAKASUGI T., HAYASHIDA N.,
MATSUBAYASHI T., ZAITA N., CHUNWONGSE J., OBOKATA J.,
YAMAGUCHI-SHINDZAKI K., OHTO C., TORAZAWA K., MENG B.Y., SUGITA M.,
DENO H., KAMOGASHIRA T., YAMADA K., KUSUDA J., TAKAIWA F., KATO A.,
TOHDOH N., SHIMADA H., SUGIURA M.;
"The complete nucleotide sequence of the tobacco chloroplast genome:
its gene organization and expression.";
[5]
                                                                                                                                                                                                                                                                                                                                                             pea),
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; Liliopsida; Poales;
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                                                                                                                                                                                                                                                                                                                                   Oryza sativa (Rice), Nicotiana tabacum (Common tobacco),
Hordem vulgare (Barley), Triticum aestivum (Wheat),
Scale cereale (Rye), Zea mays (Maize), Pisum sativum (Garden
Spinacia oleracea (Spinach), Capsicum annuum (Bell pepper),
Mesembryanthemum crystallinum (Common ice plant),
Chloroplast.
                                                                                                                                                                                                                                                      PSBL_ORYSA STANDARD, PRT; 37 AA.
P12166; P12167; Q34007;
01-007-1989 (Rel. 12, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PHOTOSYSTEM II REACTION CENTER L PROTEIN (PSII 5 KD PROTEIN)
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3.56+02;
2; Indels
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                        Score 9; DB 1;
Pred. No. 3.6e+
0; Mismatches
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                                                                                                                                  52.9%;
50.0%;
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Best Local Similarity
Matches 2; Conserv
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PSBL_ORYSA
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SPECIES-S.CEREALE;
MEDLINE; 90073796.
KOLOSOV V.L., KLEZOVICH O.N., ABDULAEV N.G., ZOLOTAREV A.S.;
Photosystem II of rye. Nucleotide sequence of genes psbE, psbE and OPC40 of chloroplast DNN.";
Bioorg. Khim. 15:1284-1286(1989).
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"RNA editing in tobacco chloroplasts leads to the formation of a
translatable psbL mRNA by a C to U substitution within the initiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZOLOTAREV A.S., KOLOSOV V.L.; "Nucleotide sequence of the rye chloroplast DNA fragment, comprising psbE and psbF genes.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SPECIES=T.AESTIYUM; STRAIN=CV. SENTRY; TISSUE=LEAF;
WEBBER A.N., HIRD S.M., PRCKMAN L.C., DYER T.A., GRAY J.C.;
WEBPER A.N., HIRD S.M., PRCKMAN L.C., DYER T.A., GRAY J.C.;
"A photosystem II polypeptide is encoded by an open reading frame co-transcribed with genes for cytochrome b-559 in wheat chloroplast
CHAUDHURI S., MALIGA P., "Sequences directing C to U editing of the plastid psbL mRNA are located within a 22 nucleotide segment spanning the editing site.";
                                                                                                                                                                                                                                                                                                                                                                                                 "Nucleotide sequence of the barley chloroplast psbE, psbF genes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
SECUES: HVULGARE; STRAIN-CV. SABARLIS;
MEDLINE; 9.2207353.
EFIMOV V.A., ANDREEVA A.V., REVERDATTO S.V., CHAKHMAKHCHEVA O.G.;
"Photosystem II of rye. Nucleotide sequence of the psbB, psbC, ps.
psbF, psbH genes of rye and chloroplast DNA regions adjacent to them."
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MEDLINE; 93395841.
MEDLINE; 93395841.
MAIR WALE WECKERMANN K., IGLOI G.L., KOESSEL H.;
"Complete sequence of the maize chloroplast genome: gene content, hotspots of divergence and fine tuning of genetic information by transcript editing.";
J. Mol. Biol. 251:614-628(1995).
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                                                                                                                                                                                                SEQUENCE FROM N.A.
SPECIES-H.VULGARE; STRAIN-CV. SABARLIS;
MEDLINE; 89240046.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      flanking regions.";
Nucleic Acids Res. 17:2858-2858(1989).
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                                                                                                                           EMBO J. 15:5958-5964(1996).
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SPECIES-S OLERACEA;
MEDLINE: 9829BIL8.
ZHELEVA D., SHARWA J., PANICO M., MORRIS H.R., BARBER J.;
ZHELEVA D., SHARWA J., PANICO M., MORRIS H.R., BARBER J.;
"ISOLATION and characterization of monomeric and dimeric
CP47-reaction center photosystem II complexes.";
J. Biol. Chem. 273:16122-16127(1998).
-:- FUNCTION: NOT KNOWN. POSSIBLY A PERIPHERAL COMPONENT OF CYTOCHROME
B559.
                                                                                                                                                                                          BOCK R., HAGEMANN R., KOESSEL H., KUDLA J.;
"Itssue- and stage-specific modulation of RNA editing of the psbF and
psbL transcript from spinach plastids -- a new regulatory mechanism?";
Mol. Gen. Genet. 240:238-244(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IKEUCHI M., TAKIO K., INOUE Y.;
"N-terminal sequencing of photosystem II low-molecular-mass proteins. 5 and 4.1 kDa components of the O2-evolving core complex from higher milants".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE: 95254673.

KUBO T., YANAI Y., KINOSHITA T., MIKAMI T.;

"The chloroplast trnP-trnW-petG gene cluster in the mitochondrial genomes of Beta vulgaris, B. trigyna and B. webbiana: evolutionary
                                                                                                                                                                                                                                                                                                  SPECIES-5.OLERACEA;
MENENNN K.C., ALT J., SCHILLER B., WIDGER W.R., CRAMER W.A.;
Huclacotide sequence of the gene for apocytochrome b-559 on the
spinach plastid chromosome: implications for the structure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KUNTZ M., CAMARA B., WEIL J.-H., SCHANTZ R.;
"The psbL gene from bell pepper (Capsicum annuum): plastid RNA editing also occurs in non-photosynthetic chromoplasts.";
Plant Mol. Biol. 20:1185-1188(1992).
                               MEDLINE; 89354671.
WILLEY D.L., GRAY J.C.;
"Two small open reading frames are co-transcribed with the pea
"Thoroplast genes for the polypeptides of cytochrome b-559.";
Curr. Genet. 15:213-220(1989).
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SPECIES-P.DELTOIDES; STRAIN-CV. STONEVILLE D121; TISSUE-LEAF;
NAITHANI S.;
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND RNA EDITING OF INITIATOR CODON. SPECIES-C.ANNUUM; STRAIN-CV. LAMUYO; TISSUE-LEAF, AND FRUIT; MEDLINE; 93099270.
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SPECIES-B.VULGARIS; STRAIN-CV. TK81-O; TISSUE-LEAF;
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SPECIES-T.AESTIVUM, AND S.OLERACEA;
MEDLINE; 89121082.
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                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-12 FROM N.A.
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MEDLINE: 94345017.
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                  SPECIES-P.SATIVUM;
SEQUENCE FROM N.A.
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Submitted (XXX-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: NOT KNOWN. POSSIBLY A PERIPHERAL COMPONENT OF CYTOCHROME
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Chlamydomonadaceae, Chlamydomonas.
-i- MASS SPECTROMETRY: MW=4365.5; METHOD=MALDI.
-i- SIMILARITY: BELONGS TO THE PSBL FAMILY.
-i- CAUTION: THE INITIATOR METHIONINE IS CREATED BY RNA EDITING
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
PHOTOSYSTEM II REACTION CENTER L PROTEIN (PSII 5 KD PROTEIN)
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
PHOTOSYSTEM II REACTION CENTER L PROTEIN (PSII 5 KD PROTEIN)
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Pred. No. 3.7e+02;
0; Mismatches 2; Indels
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3.6e+02;
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Photosystem II; Chloroplast. SEQUENCE 38 AA; 4389 MW; EECC7F31 CRC32;
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Pred. No. 3.6e
0; Mismatches
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50.0%;
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SEQUENCE FROM N.A.
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01-NOV-1995
01-NOV-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 RTSL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chloroplast.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSBL_CHLEU
P46306;
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P32974;
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PSBL_CHLEU
DY O1-NOV
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DT 01
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PSBL_CHIRE
19 PSBL_C
AC P32974
DT 01-0CT
DT 01-NOV
DT 01
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Ouery Match
Best Local Similarity
Matches 2; Conserv
                                                                                                                                                               15 RTSL 18
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                                                                                                                 1 RXXL 4
                                                                                                                                                                                                                                                                            PSBL_CYAPA
P19154;
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                                                                                                                                                                                                                                    RESULT 15
PSBL_CYAPA
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                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced theough a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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STRAIN-IAM C-27 / TAMIYA;

MEDLINE; 97303241.

WARASUGI T., NAGAI T., KAPOOR M., SUGITA M., ITO M., ITO S.,

TSUDZUKI J., NAKASHIMA K., TSUDZUKI T., SUZUKI Y., HAMADA A., OHTA T.,

INAMURA A., YSUSHINAGA K., SUGIURA M.;

"Complete nucleotide sequence of the chloroplast genome from the

green alga Chlorella vulgaris: the existence of genes possibly

proc. Natl. Acad. Sci. U.S., 94:597-5972(1997).

-!- FUNCTION: NOT KNOWN. POSSIBLY A PERIPHERAL COMPONENT OF CYTOCHROME
                                                                                                                 -!- FUNCTION: NOT KNOWN. POSSIBLY A PERIPHERAL COMPONENT OF CYTOCHROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chloroplast.
Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
Chlorellaceae; Chlorella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                   FONG S.E., SURZYCKI S.J.;
"Organization and structure of plastome psbF, psbL, petG and ORF712 genes in Chlamydomonas reinhardtii.";
Curr. Genet. 21:527-530(1992).
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
PHOTOSYSTEM II REACTION CENTER L PROTEIN (PSII 5 KD PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 38; 3.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                          PIR: S26679; S26879.
MENDEL; 2695; CHLTerpsbL;1.
Photosystem II; Chloroplast.
SEQUENCE 38 AA; 4428 MW; 2A6CC463 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB001684; BAA20643.1; -.
Photosynthesis; Photosystem II; Chloroplast.
SEQUENCE 38 AA; 4388 MW; 1A947871 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 AA.
                                                                                                                                                               -! - SIMILARITY: BELONGS TO THE PSBL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      · ! - SIMILARITY: BELONGS TO THE PSBL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 9;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X66250; CAA46978.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chlorella vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 2; Conserv
MEDLINE; 92315354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 RTSL 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RXXL 4
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P56339;
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PSBL_CHLVU
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Baloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=LB555 / PRINGSHEIM;
CANTRELL A., BRYANT D.A.;
"Nucleotide sequence of the genes encoding cytochrome b-559 from the cyanelle genome of Cyanophora paradoxa.";
Photosyn. Res. 16:65-81(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-LBSSS / PRINGSHEIM;
CANTRELL A., BRYANT D.A.;
Molecular cloning and nucleotide sequences of the genes encoding cytochrome B-559 from the cyanelle genome of Cyanophora paradoxa."
Prog. Photosyn. Res. 4:659-662(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STIREWALT V.L., MICHALOWSKI C.B., LUFFELHARDT W., BOHNERT H.J.,
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                                                                                                                                                                                                                                                                                                                       01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
PHOTOSYSTEM II REACTION CENTER L PROTEIN (PSII 5 KD PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Glaucocystophyceae; Cyanophoraceae; Cyanophora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
  Length 38,
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Score 9; DB 1; Len
Pred. No. 3.7e+02;
); Mismatches 2;
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Pred. No. 3.7e+02;
0; Mismatches 2
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4277B4E3 CRC32;
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                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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MENDEL: 7894; CYADA: Photosynthes1s; Photosystem I
SEQUENCE 38 AA; 4473 MW;
52.9%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M35129; AAA31697.1; -. EMBL; U30821; AAA81211.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-LB555 / PRINGSHEIM;
                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Cyanophora paradoxa.
Cyanelle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
2; Conserv
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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Search completed: February 8, 2000, 00:59:40

Job time: 3769 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*

8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodon.*

sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
sp_human:*
sp_invertebrate:*
sp_mhc:*

SPTREMBL_12:*

Database :

SUMMARIES

	Description	O61723 mus musculu		Q47251 escherichia	Q40183 lemna qibba	P72423 saccharopol	Q33294 zea mays (m	Q40181 lemna q1bba	O54632 escherichia	Q9xgq0 oryza sativ	Q61678 drosophila	Q9z079 hepatitis c	Q9z063 hepatitis c	Q9z058 hepatitis c	Q37005 oryza sativ	Q00491 streptomyce	Q9wux2 rattus norv	O17148 echinococcu	Q9y6h2 homo sapien	Q9xqq5 toxoplasma	Q47883 frankia aln
	ID	961723	069347	047251	040183	P72423	Q33294	040181	054632	0 0 5x6 0	261678	620260	690260	092058	037005	000491	Q9WUX2	017148	09х6н2	500x60	047883
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COUT NAC EO OO	092289 porcine cir Q64838 human adeno O50275 rhodococcus
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ALIGNMENTS

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RESULT 1

061723 PRELIMINARY; PRT; 9 AA.

10 061723 PRELIMINARY; PRT; 9 AA.

10 061723 PRELIMINARY; PRT; 9 AA.

10 070-1996 (TYEMBLE-1. 01, Last sequence update)

10 1.NOV-1996 (TYEMBLE-1. 12, Last sequence update)

10 1.NOV-1996 (TYEMBLE-1. 12, Last sequence update)

10 1.NOV-1999 (TYEMBLE-1. 12, Last sequence update)

11 NY REAL OR NF. KAPPA-B.

12 NN SEQUENCE FROM N.A.

13 NA HOLLING Of the p50 DNA binding subunit of NF-kappa B: homology to rel

14 NA HOLL CARANING N.A.

15 NA HOLL CHUNG N.A.

16 SEGUENCE FROM N.A.

17 C-terminal Sequence of the NF-kappa B p50 precursor from primary

18 NA HOLL CHUNG N.A.

18 NA HOLL CHUNG N.A.

19 NA HOLL CHUNG N.A.

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11 NA HOLL CHUNG N.A.

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12 NA HOLL CHUNG N.A.

13 12 NA HOLL CHUNG N.A.

14 NA HOLL CHUNG N.A.

15 NA HOLL CHUNG N.A.

16 Gene 139:287-288(1994).

17 NON-TER

18 NON-TER

19 NON-TER

10 NA HOLL CHUNG N.A.

10 NA HOLL CHUNG N.A.

11 NON-TER

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13 SEQUENCE 9 AA. 925 NW; CSEBD462 CRC32;

14 NON-TER

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Gaps
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                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
01-NOV-1996 (TREMBLrel. 01, Last annotation update)
NEGATIVELY LIGHT-REQUEATED PROTEIN (LG106) (FRAGMENT).
Lemna gibba (Swollen duckweed).
Lemna gibba (Swollen duckweed).
Lemna gibba (Swollen duckweed).
Lemna gibba (Spermatophyta; Embryophyta; Tracheophyta; Lemna.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03329;
01-30V-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
EITHER FRAME IS POSSIBLE (FRAGMENT)
Can mays (Maize).
Chloroplast.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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DONADIO S., STAVER M.J.;

DONADIO S., STAVER M.J.;

DONADIO S., STAVER M.J.;

Saccharopolyspora erythraea.";

Gene 126:147-151(1993).

EMBL; LO7626; AAA26506.1; -.

SEQUENCE 20 AA, 2339 MW; FB210B56 CRC32;
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Pseudonocardineae; Pseudonocardiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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50.0%; Pred. No. 9.6e+02;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10; I
9.1e+02;
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
OKUBARA P.A., FLORES S., TOBIN E.M.;
Plant Mol. Biol. 11:673-681(1988).
EMBL. M35866; AAA33395.1; -.
1 1
SEQUENCE 19 AA; 2153 MW; 76EEIF6D CRC32;
19 AA.
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01-FEB-1997 (TrEMBLrel. 02, Last sequence ul
01-NOV-1998 (TrEMBLrel. 08, Last annotation
6-DEOXYERYTHRONOLIDE B SYNTHASE (FRAGMENT).
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Pred. No.
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PRT;
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50.0%;
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PRELIMINARY;
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Best Local Similarity
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nes 2; Conserv
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ID P72423
AC P72423;
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JORDAN P.M., MGBEJE B.I.A., ALWAN A.F., THOMAS S.D.;

JORDAN P.M., MGBEJE B.I.A., ALWAN A.F., THOMAS S.D.;

JORDAN P.M., MGBEJE B.I.A., ALWAN A.F., THOMAS S.D.;

Nucleotide sequence of hemD, the second gene in the hem operon of Escherichia coli K-12.";

Nucleic Acids Res. 15.10583-10583(1987).

EMBL; Y00883; CAA68775.1;

SEQUENCE 12 AA: 1375 MW; A41CD7AF CRC32;
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Sequence and mapping analyses of the herpes simplex virus DNA polymerase gene predict a C-terminal substrate binding domain."; Proc. Natl. Acad. Sci. U.S.A. 82:7969-7973(1985).
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GIBBS J.S., CHIOU H.C., HALL J.D., MOUNT D.W., RETONDO M.J.,
WELLER S.K., COEN D.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 10;
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Pred. No. 5.9e+02;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                             human herpesvirus 1.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
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Last annotation update)
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. 5e+02;
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SEQUENCE 10 AA; 1057 MW; 223ABAlA CRC32;
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Pred. No. 5e+03
0; Mismatches
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ilarity 50.0%;
Conservative
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50.0%;
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Best Local Similarity 50.0
Matches 2; Conservative
                                                                                                                                                                                          PRELIMINARY;
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Best Local Similarity
Matches 2; Conserv
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Escherichia.

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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
"Direct Selection cloning vectors adapted to the genetic analysis of gram-negative bacteria and their plasmids.";

EMBL: Y10544: CAA71573.1;

EMBL: Y10544; CAA71573.1;

NON_TER

SEQUENCE 22 AB.
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MEDLINE; 32815917
MEDLINE; 93281592
DEAR T.N., SANCHEZ-GARCIA I., RABBITIS T.H.;
"The HOX11 gene encodes a DNA-binding nuclear transcription factor belonging to a distinct family of homeobox genes.";
Proc. Natl. Acad. Sci. U.S.A. 90:4431-4435(1993).
EMBL; LO8620; ARA286141; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (Rice).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
euphyllophytes; Spermatophyta, Magnoliophyta, Liliopsida, Poales;
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SASAKI T., MATSUMOTO T., YAMAMOTO K.;
"OLYSA SALIVA nipponbare(GA3) genomic DNA, chromosome 8, 1clone:P0026F07.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AP000364, APA81770.1; 6EE798D7 CRC32;
SEQUENCE 22 4A; 2500 MW; 6EE798D7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
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Last sequence update)
Last annotation update)
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Last annotation update)
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le+03;
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Pred. No. 1e+03;
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Pred. No. 1e+03
0; Mismatches
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Drosophila melanogaster (Fruit fly)
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50.0%;
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1998 (TrEMBLrel. 08,
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Best Local Similarity 50.0°
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Best Local Similarity
Matches 2; Conserv
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01-NOV-1996 (TEMBLrel. 01, Created)
01-NOV-1996 (TEMBLrel. 01, Last sequence update)
01-NOV-1996 (TEMBLrel. 01, Last annotation update)
SHORTEST ORF (FRAGMENT).
Emena gibba (Swollen duckweed).
Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Lillopsida; Araceae;
                                                                                                    euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
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Pred. No. 9.6e+02;
Mismatches 2; Indels
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01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
CLONING YECTOR FKILL94T (FRAGMENT).
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OKUBARA P.A., FLORES S., TOBIN E.M.;
Plant Mol. Biol. 11:673-681(1988).
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Plant Mol. Biol. 15:955-956(1990).
EMBL; X14075; CAA32238.1; -.
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20 20
20 AA; 2377 MW;
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Best Local Similarity 50.0%;
Matches 2; Conservative
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Submitted (JUN-1982) to the
EMBL; V01469; CAA24716.1;
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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepatitis C-like viruses.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
E2 REGION (FRAGMENT).
E2 PREJON (TRAGMENT).
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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"Genetic and serological evidence for multiple instances of
unrecognized transmission of hepatitis C virus in hemodialysis
units:";
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MIZUNO M., HIGUCHI T., KANMATSUSE K., ESUMI M.;
"Genetic and serological evidence for multiple instances of
unrecognized transmission of hepatitis C virus in hemodialysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 9; DB 12; Length 27;
Pred. No. 1.3e+03;
0; Mismatches 2; Indels
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27 AA; 2783 MW; 239EED5B CRC32;
                                                    08DA4C92 CRC32;
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Pred. No. 1.3e4
0; Mismatches
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EMBL; AB001390; BAA35030.1; -.
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J. Clin. Microbiol. 36:2926-2931(1998)
EMBL: AB001409; BAA35048.1; -
NON_TER 1 1 1
NON_TER 27 27
SEQUENCE 27 AA; 2783 MW; 239EED5B
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2986 MW;
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ilarity 50.0%;
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27 AA;
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MEDILINE; 89364698.

HIRATSUKA J., SHIMADA H., WHITTIER R., ISHIBASHI T., SAKAMOTO M., MONI M., KONDO C., HONJI Y., SUN C.R., MENG B.Y., LI Y.Q., KANNO A., MISHIZAWA Y., HIRAL A., SHINOZAKI K., SUGIURA M.;

"The complete sequence of the rice (Oryza sativa) chloroplast genome: intermolecular recombination between distinct tRNA genes accounts for a major plastid DNA inversion during the evolution of the cereals.";

Mol. Gen. Genet. 217:185-194(1989).
                                                    Gaps
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Hepatitis C-like viruses.
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MEDLINE; 98411405.
MIZUNO M., HIGCHI T., KANMATSUSE K., ESUMI M.;
"Genetic and serological evidence for multiple instances of unrecognized transmission of hepatitis C virus in hemodialysis
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  Length 27
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STRAIN-CV. NIPPONBARE.;
SUGUINA M.:
Submitted (JUL-1989) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                     01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
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Last annotation update)
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Pred. No. 1.3e+03;
                           1.3e+03;
     DB 12;
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  Score 9; DB 12
Pred. No. 1.3e-
0; Mismatches
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J. Clin. Microbiol. 36:2926-2931(1998)
EMBL; AB001414; BAA35053.1; -.
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01-NOV-1996 (TrEMBLREL 01,
01-NOV-1996 (TrEMBLREL 01,
01-NOV-1998 (TrEMBLREL 08,
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Hepatitis C virus.
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Chloroplast.
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[3]
SEQUENCE FROM N.A.
STRAIN-EV. NIPPONBARE.;
MEDILINE; 91212240.
SHIMADA H., SUGIURA M.;
"Fine structural features of the chloroplast genome: comparison of the sequenced chloroplast genomes.";
Nucleic Acids Res. 19:983-995(1991).
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000491;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1998 (TrEMBLrel. 03, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
HYPOTHETICAL 3.6 KD PROTEIN (FRACMENT).
Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomyces.
                                                                                           STRAIN-CV. NIPPONBARE.;
STRAIN-CV. NIPPONBARE.;
MCDLINE; 94073993.
MORTON B.R., CLEGG M.T.;
A chloroplast DNA mutational hotspot and gene conversion in a noncoding region near rbcL in the grass family (Poaceae).";
Curr. Genet. 24:357-365(1993).
EMBL; X15901; CAA33922.1; --
EMBL; X15901; CAA33922.1; --
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Pred. No. 1.3e+03;
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Pred. No. 1.5e+03;
0; Mismatches 2; Indels
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Best Local Similarity 50.0%;
Matches 2; Conservative
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Unknown.
Unclassified.
1 (bases 1 to 14)
1 (bases 1 to 14)
Hve,G.D., Bradley,M.O., Williams,T.J. and Lee,C.
Antisense oligonucleotides directed against human VCAM-1 RNA
Patent: US 5596090-A 17 21-JAN-1997;
Location/Qualifiers
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Gaps: 0
Percent Identity: 100.000
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/db_xref="taxon:32630"
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synthetic construct
artificial sequence.

| (bases 1 to 15)
Ikehara,M. and Kida,M.
Synthetic gene for human lysozyme
Patent: EP 0181634-A 39 21-MAY-1986;
Takeda Chemical Industries, Ltd
4.1e+03
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Locus A11095 15 bp
DEFINITION Oligonucleotide U20.
ACCESSION A11095
VERSION A11095.1 GI:490945
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134630.1 GI:1825421
66.6
60.6
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US-08-653-294-1 x I34630/rev
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US-08-653-294-1 x Al1095/rev
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Ratio: 2.250
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Ratio: 2.250
Percent Similarity: 100.000
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LOCUS I34630
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                                                                 seq_name: gb_pat:134630
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gb_pat:146300
gb_pat:146301
gb_pat:194267
                                                                                                                                            ACCESSION
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-Q-fcqnl_J/USPTO_Spool_VUS08653294/runat_04022000_160701_15779/app_query.fasta.1

-DB-GennEmbl -OFWI-fastap -SDFFIX-rge -GAPOP-12.000 -GAPDEXT-4.000

-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT-0.000 -OGAPOP-4.500

-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT-0.500 -FGAPOP-6.000

-FGAPDEXT=7.000 -YGAPOP-10.000 -YGAPEXT-0.500 -DELOP-6.000

-FGAPEXT=7.000 -YGAPOP-10.000 -YGAPEXT-0.500 -DELOP-6.000

-DELEXT=7.000 -START-1 -MATRIX-blosum62 -TRANS-human40.cdi

-LOTALGN=20 -THR_SCORE-PCT -ALIGN-15 -MODE-LOCAL

-OUTPWT-PFS -NORM-ext -MINLEN-0 -MAXLEN-1000000 -USER-US08653294

-NCPU-6 -ICPU-3 -NO_XLPXY -WAIT -THREADS-1
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                                                             About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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Query: US-08-653-294-1
Query length: 10
Database: GenEmbl:*
Database sequences: 821193
Database length: -1518192014
Search time (sec): 11370.480000
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OM of: US-08-653-294-1 to:
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                                                                                                             Command line parameters:
                                Date: Feb 8, 2000 4:36
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9b_pat.AR041843
9b_pat.AR041844
9b_pat.157736
9b_pat.157745
9b_pat.157745
9b_pat.AR008356
9b_pat.AR008357
9b_pat.AR0665371
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9b_pat.AR0663
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gb_pat:AR041315
gb_pat:AR041316
gb_pat:AR041841
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gb_pat:I30828
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gb_pat:130840
gb_pat:130841
gb_pat:130842
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gb_pat:I34630
gb_pat:A11095
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29-SEP-1999

PAT

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1 (bases 1 to 15)
Draper, K.G.
Method and reagent for inhibiting hepatitis C virus replication
Patent: US 5869253-A 282 09-FEB-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: 9.00 Length: 4
Ratio: 2.250 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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Sequence 282 from patent US 5869253.
AR033516
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4 c 4 g
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US-08-653-294-1 x AR033516
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US-08-653-294-1 x AR041315
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                                                                            seq_name: gb_pat:AR033516
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LOCUS AR041315
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LOCUS AR033516
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  4 AGGTCGTCACTA 15
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Quality:
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                                                                                                                                                                                                                                                                                                                                                     Unknow...
Unclassified.
1 (bases 1 to 15)
Draper,K.G.
Method and reagent for inhibiting hepatitis C virus replication
Patent: US 5869253.A 273 09.FEB-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unknown.
Unclassified.
Unclassified.
1 (bases 1 to 15)
Draper,K.G.
Method and reagent for inhibiting hepatitis C virus replication
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Ratio: 2.250 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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Gaps: 0
Percent Identity: 100.000
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LOCUS AR033507
DEFINITION Sequence 273 from patent US 5869253.
ACCESSION AR033507
VERSION AR033507.1 GI:5949112
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LOCUS AR033515 15 bp DNA
DEFINITION Sequence 281 from patent US 5869253.
ACCESSION AR033515
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US-08-653-294-1 x AR033507/rev
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Ratio: 2.250
Percent Similarity: 100.000
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US-08-653-294-1 x AR033515
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14 CGGCAACTCTC 3
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to: 15

from: 1

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Unclassified.
Unclassified.
1 (bases 1 to 15)
Sullivan,S., Draper,K., Kisich,K., Stinchcomb,D.T. and McSwiggen,J.
TNF-.alpha. ribozymes
Patent: US 5811300-A 105 22-SEP-1998;
Location/Qualifiers
               29-SEP-1999
                                                                                                                                                                                                                                                                                                                                           Length: 4
Gaps: 0
Percent Identity: 100.000
               PAT
DEFINITION Sequence 105 from patent US 5811300.
ACCESSION AR041315.1 GI:5961811
KEYWORDS
SOURCE UNKNOWN
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Percent Similarity: 100.000
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ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

FEATURES

BASE COUNT ORIGIN

ACCESSION VERSION KEYWORDS

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1 (bases 1 to 15)
Sullivan, S., Draper, K., Kisich, K., Stinchcomb, D.T. and McSwiggen, J.
TNF-.alpha. ribozyma. ribozyma.
Patent: US 5811300-A 632 22-SEP-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sullivan, S., Draper, K., Kisich, K., Stinchcomb, D.T. and McSwiggen, J. Sullivan, S., Draper, K., Kisich, K., Stinchcomb, D.T. and McSwiggen, J. TNF-.alpha. ribozymes
Patent: US 5811300-A 633 22-SEP-1998;
Location/Qualifiers
                                                                                29-SEP-1999
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Percent Identity: 100.000
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                                                                           AR041842 15 bp DNA
Sequence 632 from patent US 5811300.
AR041842
AR041842.1 GI:5962338
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Sequence 633 from patent US 5811300.
AR041843
AR041843.1 GI:5962339
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/organism="unknown"
3 c 4 g
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Ratio: 2.250
Percent Similarity: 100.000
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Ratio: 2.250
Percent Similarity: 100.000
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US-08-653-294-1 x AR041842
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US-08-653-294-1 x AR041843
                                seq_name: gb_pat:AR041842
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                                                                                                                                                                           Unknown.
Unclassified.
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LOCUS AR041843
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LOCUS AR041842
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   4 AGGICIACITIG 15
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                                                                                                                                                          Unknown.
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AUTHORS
TITLE
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SOURCE
                                                                                                                                                                                                                       1 (bases 1 to 15)
Sullivan, S., Draper, K., Kisich, K., Stinchcomb, D.T. and McSwiggen, J.
TNF-alpha. ribozyman.
Patent: US 5811300-A 106 22-SEP-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unclassified.

1 (bases 1 to 15)
Sullivan,S., Draper,R., Kisich,K., Stinchcomb,D.T. and McSwiggen,J.
TNF-alpha. ribozymes
Patent: US 5811300-A 631 22-SEP-1998;
Location/Qualifiers
                                                                                               29-SEP-1999
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Ratio: 2.250 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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Gaps: 0
Percent Identity: 100.000
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t
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LOCUS AR041316
DEFINITION Sequence 106 from patent US 5811300.
ACCESSION AR041316
VERSION AR041316.1 GI:5961812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
LOCUS AR041841 15 bp DNA
DEFINITION Sequence 631 from patent US 5811300.
ACCESSION AR041841. GI:5962337
VERSION AR041841.1 GI:5962337
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3 c 5 g
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Percent Similarity: 100.000
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US-08-653-294-1 x AR041316
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US-08-653-294-1 x AR041841
                                                 seq_name: gb_pat:AR041316
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Jnclassified.
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL FEATURES

BASE COUNT ORIGIN

us-08-653-294-1.rge

DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

source

BASE COUNT ORIGIN

REFERENCE AUTHORS TITLE JOURNAL FEATURES

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# Unknowm.
Unclassified.
Unclassified.
Unclassified.
Draper,K.G.
Enzymatic RNA molecule targeted against Hepatitis C virus
Enzymatic RNA molecule targeted against Hepatitis C virus
L Patent: US 5510054-A 281 11-MAR-1997;
Location/Qualifiers
1 .15
Vorganism="unknown" 4 t
                                             07-0CT-1997
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Draper,K.G.
Enzymatic RNA molecule targeted against Hepatitis C virus
Patent: US 5610064-A 282 11. MAR-1997;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                     Quality: 9.00 Length: 4
Ratio: 2.250 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION Sequence 282 from patent US 5610054.
ACCESSION 157745
VERSION 157745.1 GI:2482809
                       seq_documentation_block:
LOCUS 157744 15 bp DNA
DEFINITION Sequence 281 from patent US 5610054.
ACCESSION 157744
KEYWORDS 50URCE Unknown.
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4 c 4 g
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Percent Similarity: 100.000
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US-08-653-294-1 x I57744
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US-08-653-294-1 x I57745
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4 AGGTCGTCACTA 15
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seq_name: gb_pat:157744
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ORIGIN
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TITLE
JOURNAL
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AUTHORS
TITLE
JOURNAL
FEATURES
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                                                                                                                                                       Unknown.
Unknown.
Unclassified.
Unclassified.
Unclassified.
Sullivan,S., Draper,K., Kisich,K., Stinchcomb,D.T. and McSwiggen,J.
TNF-alpha. ribozymes
Patent: US 5811300-A 634 22-SEP-1998;
Location/Qualifiers
                                                              29-SEP-1999
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Unknown.
Unclassified.
I (bases 1 to 15)
Draper, K.G.
Enzymatic RNA molecule targeted against Hepatitis C virus
Patent: US 5610054-A 273 11-MAR-1997;
Patent: US 561007Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps: 0
Percent Identity: 100.000
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Percent Identity: 100.000
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                                             seq_documentation_block:
LOCUS ARQ41844 15 bp DNA
DEFINITION Sequence 634 from patent US 5811300.
ACCESSION ARQ41844.1 GI:5962340
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Sequence 273 from patent US 5610054.
157736
157736.1 GI:2482800
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US-08-653-294-1 x I57736/rev
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Ratio: 2.250
Percent Similarity: 100.000
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Ratio: 2.250
Percent Similarity: 100.000
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US-08-653-294-1 x AR041844
                seq_name: gb_pat:AR041844
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2 AGGTCTACTTTG 13
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LOCUS I57736
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13 CGGCAACCCTG 2
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

source

REFERENCE AUTHORS TITLE JOURNAL FEATURES

BASE COUNT ORIGIN

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unidentified.

ISM unidentified
unclassified.

unclassified.

(CE 1 (bases 1 to 16)
RS Schlingensiepen, R., Schlingensiepen, K. and
Brysch, W.

Brysch, W.

A PHARMACEUTICAL COMPOSITION COMPRISING ANTISENSE-NUCLEIC ACID FOR
PREVENTION AND/OR TREATMENT OF NEURONAL INJURY, DEGENERATION AND
CELL DEATH AND FOR THE TREATMENT OF NEOPLASMS
NAL BYSCH, WO SOCOSI-A 124 19-7AN-1995;
BIOGNOSTIK GES FUER BLOMOLEKUL (DE)

T Other publication AU 7345694 950206.

ES Location/Qualifiers
                 06-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
Quality: 9.00 Length: 4
Ratio: 2.250 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
                   PAT
                                                                                                                                                                                                                                                                                                                                             1. .16
/organism="unidentified"
/db_xref="taxon:32644"
a 2 c 5 g 5
               A42606 16 bp DNA
Sequence 124 from Patent W09502051.
A42606 42606.1 GI:2298055
seq_documentation_block:
LOCUS A42606
                                DEFINITION
ACCESSION
VERSION
KEYWORDS
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Align seg 1/1 to reverse of: A42606 from: 1 to: 16

alignment_block: US-08-653-294-1 x A42606/rev THIS PAGE BLANK (USPTO)

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Labelled oligonucleotide used
SY40 promoter Gal4 and bNA bindin
Capture probe 13. Reaction au
EP-893493 Seq ID 4. New endot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents a primer used in the method of the invention for this sequence represents a primer used in the method of the invention for the detection of the presence or absence of chromosomal abnormalities, each abnormality being associated with a condition in a subject and each being defined by at least one characteristic nucleic acids derived from a subject which may harbour one of the chromosomal abnormalities;

(b) subjecting the sample to a multiplex molecular amplification (MMA) procedure, where a number of the characteristic sequences, if present in procedure, where a number of the characteristic sequences, if present in constep (b), and detecting the presence and/or absence of an amplicon characteristic of the abnormal sequences to detect the presence or characteristic of the abnormal abnormalities; where the MMA procedure comprises the use of at least 7 mutually distinct primers (MDP) in one single reaction mixture, each of the primers defining an end of at least two characteristic nucleic acid sequences and where at least one of the primers defines the first end of at least two characteristic nucleic acid sequences ach being a determined in their opposite ends by MDP selected from the remainder of the MDP. The methods can be used for detecting chromosomal abnormalities associated with diseases including numerous leukaemia's, lymphoma's, andenocarinoma's,                                                                                                                                                                                                                                                              25-5EP-1998 (first entry)
Primer AMLIEVI:4905L12 for abnormality detection.
PRIMER: ATTOMOSOMAL abnormality; abnormality detection; leukaemia; lymphoma; carcinoma; adenocarcinoma; sarcoma; glioma; neuroblastoma; medullablastoma; malignant melanoma; malignant neoplastic condition; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JUN-1998.
08-DEC-1995; DKOS56.
06-DEC-1995; DK-001401.
(PALL/) PALLISGAARD N.
Hokland P, Pallisgaard N;
WPI: 98-33344/29.
Detection of chromosomal abnormalities - by subjecting patient sample nucleic acids to a multiplex molecular amplification procedure using primers specific for characteristic nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps: 0
Percent Identity: 100.000
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8888
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ID V65428 standard; DNA; 12
AC V65428;
                                                                                                                                                                                                                 V40924 standard; DNA; 12
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US-08-653-294-1 x V40924/rev
                                                                                                                                seq_name: N_Geneseq_36:V40924
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N_Geneseq_36:v30249
N_Geneseq_36:v49885
N_Geneseq_36:v45767
N_Geneseq_36:x02670
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Quality:
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                                                                                                                                                                                                                    Primer AMLIEVI:4905L12 for abnor Primer pBS7-9C used in the cours Primer pBS7-9C used in the cours Primer pBS800-89E used in the cours Primer pBS800-89E used in the comparing the primer pBS800-910E used in the comparing pBS81 which was pBS900-910E used in the comparing pBS91 which was pBS91 to CETP HH ribozyme target semblic CETP HH ribozyme target
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Primer A (Group 13, set B) for m G. oxydans T100 L.sorbose dehydr Bacterlophage T4 permuted gene 3 Adaptor directed primer Hnd.pr. 6 Adaptor direct
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Hepatitis C virus recognition se
HIV-1 gag gene antisense oligonu
                                                                                                                                                                                                        -MODEL-frame-p2n.model -DEV-x1p
-Q=/cgn1_1/USPTO_spool/US08653294/runat_04022000_160701_15807/app_query.fasta.1
-Q=/cgn1_1/USPTO_spool/US08653294/runat_04022000_160701_15807/app_query.fasta.1
-Q=/cgn1_1/USPTO_spool/US08653294 runat_04022000_16000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPENT=0.000
-QGAPOP=4.500 -QGAPEXT=0.000 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-TRANO=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-ALIGN=15 -MODE=LOCAL -OUTFMT-Pfs -NORM-ext -MINLEN-0
-MAXLEN-1000000 -USER-US08653294 -NCPU-6 -ICPU-3 -NO_XLPXY -WAIT
                                                                                                       About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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OM of: US-08-653-294-1 to: N_Geneseq_36:*
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Database sequences: 311585
Database length: 125096042
Search time (sec): 590.520000
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Query: US-08-653-294-1
Query length: 10
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                                                     Date: Feb 8, 2000 1:27
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N_Geneseq_36:V65428
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N_Geneseq_36:V65479
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N_Geneseq_36:V65488
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Examples: Page 8; 20pp; Japanese.
Sequences shown in V65401 to V65800 represent PCR primers used in the course of the invention which provides a method for determining a single stranded nucleic acid base sequence. The method comprises separation 4k oligonucleotide probe as a primer from all combinations of k base sequences and hybridising the probe and the nucleic acid to be tested. The probe is elongated to make a primer using the nucleic acid to be tested as a template and the elongated primer is determined. The base sequence of the nucleic acid is determined assed on the elongated amount. The method allows sensitive and rapid determination of nucleic by hybridisation (SBH) method. 3 G; 2 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Examples: Page 8; 20pp; Japanese.
Sequences shown in V65401 to V65580 represent PCR primers used in the course of the invention which provides a method for determining a single stranded nucleic acid base sequence. The method comprises separation of k oligonucleotide probe as a primer from all combinations of k base sequences and hybridising the probe and the nucleic acid to be tested. The probe is elongated to make a primer using the nucleic acid to be tested as a template and the elongated primer is determined. The base sequence of the nucleic acid is determined based on the elongated amount. The method allows sensitive and rapid determination of nucleic acid base sequence without mismatch in hybridisation as in sequencing
                                                                                                                                                                                                                                           Determination of nucleic acid base sequence - is sensitive and rapid without mismatch in hybridisation as in sequencing by hybridisation
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Primer pBS7-BB used in the course of the invention.
Nucleic acid determination; hybridisation; probe; mismatch; SBH; sequencing by hybridisation; PCR primer; ss.
08-DEC-1998 (first entry)
Primer 1987-9c used in the course of the invention.
NuCleic acid determination; hybridisation; probe; mismatch; SBH; sequencing by hybridisation; PCR primer; ss.
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Percent Identity: 100.000
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                                                                                                                                  14-SEP-1998.
03-MAR-1997, 047821.
03-MAR-1997; JP-047821.
(BUNS-) BUNSHI BIOHOTONICS KENKYUSHO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J10243785-A.
14-SEP-1998.
03-MAR-1997; 047821.
03-M97-1997; JP-047821.
(BUNS-) BUNSHI BIOHOTONICS KENKYUSHO KK.
WPI; 98-549781/47.
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ID V65424 standard; DNA; 12 BP
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Ratio: 2.250
Percent Similarity: 100.000
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US-08-653-294-1 x V65428/rev
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Examples; Page 10; 20pp; Japanese.

Examples shown in V65401 to V65580 represent PCR primers used in the course of the invention which provides a method for determining a single stranded nucleic acid base sequence. The method comprises separation of 4k oligonucleotide probe as a primer from all combinations of k base sequences and hybridising the probe and the nucleic acid to be tested. The probe is elongated to make a primer using the nucleic acid to be sequence of the nucleic acid is determined based on the elongated amount. The method allows sensitive and rapid determination of nucleic acid base sequence without mismatch in hybridisation as in sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Determination of nucleic acid base sequence - is sensitive and rapid without mismatch in hybridisation as in sequencing by hybridisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                08-DEC-1998 (first entry)
primer pBS800-89E used in the course of the invention.
Nucleic acid determination; hybridisation; probe; mismatch; SBH; sequencing by hybridisation; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-DEC-1998 (first entry)
Primer pBS800-89F used in the course of the invention.
                                                                                                Length: 4
Gaps: 0
Percent Identity: 100.000
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Ratio: 2.250 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BUNS-) BUNSHI BIOHOTONICS KENKYUSHO KK.
WPI; 98-549781/47.
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by hybridisation (SBH) method. Sequence 12 BP; 3 A; 2
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Sequence 12 BP; 2 A;
                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
ID V65478 standard; DNA; 12 BP.
AC V65478;
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ID V65479 standard; DNA; 12 BP.
AC V65479;
                                                                                              Quality: 9.00
Ratio: 2.250
Percent Similarity: 100.000
                                                                                                                                                                                               US-08-653-294-1 x V65424/rev
                                                                                                                                                                                                                                                                                                                                                      seq_name: N_Geneseq_36:V65478
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US-08-653-294-1 x V65478/rev
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03-MAR-1997; 047821.
03-MAR-1997; JP-047821
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7

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1 Arg*****Leu 4
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Ratio:
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                                       alignment_scores
                                                                                                                  alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
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                                                                                                                                                                                            Examples; Page 10: 20pp; Japanese.

Sequences shown in V65401 to V65800 represent PCR primers used in the course of the invention which provides a method for determining a single stranded nucleic acid base sequence. The method comprises separation of k oligonucleotide probe as a primer from all combinations of k base sequences and hybridising the probe and the nucleic acid to be tested. The probe is elongated to make a primer using the nucleic acid to be sequence of the nucleic acid is determined based on the elongated amount. The method allows sensitive and rapid determination of nucleic acid base sequence without mismatch in hybridisation as in sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Examples; Page 10: 20pp; Japanese.

Sequences shown in V6401 to V6580 represent PCR primers used in the course of the invention which provides a method for determining a single stranded nucleic acid base sequence. The method comprises separation of the oligonucleotide probe as a primer from all combinations of k base sequences and hybridising the probe and the nucleic acid to be tested. The probe is elongated to make a primer using the nucleic acid to be tested as a template and the elongated primer is determined. The base sequence of the nucleic acid is determined based on the elongated amount. The method allows sensitive and rapid determination of nucleic acid base sequence without mismatch in hybridisation as in sequencing
                                                                                                                                                  Determination of nucleic acid base sequence - is sensitive and rapid without mismatch in hybridisation as in sequencing by hybridisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Determination of nucleic acid base sequence - is sensitive and rapid without mismatch in hybridisation as in sequencing by hybridisation method
Nucleic acid determination; hybridisation; probe; mismatch; SBH; sequencing by hybridisation; PCR primer; ss.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-DEC-1998 (first entry) Primer PBS800-910D used in the course of the invention. Nucleic acid determination; hybridisation; probe; mismatch; SBH; sequencing by hybridisation; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps: 0
Percent Identity: 100.000
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1;
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G
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03-MAR-1997; JP-047821.
(BUNS-) BUNSHI BIOHOTONICS KENKYUSHO KK.
WPI; 98-549781/47.
                                                                                                               (BUNS-) BUNSHI BIOHOTONICS KENKYUSHO KK.
WPI; 98-549781/47.
                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                             3
C;
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C;
                                                                                                                                                                                                                                                                                                                                                                              by hybridisation (SBH) method Sequence 12 BP; 2 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hybridisation (SBH) method quence 12 BP; 2 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     V65486 standard; DNA; 12 BP
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US-08-653-294-1 x V65479/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: N_Geneseq_36:V65486
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 9.00
Ratio: 2.250
Percent Similarity: 100.000
                                                                    14-SEP-1998.
03-MAR-1997; 047821.
03-MAR-1997; JP-047821.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 Arg*****Leu 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 CGCGCCGCCTTA 1
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Quality:
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J10243785-A.
14-SEP-1998.
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                                                                                                                                                                                   method
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Examples; Page 10; 20pp; Japanese.
Sequences shown in V65401 to V65580 represent PCR primers used in the Sequences shown in V65401 to V65580 represent PCR primers used in the Sequences of the invention which provides amethod for determining a single stranded nucleic acid base sequence. The method comprises separation of 4k oligonucleotide probe as a primer from all combinations of k base sequences and hybridising the probe and the nucleic acid to be tested. The probe is elongated to make a primer using the nucleic acid to be tested as a template and the elongated primer is determined. The base sequence of the nucleic acid is determined based on the elongated amount. The method allows sensitive and rapid determination of nucleic acid base sequence without mismatch in hybridisation as in sequencing by hybridisation (SBH) method.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Determination of nucleic acid base sequence - is sensitive and rapid without mismatch in hybridisation as in sequencing by hybridisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Primer pBS800-910E used in the course of the invention. Nucleic acid determination; hybridisation; probe; mismatch; SBH; sequencing by hybridisation; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-DEC-1998 (first entry) prime pssecont the invention. Primer BS800-210F used in the course of the invention. Nucleic acid determination; hybridisation; probe; mismatch; SBH; sequencing by hybridisation; PCR primer; ss.
                             Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 4
Gaps: 0
Percent Identity: 100.000
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2
Gaps:
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                                                                                                                                                                                                          Align seg 1/1 to reverse of: V65486 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-SEP-1998.
03-MAR-1997; 047821.
03-MAR-1997; JP-047821.
(BUNS) BUNSHI BICHOTONICS KENKYUSHO KK.
WPI; 98-549781/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               V65487 standard; DNA; 12 BP.
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ID V65488 standard; DNA; 12 BP
AC V65488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-DEC-1998 (first entry)
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2.250
100.000
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US-08-653-294-1 x V65487/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                        seg_name: N_Geneseg_36:V65487
                         Percent Similarity: 100.000
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Percent Identity: 100.000

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Percent Similarity: 100.000
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                                                                                                        Align seg 1/1
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                                                                                                                                                                                                                                                                                                  Examples; Page 10; 20pp; Japanese.

Sequences shown in v65401 to v65580 represent PCR primers used in the Sequences shown in v65401 to v65580 represent PCR primers used in the Sequences shown in v65401 to v65580 represent PCR primer is already a single stranded nucleic acid base sequence. The method comprises separation of 4k oligonucleotide probe as a primer from all combinations of k base sequences and hybridising the probe and the nucleic acid to be tested. The probe is elongated to make a primer using the nucleic acid to be tested as a template and the elongated primer is determined. The base sequence of the nucleic acid is determined based on the elongated amount. The method allows sensitive and rapid determination of nucleic acid by hybridisation (SBH) method.

Sequence 12 BP; 3 A; 3 C; 4 G; 2 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antisense oligo:nucleotide(s) for treating septic shock - with sequence complementary to VCAM-1 mRNA transcript claim 19. HBpp. English.

The present sequence is that of an antisense oligonucleotide complementary to a region in the precursor or mature mRNA of human vascular cell adhesion molecule VCAM-1. The antisense oligonucleotide (preferably containing phosphorothioate linkages) is used for downrequiating VCAM-1 synthesis which in turn results in a reduction in adhesion of leukocytes to the endothelium and hence to a reduced
                                                                                                                                                Determination of nucleic acid base sequence - is sensitive and rapid without mismatch in hybridisation as in sequencing by hybridisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; vascular cell adhesion molecule; VCAM-1; antisense;
septic shock; downregulation; inflammation; leukocyte adhesion; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complementary to human VCAM-1 mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity: 100.000 Percent Identity: 100.000
                                                                                                   (BONS-) BUNSHI BIOHOTONICS KENKYUSHO KK.
WPI; 98-549781/47.
Determination of nucleic acid base sequence - is
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24-JUL-1992; 918256.
24-JUL-1992; US-918256.
12-OCT-1993; US-137701.
(USNA ) US SEC OF NAVY.
Bradley MO, Hoke GD, Lee C, Williams IJ;
WPL; 97-107618/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
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9
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C;
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Antisense oligonucleotide #17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
ID T64335 standard; DNA; 14 BP.
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US-08-653-294-1 x V65488/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: N_Geneseq_36:T64335
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                                                           03-MAR-1997; 047821.
03-MAR-1997; JP-047821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inflammatory response.
Sequence 14 BP; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 CGTAGCGCCTTA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
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Synthetic.
J10243785-A.
                                          14-SEP-1998
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Gaps:

Ratio:

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Example 37: Page 301: 457pp; English.

Example 37: Page 301: 457pp; English.

Cleavage of test Oligonucleotide IT-2 (17671) was examined in the presence of Invader (TM) oligonucleotides IT-1 (176718) and IT-1A4 (176719).

IT-1 is fully complementary to the 3' arm of IT-2, whereas IT-1A has a T to A substitution that results in an A/A mismatch in the Invader target duplex. Experiments were performed to show that the presence of a mismatch in the Invader oligonucleotide decreases the cleavage activity of Cleavase A/G unclease (see I76643). The invention relates to means for the oligonucleotide decreases the cleavage activity of cleavase A/G unclease (see I76643). The invention relates to means for the NA cleavage structure on a target sequence and cleaving the NA cleavage structure on a target sequence and cleaving the NA cleavage structure in a site-specific manner. The 5' unclease activity of various enzymes (see W24210-13) is used to cleave the target-dependent cleavage structure, thereby indicating the presence of specific NA sequences or specific variations of the invantion is an ideal direct detection method that combines the advantages of direct detection assays with the specificity of a dual or relational assays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermostable structure-specific nuclease(s) - used for detection and characterisation of nucleic acid sequences and variations in nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-APR-1998 (first entry).
Invader Oligonucleotide IT-1.
Nucleic acid cleavage; DNA cleavage; RNA cleavage; nuclease;
invader directed cleavage; Cleavase A/G; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (THIR-) THIRD WAVE TECHNOLOGIES INC.
Brow MAD, Dahlberg JE, Hall JG, Kaiser MW, Lyamichev VI, Olive DM, Prudent JR; WPI, 97-393613/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 4
Gaps: 0
Percent Identity: 100.000
                                                                                                    14
                                                                                                    :
::
                                                                                                to reverse of: T64335 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                      76718 standard; DNA; 14 BP.
alignment_block:
US-08-653-294-1 x T64335/rev
                                                                                                                                                                                                                                                                                                         seq_name: N_Geneseq_36:T76718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-JUL-1997,
22-JAN-1997, UO1072,
02-DEC-1996, US-759038,
24-JAN-1996, US-599491,
12-JUL-1996, US-682853,
29-NOV-1996, US-756386,
02-DEC-1996, US-758314,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ratio: 2.250
Percent Similarity: 100.000
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US-08-653-294-1 x T76718
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                                                                                                                                                                                                                                     14 CGGGCCTCACTG 3
                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
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mutation

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growth of cells in culture

Claim 10: Fig 8a: 286pp: English.

V48930-49007 represent antisense directed against

transforming growth factor-beta2 (TGF-beta2). Of these, only

oligonucleotides V48930-67 resulted in significant redcution in

TGF-beta 2 protein expression, while oligonucleotides v48968-49007 had

little effect. The oligonucleotides exemplify the invention. The

specification describes oligonucleotides that contain 8-30 nucleotides,
                                                                                                                                                               11-JUN-1998.
02-DEC-1996; WO-U19194.
(DYAD-) DYAD PHARM CORP.
Bradley MO, Hoke GD, Lee C, Williams TJ;
WPI: 98-333253/28.
Antisense Oligonucleotides to ICAM-1, E-selectin or VCAM-1 - useful
                                                                                                                                                                                                                                                                                                                               for treating diseases having an inflammatory component, e.g. claims; page 41; 48pp; Engilsh.

Claims; Page 41; 48pp; Engilsh.

The sequence is that of an antisense oligonucleotide which is substantially complementary to at least a portion of the preor mature RNA transcript of human intracellular adhesion molecule (ICAM), E-selectin or vascular cell adhesion molecule (VCAM). It can be used to inhibit expression of these proteins. Inhibition of these proteins forms the basis for treatment of conditions and diseases that have an inflammatory component, e.g. acne, psoriasis, arthitis, organ rejection, wounds, burns, septic shock or inflammatory complications of septic shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Preparation of antisense oligo:nucleotide(s) which lack long runs consecutive guanosine or inosine - and have specific ratio of residues able to form two or three hydrogen bonds, have greater activity and reduced toxicity, used therapeutically or to modulate
                    vascular cell adhesion molecule-1; antisense; inflammatory; disease; treatment; septic shock; psoriasis; wounds; burns; acne; arthritis; organ rejection; inhibition; expression; ss.
ICAM-1; intracellular adhesion molecule-; E-selectin; VCAM-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGF-beta2 antisense oligonucleotide TGF-beta2-8.
Transforming growth factor-beta2; TGF-beta2;
antisense oligonucleotide; modulate; gene expression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 4
Gaps: 0
Percent Identity: 100.000
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EP-856579-A1.
05-A06-1998
31-JAN-1997; 101531.
31-JAN-1997; EP-101531.
(BIOG) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
WPI; 98-400910/35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality: 9.00
Ratio: 2.250
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 BP;
                                                                                                                         Homo sapiens.
WO9824797-A1.
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                                                                                                Synthetic
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Example 37; Page 301; 457pp; English.

Example 37; Page 301; 457pp; English.

Cleavage of test oligonucleotide IT-2 (176717) was examined in the presence of Invader (TM) oligonucleotides IT-1 (176718) and IT-1A4

(T76719). IT-1 is fully complementary to the 3' arm of IT-2, whereas IT-1A4 has a T to A substitution that results in an A/A mismatch in the Invader tenget duplex. Experiments were performed to show that the presence of a mismatch in the Invader of show that the presence of a mismatch in the Invader oligonucleotide decreases the cleavage activity of Cleavase A/G on oligonucleotide decreases the cleavage activity of Cleavase A/G and variations in NA sequences. It also relates to methods for detection and characterisation of nucleas caid (NA) sequences and cleaving the NA cleavage structure on a target sequence and cleaving the NA cleavage structure in a site-specific manner. The 5' cleave the target-dependent cleavage structure, thereby indicating them The Invader directed cleavage reaction of the invention is an ideal direct detection method that combines the advantages of cliect detection assays with the specificity of a dual or tri-oligonucleotide hybridisation assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermostable structure-specific nuclease(s) - used for detection and characterisation of nucleic acid sequences and variations in nucleic
                                                                                                                  14-APR-1998 (first entry)
Invader oligonucleotide IT-1A4.
Nucleic acid cleavage; DNA cleavage; nuclease;
invader directed cleavage; Cleavase A/G; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-OCT-1998 (first entry)
Human ICAM-1, E-selectin, VCAM-1 antisense oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (THIR-) THIRD WAVE TECHNOLOGIES INC.
Brow MAD, Dahlberg JE, Hall JG, Kaiser MW, Lyamichev VI,
Olive DM, Prudent JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 4
Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                         Location/Qualifiers
                                             seq_documentation_block:
ID T76719 standard; DNA; 14 BP.
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/note= "T
seq_name: N_Geneseq_36:T76719
                                                                                                                                                                                                                                                                                                                                                                                                         02-DEC-1996; US-759038.
24-JAN-1996; US-599491.
12-JUL-1996; US-682853.
29-NOV-1996; US-758314.
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Percent Similarity: 100.000
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13-0CT-1998
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7 A;

14 BP;

Sednence

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Preparation of antisense oligo:nucleotide(s) which lack long runs of consecutive guanosine or inosine - and have specific ratio of residues able to form two or three hydrogen bonds, have greater activity and reduced toxicity, used therapeutically or to modulate PT activity and reduced toxicity, used therapeutically or to modulate PS (laim 10): Fig 5a: 286pp; English.

V48564-708 represent antisense oligonucleotides V4855-614 resulted in effective downrequiation of negative growth control by JunB or JunD, while v48615-708 had little effect. The oligonucleotides that counting the invention. The specification describes oligonucleotides that contain 8-30 nucleotides, which contain at most 8 nucleotides that can each form three hydrogen bonds to cytosine; do not contain four consecutive nucleotides able to form three H-bonds each to four tree consecutive cytosines; do not contain two sequences of three consecutive cytosines; and the ratio between residues able to form two H-bonds each coligonucleotides are used to modulate expression of genes, particularly cyclosines, and the ratio between residues able to form two H-bonds each coligonucleotides are used to modulate expression of genes, particularly the genes for p53, ErbB-2, junB, julm, TGF-beta 1 or beta 2 to control coligonucleotides can also be used to analyse function of proteins (by altering their expression or activity) and therapeutically, e.g. in cases of cancer or (targeting TGF) for stimulating the immune system.
which contain at most 8 nucleotides that can each form three hydrogen bonds to cytosine; do not contain four consecutive nucleotides able to form three H-bonds each to four consecutive cytosines; do not contain two sequences of three consecutive nucleotides each able to form three theory of three consecutive nucleotides each able to form three theory of three consecutive nucleotides each able to form three theory of three consecutive nucleotides are used to form three theory of the contained the contained to three such bonds (3R) is given by 2R/3R = 0.33-0.72. The oligonucleotides are used to modulate expression of genes, particularly the genes for p53, ErB-2, JunB, JunD, TGF-beta I or beta 2 to control proliferation of primary cell cultures (e.g. bone marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or keratinocytes). The oligonucleotides can also be used to analyse function of proteins (by altering their expression or activity) and therapeutically, e.g. in cases of cancer or (targeting Sequence 14 BP; 2 A; 4 C; 3 G; 5 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             V48608;
15-CCT-1998 (first entry)
junD gene antisense oligonucleotide JunD-25.
junD; antisense oligonucleotide; modulate; gene expression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio: 2.250 Length: 4 Gaps: 0 Gaps: 0 Percent Similarity: 100.000 Percent Identity: 100.000
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31-7AN-1997; 101531.
31-7AN-1997; EP-101531.
(BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
Brysch W, Schlingensiepen K;
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ID V48608 standard; DNA; 14 BP.
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15-OCT-1998 (first entry)
junD gene antisense oligonucleotide JunD-11.
junB; junD; antisense oligonucleotide; modulate; gene expression; ss.
                    Percent Identity: 100.000
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                                                         Align seg 1/1 to: V48608 from: 1
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                                                                                                                              V48594 standard; DNA; 14 BP
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Percent Similarity: 100.000
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                     Percent Similarity: 100.000
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31-JAN-1997; 101531.
31-JAN-1997; EP-101531.
                                     alignment_block:
US-08-653-294-1 x V48608
                                                                                         1 CGCTCCAGCTTG 12
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                                                                                 Quality:
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EP-856579-A1.
alignment_scores:
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Wed Feb 9 08:46:19 2000

us-08-653-294-1.rng

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us-08-653-294-1.rst

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AI096191 SWAMCAC26D07SK Brugi
AQ025526 EP(X)1597 Drosophila
C00971 HUMGS0003340 Human adu
                                                                                                                                                                                                                                          Eukaryota in Saptaca, Chordata; Craniata; Vertebrata; Mammalia; Eukaryota in Charea; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (Dasea I to 19)

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tunor Gene Index

I (Dupblished (1997)

On Mar 10, 1998 this sequence version replaced gi:2948114.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov

Life Technologies catalog #: 11548-013

Das Sequencing by; Washington University Genome Sequencing Center Clone distribution: NCL-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing Center information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.72 kb. Life Technologies catalog #: 11548-013" 5 g 5 t
                                                                                                       AIS69191 19 bp mRNA EST 14-MAY-1999
tr83f12.xl NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224943 3'
similar to SW:PRCE_HUMAN P28074 PROTEASOME EPSILON CHAIN PRECURSOR
7; mRNA sequence.
7; mRNA sequence.
A1569191 GI:4532565
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LOCUS C00979 20 bp mRNA EST 23-JUL-19
DEFINITION HUMGS0003365 Human adult (K.Okubo) Homo sapiens CDNA, mRNA
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Gaps: 0
Percent Identity: 100.000
 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. 19
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/tissue_type="adenocarcinoma"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trace considered overall poor quality Insert Length: 1117 Std Error: 0.00 Seq primer: -400P from Gibco High quality sequence stop: 1 POLYA-No.
4.1e+04
4.1e+04
4.3e+04
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Ratio: 2.250
Percent Similarity: 100.000
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US-08-653-294-1 x AI569191
                                                                                            seq_documentation_block:
LOCUS AIS69191
                                                                                                                                                                                                                                   Homo sapiens
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gb_gss8:AQ025526
gb_est8:C00971
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
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R82106 13D6 Chromosome 21 exon H
H82478 yv80e05.rl Soares melanod
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-LISP=45 -DOCALIGN=200 -THR_SCORE=PCT_ALIGN=15 -MODE=LCCAL
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-NCPU=6 -ICPU=3 -NO_XLPXY -WAIT -THREADS=1
                                                             software, version 4.5,
out_format :
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                                                             About: Results were produced by the GenCore Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                          Search information block:
Query: US-08-653-294-1
Query length: 10
Database: EST:*
Database sequences: 4538634
Database length: 1887831982
Search time (sec): 8553.36000
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                              Date: Feb 8, 2000 4:02 AM
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gb_est9:C21489
gb_est8:AO026240
gb_gss13:AO051551
gb_est5:N85094
gb_est5:N85094
gb_est1:T48676
gb_est1:T48676
gb_est2:AI723287
gb_est2:AI723287
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gb_est32:AI723287
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gb_est15:AA509644
gb_est16:AA582036
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gb_est22.AU006493
gb_est15.AA132764
gb_est15.AA519848
gb_est18.AA775377
gb_est19.AA775377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gb_est24:AI186043
gb_est29:AI573818
gb_est36:AI911947
gb_est37:AI971896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_est23:A1159689
gb_est30:A1631121
gb_est31:A1683303
gb_est32:A1720308
gb_est37:A1965919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
gb_est29:A1569191
gb_est8:C00979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gb_est9:AA109657
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gb_est3:R82106
gb_est5:H82478
                                                                                                                                                                                                                                                                                                                                                                                                                                                       score_list:
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/dev_stage="adult"
//dev_stage="adult"
//dev_stage="adult"
//dev_stage="adult"
//deb.host="Yez-Txi1-Blue MRF'"
//note="Yez-Txi1-Blue MRF'"
//dex_stage="decorated in the parasite of humans. Two adult female worms of Onchocerca volvulus were isolated from consenting patients and quick frozen. Adult female mRNA was converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNASe H and DNA poll. The library has 7 x 10E5 independent recombinants and the average insert size is "1100bp.The library was constructed by Michelle Lizotte-Wanlewski with worms provided by Dr. Sara Lustigman. The library is available from Dr. Steven A. Williams, email: genome@smith.edu."

5 a 3 c 6 g
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Email: Kousaku(&inoc).csaka-u.ac.jp
Human Gene Signature, 3'-directed cDNA sequence. We are not
Submitting the same cDNA sequence redundantly to DDBJ since 1993.
For the abundance information of clones with this sequence in this
library and as well as in other 3'-directed libraries, see '
http://www.incb.osaka-u.ac.jp/bodymap'. The sequences of the clones
represented by this GS sequences is also found there.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C21489 25 bp mRNA EST 23-OCT-1996
HUMGS0010483 Human adult (K.Okubo) Homo sapiens cDNA 3', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 25)
                                                                                                                                                                                                          /clone_lib="Onchocerca volvulus adult female cDNA (SAN98MIM-OvAF)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BodyMap; human gene expression database
Upublished (1995)
On Nov 29, 1993 this sequence version replaced gi:430468
Contact: Okubo, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps: 0
Percent Identity: 100.000
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                                                                                                                                  /organism-"Onchocerca volvulus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 20
                                                                                                                                                     /db_xref="taxon:6282"
/clone="SWOVAFCAP14E11"
Fax: 4135853786
Email: genome@smith.edu
Seg primer: pBluescript SK.
Location/Qualifiers
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                                                                                                                                                                                                                                                               /sex="female
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C21489.1 GI:1622599
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Ratio: 2.250
Percent Similarity: 100.000
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US-08-653-294-1 x AI253456
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LOCUS C21489
DEFINITION HUMGS0010483
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                     1-3, Yamada-Oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111(ex.315)
Email: Kousaku@inob.osaka-u.ac.jp
Human Gene Signature, 3'-directed cDNA sequence. We are not
Submitting the same cDNA sequence redundantly to DDBJ since 1993.
For the abundance information of clones with this sequence in this
library and as well as in other 3'-directed libraries, see '
http://www.imcb.osaka-u.ac.jp/bodymap'. The sequences of the clones
represented by this GS sequences is also found there.
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LOCUS AI253456 20 bp mRNA EST 06-NOV-1998

DEFINITION SWOVAFCAP14E11SK Onchocerca volvulus adult female cDNA (SAW98MLW-OvAF) Onchocerca volvulus cDNA clone SWOVAFCAP14E11 5',

RRNA sequence.

ACCESSION AI253456
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Onchocerca volvulus
Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Secernentea; Spiruria; Spirurida;
Filarioidea; Onchocercidae; Onchocerca.
I (bases 1 to 20)
Lizotte-Waniewski, n. and Milliams, S.A.
Genes expressed in adult female stage of Onchocerca volvulus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 20)
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On Jan 17, 1998 this sequence version replaced g1:2043512
Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human adult (K.Okubo)"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: 20
                                                                                                                                                                                                                                                          BodyMap; human gene expression database Unpublished (1995) Contact: Okubo, K. Institute for Molecular and Cellular Biol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
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                                                     C00979.1 GI:1433209
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Percent Similarity: 100.000
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US-08-653-294-1 x C00979/rev
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       sequence.
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AUTHORS
TITLE
JOURNAL
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TITLE
JOURNAL
COMMENT
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KEYWORDS
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FEATURES

Percent Identity: 100.000

Gaps:

:: t2

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seq_documentation_block:
LOCUS AQ026240 28 bp DNA GSS 30-JUN-1998
DEFINITION 1(3)11231 Drosophila melanogaster P lethal line Drosophila
melanogaster genomic Sequence recovered from 5' end of P element,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Endit fly.

Bukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda: Insecta; Bukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda: Insecta; Pterygota: Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha: Bphydroidea; Drosophilidae; Drosophila.

E loases 1 to 28)

S Spradling.A.C., Stern,D., Beaton,A., Rehm,E.J., Laverty,T., Morden,N., Misra,S. and Rubin,G.M.

The BDGP gene disruption project: Single P element insertions mutating 30% of Drosophila autosomal genes
Unpublished (1998)

Contact: Gerald Rubin
Berkeley Drosophila Genome Project
University of California, Berkeley
Exa Building, Berkeley, CA 94720-3200, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence orientation is forward strand relative to 5' end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence recovery method was inverse PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: gerry@fruitfly.berkeley.edu
                                                                                                                                                                                                                                                      Align seg 1/1 to reverse of: A1625681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genomic survey sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQ026240.1 GI:3266525
                                                                                                                                                                          alignment_block:
US-08-653-294-1 x AI625681/rev
                                                                        Uuality: 9.00
Ratio: 2.250
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: gb_gss8:AQ026240
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                                                      alignment_scores
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 28)

NCI-GCAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-GCAP http://www.obi.nlm.nih.gov.ncicgap.

NCI-GCAP http://www.obi.nlm.nih.gov.ncicgap.

NCI-GCAP close distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
LOCUS Af625681
LOCUS Af625681
DEFINITION LY595006.x1 NOT_CGAP_UT2 Homo sapiens CDNA clone IMAGE:2283370 3'
DEFINITION LY595006.x1 NOT_CGAP_UT2 Homo sapiens CDNA clone IMAGE:2283370 3'
i, mRNA sequence.

ACCESSION Af625681
VERSION Af625681. GI:4650612
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/lab_host="bind" 3 pooled tumors.
/lab_host="bind" 3 pooled tumors.
/lab_host="bind" 1 pooled tumors.
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.85 kb. Life Technologies catalog #:
11539-012"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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/tissue_type="moderately_differentiated endometrial
                                                                                                                                                                                                                                                                             Gaps: 0
Percent Identity: 100.000
1. .25
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human adult (K.Okubo)"
/dev_stage="adult"
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High quality sequence stop: 1.
Location/Qualifiers
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US-08-653-294-1 x C21489/rev
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Percent Similarity: 100.000
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/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/dlome_llb="brosophila melanogaster P lethal line"
/clone_llb="brosophila melanogaster P lethal line"
/note="Inverse PCE was performed on prosophila
melanogaster strains each of which contains a single P
transposable element insertion that is thought to cause
either lethality or sterility. The resultant fragment for
each strain was directly sequenced to determine the
genomic sequence at the site of insertion. Details of the
protocols used can be found at
http://fruitily.berkeley.edu/p_disrupt/inverse_pcr.html."
3 a 5 C 13 t.
The P element insertion position is base 021 in the 28 bases. This insertion position refers to the first base of the 8 base target
                                                                                                                                                                    Class: transposon-tagged.
Location/Qualifiers
                                                                                        recognition sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.00
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us-08-653-294-1.rst

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human.
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//db xref="taxon:453"
//clone="hbxb0002006r"
//clone="hbxb0002006r"
//clone="hbxb0002006r"
//clone="hbxb0002006r"
//tssue_type="redi"
//lab_host="redi"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
LOCUS AQ051551 28 bp DNA GSS 24-MAR-1999
DEFINITION nbxD0002bH03r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0002006r, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Poaceae; Oryza.

1 ( Abases 1 to 28)

Wing, R.A. and Dean, R.A.

A BAC End Sequencing Framework to Sequence the Rice Genome

Unpublished (1998)

On Mar 23, 1999 this sequence version replaced g1:3324109.
Gaps: 0
Percent Identity: 100.000
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Clemson University
100 Uordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                    Align seg 1/1 to reverse of: AQ026240 from: 1
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/organism="Oryza sativa"
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/cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: rwing@clemson.edu
Seq primer: GGAAACAGCTATGACCATG
Class: BAC ends
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Location/Qualifiers
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                                                                                                    alignment_block:
US-08-653-294-1 x AQ026240/rev
Ratio: 2.250
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: gb_gss13:AQ051551
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Oryza sativa
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="12591"
/clone_lib="Human fetal heart, Lambda ZAP Express"
/lab_host="E. coli XLI-Blue"
/note="Vector: Lambda ZAP Express; Site_l: EcoRI: Site_2:
/note="Vector: Lambda ZAP Express; Site_l: EcoRI: Site_2:
Xho!; mRNA was purified from human fetal hearts (8-10
weeks). cDNA was synthesized using a XhoI-Oligo dT
adaptor-primer. EcoRI adaptors were ligated, followed by
digestion with XhoI, for directional cloning into
predigested lambda ZAP Express."
8 a 6 c 10 g 5 t
                                                                                                                                                                                                                                                                                                                                                       LEST 01-APR-1996 CLODE 12291 5' SIMILIAR TO RAB7P, MRNA Sequence. N85094.1 GI:1260719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 29)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Liew CC
Department of Laboratory Medicine and Pathobiology
University of Toronto
Banting Institute, 100 College St., Toronto, Ontario, M5G1L5
Tel: 4169788758
Fax: 4169785550
Email: liewcceutcc.utoronto.ca
Email: liewcceutcc.utoronto.ca
Seq primer: GAAATGAACCTCACTAAAGGG.
  Length: 4
Gaps: 0
Percent Identity: 100.000
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Ratio: 2.250 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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Unpublished (1996)
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US-08-653-294-1 x AQ051551/rev
Quality: 9.00
Ratio: 2.250
Percent Similarity: 100.000
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US-08-653-294-1 x N85094
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AQÓ25148
AQO25148.1 GI:3265500
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US-08-653-294-1 x C01074/rev
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Ratio: 2.250
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus domesticus"
/strain="C57BL/6J"
/db_xref="taxon:10092"
/clone="mad188"
/clone=lib="Muouse 3'-directed"
/tissue_type="decidual tissue (day 6.5-8.5 of gestation)"
a 12 c 4 g 5 t
                                                                                                                                                Mus musculus domesticus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 30)
Kawamoto,S., Okubo,K., Yoshil,J., Katsuki,M. and Matsubara,K.
D18723 30 bp mRNA EST 12-DEC-1995 WUSGS01785 Mouse 3'-directed Mus musculus domesticus cDNA clone md0188 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JUL-1996
CDNA, mRNA
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                                                                                                                                                                                                                                                 cDNA sequencing
Unpublished (1995)
On May 18, 1995 this sequence version replaced gi:811444.
Contact: Kawamoto,S., Okubo,K., Yoshii,J., Katsuki,M. and
Matsubara,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C01074 30 bp mRNA EST
HUMGS0007722 Human adult (K.Okubo) Homo sapiens
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BodyMap; human gene expression database Unpublished (1995) Contact: Okubo.K.
Institute for Molecular and Cellular Biol Osaka University
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                                                                                                                                                                                                                                                                                                                              Matsitute for Cellular and Molecular Biology Osaka University
3-1 Yamada-Oka, Suita, Osaka 565, Japan
Binsert Length; 783 Std Error: 0.00
High quality sequence stop: 354.
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Gaps: 0
Percent Identity: 100.000
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Tel: 06-877-5111(ex.3315)
Email: kousaku@imcb.osaka-u.ac.jp
                                                                                                                                  western European house mouse.
                                                                                               D18723.1 GI:1100692
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C01074
C01074.1 GI:1433304
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US-08-653-294-1 x D18723/rev
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Percent Similarity: 100.000
              seq_documentation_block:
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Human Gene Signature, 3'-directed cDNA sequence. We are not submitting the same cDNA sequence redundantly to DDBJ since 1993. For the abundance information of clones with this sequence in this library and as well as in other 3'-directed libraries, see 'http://www.imcb.osaka.u.ac.jp/bodymap'. The sequences of the clones represented by this GS sequences is also found there.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
LOCUS AQ055148 30 bp DNA GSS 14-OCT-1998
DEFINITION EP(3)1001 Drosophila melanogaster EP line Drosophila melanogaster genomic Sequence recovered from 5' end of P element, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fruit fly.

SM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Meoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

E 1 (bases 1 to 310)

S Rehm, E.J. and Rubin, G.M.

The BDGP gene disruption project: single EP element insertions

L Unpublished (1998)

Contact: Gerald Rubin

Berkeley Drosophila Genome Project

University of California, Berkeley

LSA Building, Berkeley, CA 94720-3200, USA

Fax: 5106439947
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/db_xref="taxon:7227"
/clone_lib="Drosophila melanogaster EP line"
/note="Inverse PCR was performed on Drosophila
melanogaster strains each of which contains a single EP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Δ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 4
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/organism="Homo sapiens"
/db_xxeef="taxon:9606"
/clone_lib="Human adult (K.Okubo)"
/dev_stage="adult"
for 6 9 9 t
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Location/Qualifiers
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Align seg 1/1 to: T48676
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US-08-653-294-1 x T48676
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TITLE
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transposable element insertion. (The generation of these insertion strains is described in Rorth P, Szabo K, Bailey A, Laverty T, Rehm J, Rubin GM, Weigmann K, Milan M, Benes V, Ansorge W, Cohen SM. 1998. Systematic gain-of-function genetics in Drosophila. Development 6:1049-1057.) The resultant fragment for each strain was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://fruitily.berkeley.edu/p_disrupt/inverse_por.html."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Butheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 31)

(hases 1 to 31)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Generation and analysis of 280,000 human expressed sequence tags Genome_Res. 6 (9), 807-828 (1996)
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Gaps: 0
Percent Identity: 100.000
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/db_xref="taxon:9606"
/clone="IMAGE:69913"
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Insert Size: 362
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Contact: Wilson RK
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Ratio: 2.250
Percent Similarity: 100.000
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US-08-653-294-1 x AQ025148
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AUTHORS
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MEDLINE
COMMENT
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KEYWORDS
SOURCE
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/clone_"md0435"
/clone_lib="Mouse 3'-directed"
/tissue_type="decidual tissue (day 6.5-8.5 of gestation)"
/ 7 c
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Kawamoto, S., Okubo, K., Yoshii, J., Katsuki, M. and Matsubara, K. Analysis of gene expression in mouse embryogenesis by 3'-directed cDNA sequencing Unpublished (1995).

On May 18, 1995 this sequence version replaced gi:811441.

Contact: Kawamoto, S., Okubo, K., Yoshii, J., Katsuki, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D18720 31 bp mRNA EST 12-DEC-1995 MUSGS01782 Mouse 3'-directed Mus musculus domesticus cDNA clone md0435 3', mRNA sequence.
                                                /lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Stratagene placenta (#937225)"
/sex="male"
                                                                                                                                                                                                                                                                                                 Length: 4
Gaps: 0
Percent Identity: 100.000
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Gaps: 0
Percent Identity: 100.000
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/strain="C57BL/6J"
/db_xref="taxon:10092"
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High quality sequence stop: 370.
Location/Qualifiers
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Mus musculus domesticus
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Ratio: 2.250
Percent Similarity: 100.000
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US-08-653-294-1 x D18720/rev
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Ratio: 2.250
Percent Similarity: 100.000
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SOURCE ORGANISM

REFERENCE AUTHORS

ACCESSION VERSION KEYWORDS TITLE JOURNAL COMMENT

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Tal: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be-
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jobe "Vector: pT713D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pooled bulk breast tumor tissue, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. This library is the normalized version of NCI_CGAP_BII.1. Library was constructed by Bento Soares and M. Fatina Bonaldo.
                                                                                                                                                                                                                                                                                      seq_documentation_block:

LOCUS A.1032352 31 bp mRNA EST 23-JUN-1998

DEFINITION OU486008.X1 NCI_CGAP_BT2 Homo sapiens CDNA clone IMAGE:1631055 3'

DEFINITION TR:062098 062098 PUTATIVE PRIMORDIAL PROTEIN TRANSCRIPT ', mRNA sequence.

ACCESSION A1032352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 31)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index

Jupublished (1997)

On Jun 19, 1998 this sequence version replaced gi:2151514.

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 4
Gaps: 0
Percent Identity: 100.000
                                                                                  to: 31
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Location/Qualifiers
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/sex="female, pooled"
/tissue_type="breast"
/lab_host="DH10B"

    .31
    /organism="Homo sapiens"

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/clone="IMAGE:1631055"
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                                                                               Align seg 1/1 to reverse of: AI021071
                                                                                                                                                                                                                                                                                                                                                                                                                                                AI032352.1 GI:3250564
alignment_block:
US-08-653-294-1 x AI021071/rev
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Ratio: 2.250
Percent Similarity: 100.000
                                                                                                                                                                                                                                    seq_name: gb_est22:AI032352
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US-08-653-294-1 x AI032352
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ORIGIN
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AUTHORS
TITLE
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                                                                                                                                                                                seg_documentation_block:
LOCUS ALO21071
DEFINITION u999f05.r1 Soares mouse mammary gland NbMMG Mus musculus CDNA clone IMAGE:1365633 5' similar to SW:PERL_RAT P43884 PERILIPIN A/B ;
                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 31)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The Washu-HHMI Mouse EST Project
Unpublished (1996)
Unpublished (1996)
Unpublished (1996)
Contact: Marsa M/Mouse EST Project
Washu-HHMI Mouse EST Project
Washington University School of MedicineP
H44 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
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/strain="c57BL/65"
/db_xrse="taxon:10090"
/clone="INAGE:1365633"
/clone_lib="Soares mouse mammary gland NDMMG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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Percent Identity: 100.000
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/dev_stage="4 weeks"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bonaldo.'
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Percent Similarity: 100.000
                                                                                                                              seq_name: gb_est22:AI021071
                                                                                                                                                                                                                                                                                        mRNA sequence.
AI021071
                                                 11 AGGTCGACTCTA 8
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FEATURES

BASE COUNT

ORIGIN

Align seg 1/1 to: AI032352 from: 1 to: 31

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February 8, 2000, 01:29:33 ; Search time 122.56 Seconds (without alignments) 1.933 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                      OM protein - protein search, using sw model
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Total number of hits satisfying chosen parameters:

188963

A_Geneseq_36:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		omogen	4	in N	ø	Protein tyrosine k	c	a14	PTK catalytic doma	Brain homing pepti	£	Growth hormone rel	PTK kinase domain	Peptide inhibiting	Hepatitis C virus	Hepatitis C virus	U	d art	PTK subdomain IV.	cel	mast cell	de s	t of hun	Peptide fragment (Peptide HER2/neu C	PYK1 subdomain TK6		_	Human leucocyte an	Truncated GHRH ana	Truncated GHRH ana	ce at antig	atelet g	Internal neurturin
	ΙΩ	R14267	P40822	W00248	R57725	W48376	W93209	R37709	R71101	W11186	W49919	W50983	W81413	X04013	R36108	R36109	R36110	R69855	R63089	W75839	W75808	W64270	Y00373	R59247	R80215	R89172	σ	R99915	W13412	W49303	W79626	W79610	4	ന	W13715
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	and	GOT H WHICE	TATE SERVICE S	1m1 10 4	anda: 92 06 f: c gr. dwar: prot. ens.
www.ww44444 www.ww4w www.ww4w www.www wwww	1 14267 14267;	O2-JAN-1992 Chromogenic Identificatid Synthetic. Key modified_site W09114787-A. 03-OCT-1991. 22-MAR-1991.	Dark of the control o	Query Match Best Local Si Matches 2: 7 LXXR	40822 st 40822; 3.4MG-19 equence ancreati ormone; omobolic omo sapi ey ey odified_
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TARRINGS TO SERVINGS THE SERVINGS TO SERVI
                                                                                                                                                                                                            18-MAR-1995 (first entry)
Rheumatoid arthritis-predictive factor.
Rheumatoid arthritis; dlagnosis; therapy; fibronectin; streptokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       claim 1; Page 54: 83pp; English.

The peptide corresponds to a common region/epitope shared by streptokinase (SK) and fibronectin that is recognized by anti-SK antibodies taken from rheumatoid arthritis (RA) patients. The peptide is used in the diagnosis of the onset/presence of RA, for monitoring the progress of therapy, or for therapy.

Sequence 6-AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein tyrosine kinase conserved peptide.
RAFTK; related adhesion focal tyrosine kinase; human; protein tyrosine kinase; PTK; cell growth; cell differentiation; cell adhesion; cell migration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diagnosis and treatment of rheumatoid arthritis - using a predictive factor peptide corresp. to a region common to fibronectin and streptokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52.9%; Score 9; DB 1; Length 6; 50.0%; Pred. No. 1.5e+05; 1ve 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                  WO941,***
04-AUG-1994, 001077, 27-JAN-1994, U01077, 3 27-JAN-1993; US-009471, A (TRIN-) TRINITY LAB INC.
A (UYDU-) UNIV DUKE.
A (UYDU-) UNIV DUKE.
A GONZALEZ-Gronow M, Pizzo SV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                    R57725 standard; peptide; 6 AA.
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Best Local Similarity 50.0
Matches 2; Conservative
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12-AUG-1997; U14093.
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2 LTAR 5
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                                                                                                                                                                                                                                                                                             peptide fragments
Claim 4: Page 67: 76pp: French.
Claim 4: Page 67: 76pp: French.
The inventors claim hipGRF fragments used for the synthesis of hpGRF.
Using the method somatocrinin can be obtd. on a large scale with
good yield and good purity. The prod. is used in man for the
treatment of dwarfism and retarded growth and for anabolic protein
deficiencies. In animals it is useful for promoting wt. growth for
increased prodn., lactation etc. This index is based on EP-122818,
which is the equivalent of AU8424774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A phage display system was used to screen 5-residue substrate
linkers for cleavage by subtilisin BNN N62D/G166D double mutant
(W00247). The library was subjected to 9 rounds of selection, and
clones that were increasingly sensitive or resistant to cleavage
were selected. Of 21 clones in the sensitive pool, 3 contained a
monobasic substrate linker sequence (W00248) contg. a hydrophobic
residue at P4; the remaining 18 were dibasic (see also W00249-53).
Of 10 substrates selected from the protease resistant pool (W00254-
63), 7 contained no basic sites, 2 were monobasic and 1 was dibasic.
The NGD/G166D double mutant specifically cleaves protein substrates
sequence 5 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-DEC-1996 (first entry)
Subtilisin N62D/G166D substrate peptide.
Subtilisin BPN'; protease; enzyme engineering; protein engineering;
Bacillus amyloliquefaciens; mutagenesis; substrate specificity;
phage display.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ballin, Wells JA;
WPI: 96-425431/42.
Subtilisin variants for cleaving substrates contg. basic residues
allow effective cleavage of fusion proteins with basic linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                          (SNFI ) SANNFI SA.
Diaz J, Demarne H, Roncucci R, Schmelck PH;
WPI; 84-256760/42.
Synthesis of hpGRf in liquid phase reactions - with use of new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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   /label- R-OH
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Best Local Similarity 50.0
Matches 2; Conservative
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                                                                                                                  21-FEB-1983; FR-002781.
29-NOV-1983; FR-019058.
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03-MAR-1995; US-398028.
19-JUL-1995; US-504265.
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WO9627671-A1.
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                                  AU8424774-A
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RESULT W00248

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Query Match

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Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Foliated nucleic acid molecules encoding vertebrate activin receptor polypeptides - useful as probes for detecting similar sequences and for investigating the function of the receptor in conditions such as carcinogenesis, wound healthing and disorders of the immune, central nervous and reproductive systems

Practinogenesis, wound healthing and disorders of the immune, central nervous and reproductive systems

Prample VIII; Column 35; 28pp; English

This sequence represents an activin receptor polypeptide predictive kinase domain motif. The nucleic acid molecules of the invention are useful as probes for the identification of additional members of the useful as probes for the recombinant expression of the receptor proteins, and the coding sequences can be used for the recombinant expression of the receptor proteins or functional fragments of them. They may also be used to study the function and activity of activin receptor polypeptides in cells and to identify agents which will modulate activin receptor expression and activity for use in treating conditions such as carcinogenesis, wound healing, use in treating conditions such as carcinogenesis, wound healing, reproductive system (where they may be used to control fertility in humans, domestic and commercial animals).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the function
                                                                                                                                                                                                                                                27-MAY 1999 (first entry)
Activin receptor predictive kinase domain #5.
Activin receptor; activin/TGF superfamily; receptor protein; function; activity; modulate; treatment; carcinogenesis; wound healing; fertility; immune system disorder; central nervous system disorder; kinase domain;
                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-529-1993 (first entry)
Deltal4 Serl7 hCNTF primer design peptide #2.
Human; ciliary neuronotrophic factor; hCNTF; intrinsic muscle; eye; choroid; ciliary body; iris; growth; chromaffin adrenal cell; ChAT;
focal tyrosine kinase (RAFTK), was assembled from 8 overlapping clones.
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                                                                                                   2; Indels
                                                                           52.9%; Score 9; DB 1; Length 6; 50.0%; Pred. No. 1.5e+05;
                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                               reproductive system.
Unidentified.
Unidentified.
US588794-A.
23-WAR-1994.
02-SEP-1994; 300584.
08-MAY-1991; US-698709.
09-CCT-1991; US-773229.
02-SEP-1994; US-300584.
Mathews LS, Vale WW;
WPI; 99-228534/19.
                                                                                                   ö
                                                                                                                                                                                                                       W93209 standard; Protein; 6 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 50.0.
                                                                          Query Match 52.9
Best Local Similarity 50.0
Matches 2; Conservative
                                     6 AA;
                                                                                                                             7 LXXR 10
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W93209
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Disclosure; Page 27; 66pp; English.

Disclosure; Page 27; 66pp; English.

This sequence was used in the design of a primer which was used in the production of a human ciliary neuronotrophic factor (hCNFS) analogue a lacking the N-terminal 14 amino acids and Cys17 replaced by Ser. This modification reduces the formation of CNFF dimers thereby maintaining biological activity. This primer contains a BglII site in the 5' end and the seventeenth codon is changed to TCT. The amplified sequence was ligated into plasmid pRSETB and transcribed. Wild-type CNFF enhances the survival and development of some sympathetic neurons, spinal neurons of cranial ganglia, motoneurons of the spinal cord and intipocampal neurons. It has been shown to influence the different. Attion of the progenitor glial cells known as 0-2A which differentiate in oligodendrocytes and astrocytes. Truncated forms of CNFF are useful a pharmaceutical composition, which may also comprise a natural of anguloside or derivative or a semisynthetic analogue. for treating nervous disorders. The truncated proteins maintain, prevent loss of correct near page of the provent and processed to the processed for the cover nearons. The truncated proteins maintain, prevent loss of correct nearous disorders.
chick; retinal cell; cholinergic neuron; pontine basal region; brain; cholinergic neurotrophic factor; sympathetic neuron; spinal neuron; cranial ganglia; mottoneuron; spinal cord; hippocampal neuron; 0-2h; differentiation; progenitor; gilal cell; oligodendrocyte; astrocyte; ganglioside; nervous disorders; PCR; amplify; primer; pT7.7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ological conditions caused by aging of the nervous system or diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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(WELL.) WELLCOME FOUND LTD.

Matchell PJ, Page MJ, Spence P;

Mitchell PJ, Page MJ, Spence P;

MPI: 95-06691/09.

MPI: 96-0691/09.

MPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-AUG-1995 (first entry)
PTK catalytic domain conserved region.
Protein-tyrosine-Kinase; PTK; discoidin domain receptor; cancer;
breast tumor; mamma carcinoma; diagnosis; prognosis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Truncated and/or mutein human ciliary neuronotrophic factor - useful for treating neuro:pathological disorders due to loss of nervous function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.9%; Score 9; DB 1; Length 7; 50.0%; Pred. No. 1.5e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R71101 standard; Peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-MAY-1993.
11-NOV-1992; E02586.
11-NOV-1991; IT-PD0207.
20-MAY-1992; IT-PD0087.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JAN-1995.
08-JUL-1994; G01480.
09-JUL-1993; GB-014271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (FIDI-) FIDIA SPA.
Callegaro L, Negro A;
WPI; 93-182549/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity Matches 2; Conserv
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RESULT W11186

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Query Match
Best Local Similarity 50.0°,
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12-OCT-1988; 579916.
12-OCT-1988; CA-579916.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 98-207809/19.
                                                                                                                                                                                                                                                                                                                                                                                                           7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified_site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 LXXR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CA1339631-C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gauthier J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 LAAR
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                  proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
W50983
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vivo panning method, specifically to identify brain, kidney, angiogenic vasculature or timour tissue homing peptide(s).

This synthetic peptide is an example of a brain-homing peptide (s) pisclosure; page 45; 75pp; English.

This synthetic peptide is an example of a brain-homing peptide that was identified using a claimed method for obtaining molecules that home to a selected organ or tissue. This in vivo panning method typically involves administering a phage display companing method typically involves administering a phage display involves administering a phage display in vivo as the factor of the desired organ or tissue. The isolated peptides which home to the desired organ or tissue. The isolated peptides (see this solate tasget or tumour tissue. The isolated peptides (see this solate target molecules (claimed) or to identify and/or isolate target molecules (claimed). The peptides can be directly methods, which require further examination to see if they maintain specificity in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                      Gaps
identified in an isolated subclone. The 3' sequence of PTK22 was obtained by reverse transcription (using the primer of 084786) and PCR amplification (primers Q84787-88) of RNA of human breast carcinoma cell line MDA MG 468. The partial DNA sequence of PTK22 is given in Q84782.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JUL-1998 (first entry)
CLK serine/threonine kinase consensus peptide.
CLK serine/threonine kinase; protein kianse; mCLK1; mCLK2; mCLK3;
SMCLK4; mouse; signal transduction.
Synthetic.
W09748723-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Obtaining compound that homes to selected organ or tissue - by in
                                                                                                                                                                                                                                                                                                                                    Brain homing peptide.
Brain homing peptide; in vivo panning; screening; phage display;
                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                    2; Indels
                                                                                                                      Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 9; DB 1; Length 7; Pred. No. 1.5e+05;
                                                                                                                      DB 1; Le
1.5e+05;
                                                                                                                      Score 9; DB 1
Pred. No. 1.5e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      10-SEP-1996; U14600.
11-SEP-1995; US-526710.
11-SEP-1995; US-526708.
(LJOL-) LA JOLLA CANCER RES FOUND.
Pasqualini R, Ruoslahti E;
WPI; 97-202359/18.
                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                        W11186 standard; Peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W49919 standard; Peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.9%;
50.0%;
                                                                                                                      52.9%;
50.0%;
                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Conservative
                                                                                                                      Query Match
Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                  drug delivery.
Synthetic.
WO9710507-A1.
                                                                                                                                                                                 LXXR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 LXXR 10
                                                                                                                                                                                                                                                                                                                      15-JAN-1998
                                                                                                                                                                                                               3 LAAR 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LSSR 4
                                                                                                                                                                                                                                                                                                                                                                                                              20-MAR-1997
                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W49919;
                                                                                                                                                                                                                                                                                                       W11186;
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Preparation of human growth hormone releasing factor (hGRF) fragment by assembling blocks of a few amino acids each on separate resins, cleaving, coupling, and deprotecting; is adaptable to scale up claim 1; Page 22: 25pp; English.

The invention relates to an improved process for preparing an active fragment of human growth hormone releasing factor (hGRF). The invention relates to an efficient process for preparing the amidated fragment of hGRF containing the first 29 amino acids of the N-terminal portion and comprises assembling blocks of a few amino acids each on separate
24-DEC-1997, 1B0946.

28 17-JUN-1997; 1B0946.

29 17-JUN-1997; 1B0946.

20 2034286.

30 9-AUG-1996; US-0034886.

31 7-JUN-1996; US-0130629.

31 17-JUN-1996; US-0130640.

32 18-NOV-1996; US-0130860.

33 15-NOV-1996; US-0130860.

34 Noki N, Chen Z, Kharitonenkov AI, Kim YW, Nayler O, Ullrich A, Wang HY;

35 WPI: 98-120302/11.

36 WPI: 98-120302/11.

37 Treatment of signal transduction disorders

38 Example 8; Page 88; 138pp; English.

39 Treatment of signal transduction disorders

30 Example 8; Page 88; 138pp; English.

30 This is a consensus sequence derived from known CLK

30 Example 8; Page 88; 138pp; English.

31 Treatment of signal transduction disorders

32 Example 8; Page 88; 138pp; English.

33 Example 8; Page 88; 138pp; English.

34 Consensus peptide (see W49910) were used in the RT-PCR

35 another consensus peptide (see W49910) were used in the RT-PCR

36 another consensus peptide (see W49910-14) from a mouse embryo 11.5 p.c. 12AP cDNA library.

33 Example 8; Page 88; Probes 80;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Growth hormone releasing factor peptide fragment intermediate.
Growth hormone releasing factor; GRF; synthesis; intermediate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.9%; Score 9; DB 1; Length 7; 50.0%; Pred. No. 1.5e+05; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Alpha-amino protecting group'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note "Side-chain protecting group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note- "Side-chain protecting group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Side-chain protecting group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BOEH ) BOEHRINGER INGELHEIM CANADA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W50983 standard; pept1de; 7 AA. W50983;
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RESULT 12

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Abajian HB. Hlawka JJ. Kende AS, Noble JF, Pincus MR;

WPI; 97-202613/18

The prides, cyclised peptides and peptidomimetics - for use in peptides, cyclised peptides, cyclised pertides are considered action of p21 ras protein

Claim 1; Page 93; 100pp; English.

Claim 1; Page 93; 100pp; English.

Claim 1; Page 93; 100pp; English.

Capable of inhibiting the oncogenic action of p21 ras. They may be used in the treatment of adenocarcinomas of the colon, pancreatic carcinomas, neuroblastomas and other cancers of undefined germ cell carcinomas, neuroblastomas and other cancers of undefined germ cell cargin. The cyclised peptides correspond to domains of the oncogenic ras protein which are most flaxible and important in interacting with target proteins upstream and downstream from ras. The peptidomimetics are obtained by molecular modelling. The present sequence represents sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example A; Page 38; 80pp; English.

This octamer was found to be immunoreactive with anti-HCV anti-sera.

In the epitope mapping experiment three different samples of anti-sera were reacted with the peptide octamer, and then incubated with HRP-labelled goat anti-human Ig antisera, to enable detection of binding. This epitope starts from amino acid 2345 of the HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus (HCV) epitope Ep36.
Hepatitis: liver disease; HCV1; monoclonal antibody; epitope;
immobilised reagent; immunoassay; diagnosis; detection; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polypeptide(s) comprising truncated hepatitis C virus sequences for detection, prevention and treatment of hepatitis C infection
             pancreatic carcinoma;
antitumour; anticancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Le...
n. 1.5e+05;
2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 9; DB 1; LA
Pred. No. 1.5e+05;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 9; DB 1;
Pred. No. 1.5e+
0; Mismatches
          p21 ras; adenocarcinoma; colon cancer;
neuroblastoma; oncogenesis inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This was found to be a strong epitope. Sequence 8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52.9%; Scu.
50.0%; Pred
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R36108 standard; protein; 8 AA.
R36108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 52.9%;
Best Local Similarity 50.0%;
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-MAY-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 52.9
Best Local Similarity 50.0
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus type 1. W09300365-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JAN-1993.
24-JUN-1992; U05388.
24-JUN-1991; US-722489.
(CHIR) CHIRON CORP.
                                                                                                                                                                                         20-SEP-1996; U15098.
21-SEP-1995; US-531525.
21-SEP-1995; US-004091.
                                                                                                                                                                                                                                                                                                             (INNA-) INNAPHARMA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rutter W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chien DY, Rutter w
WPI; 93-036334/04.
                                                                                                          Homo sapiens.
WO9710836-A1.
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Sequences W81413 to W81415 represent peptides flanking a highly conserved tegion of the Kniase domain of receptor protein tyrosine kinase (PTK).

These are used for designing primers to amplify PTK related sequences.

The invention provides sequences v65308 to v65313, v65315, and v65317 to v65319 that encode proteins having a tyrosine kinase domain and a tissue expression pattern of a receptor PTK subtype selected from tyro-1, tyro-3, tyro-4, tyro-5, tyro-6, tyro-10, tyro-10, tyro-11, and tyro-12, respectively. The polynucleotides are useful for the detection of tyrosine kinase domain sequences and detection of tissue expression patterns of PTK subtypes. The polynucleotides are useful for the detection of tyrosine kinase domain sequences and detection of tissue expression patterns of PTK subtypes. The colvas can also be injected into cocytes, the protein expressed, and expression products screened for using antibodies against tyrosine kinase epitopes. These subtypes sequences can be used for the design of oligonucleotides, for use in amplification are used in the diagnosis of diseases associated with (receptor) PTKs.

Recombinant vectors expressing the subtypes can be used to treat related diseases e.g. tumours, by introduction of the vectors into skin transplants, thus specifically targetting tumours as the proteins are released from the matrix.
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02-MAY-1994: 237401.
15-MAY-1994: US-284486.
15-MAY-1994: US-237401.
(SALK ) SALK INST BIOLOGICAL STUDIES.
Lai CHC, Lanke GE.
MWPI: 99-023436/02.
Nucleic acids encoding protein tyrosine kinase sub:types - for
                                                                                                                                                                                                                                            Gaps
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resins, cleaving, coupling, and deprotecting. The present sequence represents a specifically claimed intermediate of the process. Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTK kinase domain conserved region flanking peptide sequence 1. PTK; receptor; protein tyrosine kinase; recombinant; grafting; diagnosis; tumour; skin transplant; connective tissue.
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Peptide inhibiting the oncogenic action of p21 ras.
                                                                                                                                                             52.9%; Score 9; DB 1; Le
50.0%; Pred. No. 1.5e+05;
ive 0; Mismatches 2;
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Pred. No. 1.5e4
0; Mismatches
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Best Local Similarity 50.0
Matches 2; Conservative
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Indels Length 8; 7

> RESULT 13 X04013

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AC MANY-1993 (first entry)

E Hepatitis C virus (HCV) epitope.

Hepatitis C virus (HCV) epitope.

WHE Hepatitis C virus (HCV) epitope.

WHE Hepatitis C virus type 1.

WHE HEPATITIS C virus type 1.

WHE HEPATITIS C virus type 1.

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                                                                       R36109 standard; protein; 8 AA.
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RESULT 15
R36109
ID R36109
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Search completed: February 8, 2000, 01:29:34 Job time: 1746 sec

2 LASR 5

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

sw model - protein search, using OM protein Run on:

February 7, 2000, 11:54:09; Search time 117.7 Seconds (without alignments) 4.008 Million cell updates/sec

US-08-653-294-2

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 XXXXXXLXXR 10 Title: Perfect score: Sequence: Scoring table:

142080 segs, 47169319 residues Searched:

142080 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description			S-locus specific g	or integral me	lass II	Ig kappa chain V r	ectrin -	ycf12 protein - Ch		₽		cytotoxic T-lympho	٠ĭ	hypothetical prote	lysis protein t -	ferritin heavy cha	hypothetical prote	О	hypothetical prote	hemoglobin gamma-G	ma	somatoliberin - pi	å		l pro	ď	c	hypothetical prote	tical	sdu	calpain I - rat (f
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histone H2A.X - human (fragment)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: Ol.Nov-1996 #sequence_revision 01-Nov-1996 #text_change 28-Feb-1997
C; Accession: 155411
R; Ivanova, V.S.; Hatch, C.L.; Bonner, W.M.
J; Biol. Chem. 2569 24189-24194, 1994
A; Title: Characterization of the human histone H2A.X gene. Comparison of its promoter A; Reference number: 155411; MUID: 95014156
A; Accession: 155411
A; Molecule type: DNA
A; Residues: 1-8 <RES>
A; Accessives: 1-8 <RES>
C; Genetics: A; Cross: referenced: GB:S73863; NID: 9765295
C; Genetics: A; Gene: H2A.X

Gaps ö 2; Indels 52.9%; Score 9; DB 2; Length 8; 50.0%; Pred. No. 1.4e+05; 1ve 0; Mismatches 2; Indel. Query Match 52.9 Best Local Similarity 50.0 Matches 2; Conservative

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7 LXXR 10 3 LAAR 6 ò g

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5-Jocus specific glycoprotein (allele S2) - wild cabbage (fragment)
C;Species: Brassica oleracea (wild cabbage)
C;Saccession: E56661
R;Caude, T.; Denoroy, L.; Dumas, C.
Electrophoresis 12, 646-653, 1991
A;Title: Use of a fast protein electrophoretic purification procedure for N-terminal A;Reference number: A56661; MUID:92090397
A;Reference number: A56661; MUID:92090397
A;Reference type: protein
A;Residues: 1-19 cGaUc
A;Residues: 1-10 cGaU

Gaps ; 0 Query Match
52.9%; Score 9; DB 2; Length 19;
Best Local Similarity 50.0%; Pred. No. 3.6e+02;
Matches 2; Conservative 0; Mismatches 2; Indels

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R;Khrebtukova, I.; Spreitzer, R.J.
submitted to the EMBL Data Library, November 1995
A;Reference number: 216296
A;Accession: 108018
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A, Genome: chloroplast
C, Keywords: chloroplast
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MHC class II histocompatibility antigen HLA-DR beta-3 - human (fragment)
C;Species: Homo saplens (man)
C;Species: 137301; 137302

R;Louis, P: Eliaou, J.F.; Kerlan-Candon, S.; Pinet, V.; Vincent, R.; Clot, J.
Immunogenetics 38, 21-26, 1993
A;Title: Polymorphism in the regulatory region of HLA-DRB genes correlating with haploty
A;Reference number: 137301
A;Reference number: 137301
A;Reference number: 137301
A;Retus: preliminary: translated from GB/EMBL/DDBJ
A;Retus: preliminary: translated from GB/EMBL/DDBJ
A;Retus: preliminary: translated from GB/EMBL/DDBJ
A;Rotes: preliminary: translated from GB/EMBL/DDBJ
A;Retus: preliminary: transla
                                                                                                                                                RESULT 3
S21285
S21285
Mis musculus (house mouse)
C:Species: Mis musculus (house mouse)
C:Accession: S12185
R:Chacession: S21285
R:Chem. V.; Crane, D.I.
Biochem. J. 283, 605-610, 1992
A:Title: Induction of the major integral membrane protein of mouse liver peroxisomes by A:Reference number: S21285
A:Accession: S21285
A:Acces
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PH0882
IG kappa chain V region (REN) - human (fragment)
IS kappa chain V region (REN) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0882
C;Accession: PH0882
A; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B. J. Exp. Med. 174, 1639-1652, 1991
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3.6e+02;
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Pred. No.
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50.0%;
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4 LSSR 7
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A,Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiot A,Reference number: PH0862; MUID:92078875
A;Accession: PH0882
A;Molecule type: protein
A;Residues: 1-30 <MAN> calelectrin - marbled electric ray (fragments)
C;Species: Torpedo marmorata (marbled electric ray)
C;Species: Torpedo marmorata (marbled electric ray)
C;Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 18-Jun-1993
C;Accession: C26393
R;Geisow, M.J.; Fritsche, U.; Hexham, J.M.; Dash, B.; Johnson, T.
Nature 320, 636-638, 1986
A;Title: A consensus amino-acid sequence repeat in Torpedo and mammalian Ca(2)+-depen A;Reference number: A3379; MUID:86203621 ö ö ö ycf12 protein - Chlamydomonas reinhardtii chloroplast C;Species: chloroplast Chlamydomonas reinhardtii C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 21-May-1999 Gaps Gaps Gaps ; 0 ; 0 ö C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin E;1-23/Region: framework 1 F;24-30/Region: complementarity-determining 1 Score 9; DB 2; Length 30; Pred. No. 5.8e+02; 0; Mismatches 2; Indels Score 9; DB 2; Length 32; Pred. No. 6.2e+02; 0; Mismatches 2; Indels Indels Length 33; A;Cross-references: EMBL:U40346; NID:g1101912; PID:g1101913 Score 9; DB 2; Len Pred. No. 6.4e+02; 0; Mismatches 2; A:Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-33 <KHR>

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- Charles Annual

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Oytotoxic T-lymphocyte-associated protein 4 - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Data                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complement factor H - mouse (fragment)
C)Species: Mus musculus (house mouse)
C)Species: Mus musculus (house mouse)
C)Accession: 15272
R)Vik, D.P.; Keeney, J.B.; Munoz-Canoves, P.; Chaplin, D.D.; Tack, B.F.
R;Vik, D.P.; Keeney, J.S.; Munoz-Canoves, P.; Chaplin, D.D.; Tack, B.F.
A;Title: Structure of the murine complement factor H gene.
A;Reference number: 155272; MJID:89034160
A;Accession: 155272
A;Molecule type: DNA
A;Residues: 1.37 RES>
A;Molecule type: Chaple (from GB/EMBL/DDBJ)
A;Coss-references: GB:M23553; NID:9340946; PIDN:AAA39530.1; PID:9554202
C;Superfamily: complement factor H; complement factor H repeat homology
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C;Species: chloroplast Chlorella vulgaris
C;Date: 14-May-1999 *sequence_revision 14-May-1999 *text_change 22-Jun-1999
C;Accession: T07292
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                                                                                                                                                                             Length 34;
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                                                                                                                                                                         52.9%; Score 9; DB 2; L
50.0%; Pred. No. 6.6e+02;
11ve 0; Mismatches 2
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A;Residues: 1-34 <MON>
C;Superfamily: phage T4 lysis protein t
C;Keywords: host cell lysis
                                                                                                                                                                     Query Match
Best Local Similarity 50.03
Matches 2; Conservative
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Best Local Similarity 50.0
Matches 2; Conservative
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A; Residues: 1-36 <RES>
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C;Species: phage M1
C;Species: phage M1
C;Species: phage M1
C;Species: phage M1
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 16-Dec-1996
C;Accession: PS0065 I.; Eschbach, M.L.; Degen, M.; Henning, U.
J. Mol. Biol. 196, 165-174, 1987
A;Title: Receptor-recognizing proteins of T-even type bacteriophages. Constant and hyper A;Reference number: A94692; MUID:88011316
A;Reference phage: DNA
A;Molecule type: DNA
"ypuchetical protein 33 - liverwort (Marchantia polymorpha) chloroplast
C; Species: chloroplast Marchantia polymorpha
C; Date: 05-50un-1987 #sequence_revision 05-Jun-1987 #text_change 31-Oct-1997
C; Accession: S01581, A05010
R; Umesono, K.; Inokuchi, H.; Shiki, Y.; Takeuchi, M.; Chang, Z.; Fukuzawa, H.; Kohchi, T. J. Mol. Biol. 203, 299-331, 1988
A; Title: Structure and organization of Marchantia polymorpha chloroplast genome. II. Gen A; Reference number: S01567; MUD:89068686
A; Moleonia S01581
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R.Chyama, K.: Fikuzawa, H.: Kohchi, T.: Shirai, H.: Sano, T.: Sano, S.; Umesono, K.: Shi Mature 322, 572-574, 1986
A;Title: Chloroplast gene organization deduced from complete sequence of liverwort March A;Reference number: A38014
A;Contents: annotation; gene organization, sites, features
C;Genetics: A;Genome: chloroplast
C;Keywords: chloroplast
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5. 6.4e+02; Indels
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Pred. No. 6.6e+02;
0; Mismatches 2; Indels
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A;Genome: plasmid
C;Superfamily: streptomycin 3''-adenylyltransferase
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50.0%;
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Best Local Similarity 50.v.
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A; Residues: 1-33 <UME>
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A; Residues: 1-34 <STO>
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R;Wakasugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; Ito, S.; Tsudzuki, J.; Nakas Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997
A:Title: Complete nucleotide sequence of the chloroplast genome from the green alga Chld A;Reference number: 215985; MUID:97303241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Montag, D.; Riede, I.; Eschbach, M.L.; Degen, M.; Henning, U.
J. Mol. Biol. 196, 165-174, 1987
J. Mol. Biol. 196, 165-174, 1987
J. Mol. Biol. 196, 165-174, 1987
A;Title: Receptor: recognizing proteins of T-even type bacteriophages. Constant and hyper A;Reference number: A94692; MUID:88011316
A;Accession: PS0063
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C;Species: Absidia spinosa (itaywent)
C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 07-May-1999
C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 07-May-1999
C;Accession: 570494
R;Carrano C, J; Boehnke, R; Matzanke, B.F.
FEBS Lett. 390, 261-264, 1996
A;Title: Fungal ferritins: the ferritin from mycelia of Absidia spinosa is a bacteriofer A;Reference number: 570494; MUID:96311417
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Species: phage Ox2
Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 20-Sep-1999
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A;Residues: 1-39 <MON>
A;Residues: 1-39 <MON>
A;Cross-references: GS.705675; NID:g15124; PIDN:CAA29159.1; PID:g15127
C;Superfamily: phage T4 lysis protein t
C;Keywords: host cell lysis
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Pred. No. 7.2e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                             A; Cross-references: EMBL: AB001684; NID: d1110444; PID: d1021518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 9; DB 2; Length 39;
Pred. No. 7.6e+02;
0; Mismatches 2; Indels
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                                                                                                                                          A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-37 <WAK>
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A.Residues: 1-40 <CAR>
A.Experimental source: strain Tue268
C.Superfamily: bacterioferritin
C.Keywords: heme; iron storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52.9%;
50.0%;
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Best Local Similarity 50.0%;
Matches 2; Conservative
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Best Local Similarity 50.0
Matches 2; Conservative
                                                                                                                                                                                                                                                                                  A;Gene: ycf12
A;Genome: chloroplast
C;Keywords: chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: PS0063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 LXXR 10
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19 LAAR 22

Search completed: February 7, 2000, 11:54:11 Job time: 24321 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

February 8, 2000, 00:59:40 ; Search time 63.71 Seconds
(without alignments)
4.688 Million cell updates/sec Run on:

US-08-653-294-2 17 1 XXXXXLXXR 10 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

82229 seqs, 29864866 residues Searched:

82229 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

SwissProt_38:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		P50370 chlamydomon					pos	s sns	P07217 ovis aries	P21153 micrococcus				_		Q37871 bacteriopha				_		budg					_	P05998 bacteriopha	P13967 escherichia	1		50 arab)	11	6291 lycor	5
11		YC12_CHLRE	YC12_MARPO	VLYS_BPM1	YC12_CHLVU	VLYS_BPOX2	SLIB_BOVIN	SLIB_PIG	SLIB_SHEEP	RL34_MICLU	RL34_STRCO	SLIB_CYPCA	CCMC_RHILV	VG62_BPML5	VO7K_FXMV	NINE_BP82	NINE_ECOLI	V193_BPT7	SASO_CLOPE	SAS2_CLOPE	HBX4_ECHGR	DNBI_BFDV	UCRX_BOVIN	VX2A_CVPFS	YORQ_TTV1	BVCP_NPVBM	SAS2_CLOBI	VXIS_BPPH8	KED2_ECOLI	Y7KD_STRLI	H6_ONCMY	RL38_ARATH	RL38_HUMAN	RL38_LYCES	Y4ON_RHISN
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TRY5_ECOLI VIP_CAVPO	VP13_BPPH6 CXO6_CONGE ABL_CALVI	Y059_TREPA Y13H_BPT4 RS20_CAUCR	YQFE_ECOLI YFL2_BACLI Y65_BPT3
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ALIGNMENTS

PUTCH 1 10.2CHERE STANDARD; PRT; 33 AA. PUTCH 200370; 10COT1996 (Rel. 34, Created) 10COT1996 (Rel. 34, Last sequence update) 11UUL-1996 (Rel. 34, Last sequence update) 11UUL-1998 (Rel. 34, Last sequence update) 11UUL-1998 (Rel. 35, Last sequence update) 11UUL-1998 (Rel. 36, Last sequence update) 11UUL-1998 (Rel. 36, Last sequence update) 11UUL-1998 (Rel. 37, PROTEIN VCF12. Chlamydomonas reinhardtii. SEQUENCE FROM N.A. STRAIN-2177 STRAIN-2177 STRAIN-2177 STRAIN-2177 (In) Plant genes of the chlorophyta; Chlorophyceae; Volvocales; Chlamydomonas reinhardtii. (In) Plant genes of the chlorophyta; Chlorophyceae; Volvocales; SEQUENCE FROM N.A. STRAIN-2177 STRAIN-2177 (In) Plant genes of the chlorophyta; Chlorophyceae; Volvocales; (In) Plant genes Sequences of the chlorophast trnS-GCU and ycf12 genes of Chlamydomonas reinhardtii. (In) Plant genes Register Persy-177 (In) Plant genes Register Reg
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Gaps

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2; Indels Length 34;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chloroplast.
Eukaryota: Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 9; DB 1; Length 3/;
Pred. No. 3.36+02;
                                                                                                                                  DB 1;
3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
01-AUG-1988 (Rel. 08, Last annotation update)
LYSIS PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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                                                                           E8C6763A CRC32
                                                                                                                                  Score 9; DB 1
Pred. No. 3e+0;
0; Mismatches
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15-JUL-1998 (Rel. 36, Last sequ
15-JUL-1998 (Rel. 36, Last anno
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50.0%;
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34 AA; 3694 MW;
EMBL; X05676; CAA29162.1; PIR; PS0065; PS0065.
Phage lysis protein.
NON IER 34 AA; 3694 MW;
                                                                                                                                                      Local Similarity 50.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chlorellaceae; Chiorella
                                                                                                                                                                                                                                                                                                                                               STANDARD;
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es 2; Conserv
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AC VLYS_BPOX2
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DT 01-AUG-1988
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DE LYSIS PROTEI
GN T.
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P56328;
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Best Local 8
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                                                                       FUCUSAMA H., KOHCHI T., SANO T., SHIRAI H., UMESONO K., INOKUCHI H., OZEKI H., OHYAMA K.;
"Structure and organization of Marchantia polymorpha chloroplast genome. III. Gene organization of the large single copy region from the to trnI(CAU).";
J. Mol. Biol. 203:333-351(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                              COMPLETE GENOME.
OHYAMA K., FUKUZAWA H., KOHCHI T., SHIRAI H., SANO T., SANO S.,
UMESONO K., SHIKI Y., TAKEUCHI M., CHANG Z., AOTA S., INOKUCHI H.,
                                                                                                                                                                                                                                                                                   "Chloropiast gene organization deduced from complete sequence of liverwort Marchantia polymorpha chloroplast DNA."; Nature 322:572-574(1986).
-i- SIMILARITY: BELONGS TO THE YCF12 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteriophage M1.
Viruses; dSDNA viruses, no RNA stage; Tailed phages; Myoviridae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 9; DB 1; Length 33;
Pred. No. 2.9e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
01-MAR-1989 (Rel. 10, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A05010; A05010.
PIR; S01581; S01581.
MENDEL; 5293; MARPO; ycf12;1.
SEQUENCE 33 AA; 3386 MW; A80804E5 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 AA.
   Marchantiales; Marchantiaceae; Marchantia
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50.0%;
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Best Local Similarity
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                                       SEQUENCE FROM N.A
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                                                           89068687
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P07217;
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SLIB_SHEEP
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-!- FUNCTION: GRF IS RELEASED BY THE HYPOTHALAMUS AND ACTS ON THE ADENOHYPOPHYSE TO STIMULATE THE SECRETION OF GROWTH HORMONE.
-!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 84127993.
ESCH F., BOHLEN P., LING N., BRAZEAU P., GUILLEMIN R.;
"Isolation and characterization of the bovine hypothalamic growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine), and Capra hircus (Goat).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Mammalia:
Eutheria: Cetartiodactyla: Ruminantia: Pecora: Bovoidea: Bovidae;
                    dsDNA viruses, no RNA stage; Tailed phages; Myoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                           MONTAG D., RIEDE I., ESCHBACH M.-L., DEGEN M., HENNING U., "Receptor-recognizing proteins of T-even type bacteriophages. Constant and hypervariable regions and an unusual case of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
SOMATOLIBERIN (GROWTH HORMONE-RELEASING FACTOR) (GRF) (GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 9; DB 1; Length 39;
Pred. No. 3.5e+02;
); Mismatches 2; Indels
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GUILLEMIN R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hormone releasing factor.";
Biochem. Biophys. Res. Commun. 117:772-779(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 39 39 39 39 39 AA; 4176 MW; B96B98A6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HORMONE-RELEASING HORMONE) (GHRH)
                                                                                                                                                                                                                    J. Mol. Biol. 196:165-174(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A01554; RHBOS.
PROSITE; PS00260; GLUCAGON; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52.9%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X05675; CAA29159.1; -. PIR; PS0063; PS0063. PNON TER 39 AA; 4176 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM; PF00123; hormone2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 2; Conserv
                                                                                    SEQUENCE FROM N.A. MEDLINE; 88011316.
  Bacteriophage Ox2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES=C.HIRCUS;
MEDLINE; 85096956
                      Viruses; dsDNA v
T4-like phages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES=BOVINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LXXR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31 LASR 34
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P01288;
                                                                                                                                                                                               evolution.
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                                                                                                                                                                                                                                                                                                                                      Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
Caprinae; Ovis.
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21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 34, Last annotation update)
SOMATOLIBERIN (GROWTH HORMONE-RELEASING FACTOR) (GRF) (GROWTH HORMONE-RELEASING FACTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
SOMATOLIBERIN (GROWTH HORNONE-RELEASING FACTOR) (GRF) (GROWTH HORNONE-RELEASING FACTOR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                    Length 44;
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                                                                                                                                                                                                                                    DB 1;
4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.9%; Score 9; DB 1; 50.0%; Pred. No. 4e+02;
                                                            AMIDATION.
9FA0D0EE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMIDATION.
B75EF294 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44 AA
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                                                                                                                                                                                                                                                                                                                             Mismatches
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Glucagon family; Amidation; Hypothalamus.
MOD_RES 44 44 ANIDATION.
SEQUENCE 44 AA; 5109 MW; 9FAODOEE CRC?
                                                                                                                                                                                                                                         Score 9;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                    52.9%;
ilarity 50.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 52.9
Best Local Similarity 50.0
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=HYPOTHALAMUS;
MEDLINE; 84079886.
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us-08-653-294-2.rsp

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                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 92250416.
CALCUTM N.J., SCHMIDT F.J.;
CALCUTM N.J., SCHMIDT F.J.;
"Conserved gene arrangement in the origin region of the Streptomyces coelicolor chromosome.";
J. Bacteriol. 174:3220-33226(1992).
-: SIMILARITY: BELONGS TO THE L34P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-HYPOTHALAMUS;
MEDLINE; 93116845.
VAUGHAN J.M., RIVIER J., SPIESS J., PENG C., CHANG J.P., PETER R.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cyprinus carpio (Common Carp).
Bukaryota, Metazoa, Chordata Craniata; Vertebrata; Actinopterygli;
Neopterygli; Teleostel; Euteleostel; Ostariophysi; Cypriniformes;
Cyprinoidea; Cyprinidae; Cyprininae; Cyprinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Isolation and characterization of hypothalamic growth-hormone releasing factor from common carp, Cyprinus carpio.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
01-NOV-1995 (Rel. 32, Last annotation update)
SOMATOLIBERIN (GROWTH HORMONE-RELEASING FACTOR) (GRF) (GROWTH HORMONE-RELEASING HORMONE) (GHRH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Le
                                                                                             Last sequence update)
Last annotation update)
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           45 AA
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M82836; AAA26733.1; -. PROSITE; PS00784; RIBOSOWAL_L34; 1. PFAM; PF00468; Ribosomal_L34; 1. Ribosomal protein.
           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                   Created)
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50.0%;
                                                                                                                                      50S RIBOSOMAL PROTEIN L34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                            Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45 AA;
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 LXXR 10
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                                                                01-AUG-1992
                                                                                             01-AUG-1992
01-DEC-1992
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P42692;
        RL34_STRCO
P27901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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SEQUENCE FROM N.A.
MEDLINE; 91033019.
FUJITA M.O., YOSHIKAWA H., OGASAWARA N.;
FUJITA M.O., YOSHIKAWA H., OGASAWARA N.;
"Structure of the dnaA region of Micrococcus luteus: conservation and
"Structure of the dnaA region of Micrococcus luteus:
                                                                                             Growth hormone-releasing factor from ovine and caprine hypothalamus:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                              isolation, sequence analysis and total synthesis."
Biochem. Blophys. Res. Commun. 125:606-614(1984).
-!-FUNCTION: GRE IS RELEASED BY THE HYPOTHALAMUS AND ACTS ON THE ADENOHYPOPHYSE TO STIMULATE THE SECRETION OF GROWTH HORMONE.
-!-SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
PROSITE; PSO0260; GLUCAGON; 1.
PRAM: PF00123; hormone2; 1.
Glucagon family; Amidation; Hypothalamus.
MOD_RES 44 Amidation.
SEQUENCE 44 AA; 5123 MW; D97898C6 CRC32;
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Actinomycetales; Micrococcineae; Micrococcaceae; Micrococcus.
MEDLINE; 85086956.
BRAZEAU P., BOHLEN P., ESCH F., LING N., WEHRENBERG W.B.,
GUILLEMIN R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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50.0%; Pred. No. 4.1e+02;
Atematches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Micrococcus luteus (Micrococcus lysodeikticus).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
50S RIBOSOWAL PROTEIN L34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 9; DB 1;
Pred. No. 4e+02
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5309 MW; 46A593A0 CRC32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 52.9
Best Local Similarity 50.0
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Best Local Similarity
Matches 2; Conserv
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SEQUENCE 45 AA;
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RESULT 10 RL34_STRCO

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Length 45; 2; Indels us-08-653-294-2.rsp

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                                                           HATFULL G.F., SARKIS G.J.;
"DNA sequence, structure and gene expression of mycobacteriophage L5:
a phage system for mycobacterial genetics.";
Mol. Microbiol. 7:395-405(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-MAY-1992 (Rel. 22, Last annotation update)
7 KD PROTEIN (ORF 4).
                                                                                                                                                                                                                                                                                                                                                                                       DE68F8AC CRC32;
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50.0%;
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SEQUENCE FROM N.A.
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P22171;
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-!- FUNCTION: REQUIRED FOR THE EXPORT OF HEME TO THE PERIPLASM FOR THE BIOGRAESIS OF C-TYPE CYTOCHROMES.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE (PROBABLE).
                                                                                    Gaps
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
HEME EXPORTER PROTEIN C (CYTOCHROME C-TYPE BIOGENESIS PROTEIN CYCZ)
                                                                                                                                                                                                                                                                                                                                                                                                                             Rhizobium leguminosarum (biovar viciae).
Bacteria: Proteobacteria: alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARGAS C., WU G., DAVIES A., DOWNIE J.A.;
"Identification of a gene encoding a thioredoxin-like product
necessary for cytochrome c biosynthesis and symbiotic nitrogen
fixation in Rhizobium leguminosarum.";
                          DB 1; Leny...
5. 4.1e+02; 1ndels
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Pred. No. 4.5e+02;
); Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, X79307; CAA55886.1; -.
Cytochrome c-type biogenesis; Transport; Transmembrane;

    -!- SIMILARITY: BELONGS TO THE CCMC/CYCZ/HELC FAMILY.

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01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
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                                          Score 9; DB 1
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50.0%;
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                                          Query Match 52.9
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Matches 2; Conservative
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Viruses.
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CCMC_RHILV
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Foxtail mosaic virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Potexvirus.
                                                                                               SEQUENCE FROM N.A.
MEDLINE; 91374015.
BANCROOT J.B., ROULEAU M., JOHNSTON R., PRINS L., MACKIE G.A.;
"The entire nucleotide sequence of foxtail mosaic virus RNA.";
J. Gen. Virol. 72:2173-2101(1991).
-: SIMILARITY: TO OTHER 7 KD PROTEINS (ORF4) FROM POTEXVIRUSES
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Pred. No. 4.8e+02;
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Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae;
Lambda phage group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAHDI A.A., SHARPLES G.J., MANDAL T.N., LLOYD R.G.; "Holliday junction resolvases encoded by homologous rusA genes in Escherichia coli K-12 and phage 82."; J. Mol. Biol. 257:561-573(1996).
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                                                                                                                                               15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
NINE PROTEIN.
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SEQUENCE 56 AA; 6493 MW; D1CD97AO CRC32;
                                                   56 AA.
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Babesia bovis.
Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
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SILING G.U., BLAKELEY R.L., RIDDLES P.W.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U44917; ABB66362.1; -.
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01.NOV-1996 (TEMBLEEL: 01, LE
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RIDDLES P.W.; EMBL/GenBank/DDBJ

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OTHER RHIZOBIUM NODB GENES.

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14 AA.

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                                                     Length 20;
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HSIEH Y.H., BOBD L.D.;
Submitted Mar-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF065436; AAC17176.1; -
NON_TER 1 1 1
NON_TER 20 20
SEQUENCE 20 AA: 1929 MW; 10DF99C2 CRC32;
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
MAJOR OUTER MEMBRANE PROTEIN (FRAGMENT).
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Last annotation update)
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01-JUN-1998 (TIEMBLrel. 06, Last sequence update)
01-JUN-1998 (TIEMBLrel. 06, Last annotation update)
OUTEN WERANE PROTEIN (FRAGMENT).
Chlamydia trachomatis: Chlamydiaceae; Chlamydia.
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Bacteria, Chlamydiales, Chlamydiaceae, Chlamydia
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1e+03;
                                                  Score 9; DB 2;
Pred. No. 1e+03;
0; Mismatches
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Pred. No. 1e+03;
0; Mismatches
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Pred. No.
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SEQUENCE FROM N.A.
BOBO L., NOVAK N.G.;
J. Infect. D1s. 0:0-0(1998).
EMBL; AF015549; AAB95377.1; -.
NON_TER
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50.0%;
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50.0%;
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                                                     Query Match 52.9
Best Local Similarity 50.0
Matches 2; Conservative
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Best Local Similarity 50.0
Matches 2; Conservative
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Best Local Similarity
Matches 2; Conser
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SEQUENCE
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051951;
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ID Q53520
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
Rhizobium loti.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phylobacteriaceae; Mesorhizobium.
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
VACUGLAR PROTON ATPASE 16 KDA PROTEOLLIPID SUBUNIT (FRAGMENT).
                                                                                                     SEQUENCE FROM N.A.
MEDLINE; 97002748.
SCOTT D.B., YOUNG C.A., COLLINS-EMERSON J.M., TERZAGHI E.A.,
ROCKMAN E.S., LENTELS P.E., PANKHURST C.E.,
"Novel and complex chromosomal arrangement of Rhizobium loti
nodulation genes.";
MOI. Plant Microbe Interact. 9:187-197(1996).
EMBL; L06241; AAB47352.1; -.
SEQUENCE 14 AA; 1600 MW; 30AC228C CRC32;
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YAMAMOTO E., BAIRD W.V.;
Submitted (MAX-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF064202; AAC16556.1; -...
NON_TER 1 1 1
SEQUENCE 17 AA: 1770 MW; 989B605C CRC32;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 06, Last annotation update)
MAJOR OUTER MEMBRANE PROTEIN (FRAGMENT).
Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
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Best Local Similarity 50.0%;
Matches 2; Conservative
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BOBO L., NOVAK N.G.;
J. Infect. Dis. 0:0-0(1998).
EMBL; AF015547; AAB95375.1;
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Best Local Similarity 50.0
Matches 2; Conservative
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NON_TER
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STRAIN-B;
HSIEH Y. H., BOBO L.D.;
"Diversity of major outer membrane protein (omp-1) of Chlamydia
trachomatis in trachoma endemic villages, Kongwa, Tanzania.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF070235; AAC22205.1; -.
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"Diversity of major outer membrane protein (omp-1) of Chlamydia trachomatis in trachoma endemic villages, Kongwa, Tanzania.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF070239; AAC25209.1; -.
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01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MAJOR OUTER MEMBRANE PROTEIN (FRAGMENT).
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MAJOR OUTER MEMBRANE PROTEIN (FRAGMENT).
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Last annotation update)
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation updat MAJOR OUTER MEMBRANE PROTEIN (FRAGMENT).
OMP-1.
Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
                                                                                         Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia
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Pred. No. 1e+03;
0; Mismatches
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Pred. No. 1e+03;
0; Mismatches
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20 AA; 1929 MW; 10DF99C2 CRC32
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nilarity 50.0%;
Conservative 0
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Best Local Similarity 50.0%;
Matches 2; Conservative
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Best Local Similarity
Matches 2; Conserv
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                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE; 95318541.
MEDLINE; 95318541.
MARD M.E.;
MAREY D.C., WATT P.J., WARD M.E.;
"Extent and kinetics of genetic change in the omp1 gene of Chlamydia trachomatis in two villages with endemic trachoma.";
J. Infect. Dis. 172:268-272(1995).
EMBL. S77980; AAB34695.1; -.
EMBL. S77980: AAB34695.1; -.
EMBL. S77980: AB34695.1; -.
EMBL. S77980: AB34695.1; -.
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MAJOR OUTER MEMBRANE PROTEIN VARIABLE DOMAIN I (FRAGMENT).
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Pred. No. 1e+03;
0; Mismatches 2; Indels
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LAMPE M.F., SUCHLAND R.J., STAMM W.E.;

LAMPE M.F., SUCHLAND R.J., STAMM W.E.;

SULLILED (OCT-1992) to the EMBL/GenBank/DDBJ databases.

EMBL, L03760; ABS59032.1; -.

NON_TER 11 11 V -> A (IN REF. 2 AND 1).

SEQUENCE 20 AA: 2017 MW; FB2B029E CRC32;
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                01-NOV-1996 (TIEMBLIEL 01, Created)
01-NOV-1996 (TIEMBLIEL 01, Last sequence update)
01-NOV-1998 (TIEMBLIEL) 08, Last annotation update)
MAJOR OUTER MEMBRANE PROTEIN (FRAGMENT).
                                                                                     OMP1.
Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
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HSIEH Y.-H., BOBO L.D.;
HSIEH Y.-H., BOBO L.D.;
Haisely of major outer membrane protein (omp-1) of Chlamydia trachomatis in trachoma endemic villages, Kongwa, Tanzania.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF070255; AAC2225.1;
                                                                  HSIEH Y.-H., BOBO L.D.; "Diversity of major outer membrane protein (omp-1) of Chlamydia
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EMBL; AF070251; AAC25221.1; -...
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SEQUENCE 20 AA: 1929 MW; 10DF99C2 CRC32;
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia
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"Diversity of major outer membrane protein (omp-1) of Chlamydia trachomatis in trachoma endemic villages, Kongwa, Tanzania."; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
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DEFINITION Oligonucleotide CRN2.
ACCESSION A06950 GI:489035
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DEFINITION Oligonucleotide CRN2
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Oligonucleotide CRN5F.
A06959
A06959.1 GI:489044
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Oligonucleotide CRN5C.
A06956
A06956.1 GI:489041
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synthetic construct
artificial sequence.
1 (bases 1 to 14)
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1 (bases 1 to 14)
Carr, F.J.
                                                                                                                                                                                                                                  synthetic construct.
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Ratio: 2.250
Percent Similarity: 100.000
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                                        Align seg 1/1 to: A06954
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US-08-653-294-2 x A06956
alignment_block:
US-08-653-294-2 x A06954
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LOCUS A06959
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LOCUS A06956
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                                                                                             3 TIGICIGCCGT 14
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Ratio: 2.250 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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Percent Identity: 100.000
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/organism="synthetic construct"
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Patent: EP 0246864-A 11 25-NOV-1987;
IMPERIAL CHEMICAL INDUSTRIES PLC
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Patent: EP 0246864-A 12 25-NOV-1987;
IMPERIAL CHEMICAL INDUSTRIES PLC
Location/Qualifiers
 to: 14
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 from: 1
                                                                                                                     Oligonucleotide CRN6C.
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Oligonucleotide CRN5A.
A06954
A06954.1 GI:489039
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synthetic construct
artificial sequence.
[ (bases 1 to 14)
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synthetic construct
artificial sequence.
[ (bases 1 to 14)
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Quality: 9.00
Ratio: 2.250
Percent Similarity: 100.000
Align seg 1/1 to: A06950
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US-08-653-294-2 x A06953
                         7 Leu*****Arg 10
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LOCUS A06953
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LOCUS A06954
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14-0CT-1993
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                                            Quality: 9.00 Length: 4
Ratio: 2.250 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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Ratio: 2.250 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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/db_xref="taxon:32630"
5 c 3 q 5 t
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/organism="synthetic construct"
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M synthetic construct
artificial sequence.

1 (bases 1 to 14)
Carr,F.J.
Hybridisation probes
Patent: EP 0246864-A 26 25-NOV-1987;
IMPERIAL CHEMICAL INDISTRIES PLC
Location/Qualifiers
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Patent: EP 0246864-A 27 25-NOV-1987;
IMPERIAL CHEMICAL INDUSTRIES PLC
LOCATION/QUALIFIERS
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Oligonucleotide CRN3B.
AU6967
AU6967.1 GI:489052
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14 bp
10CUS A00968 14 bp
ACCESSION 011gonuclectide CRN3C.
ACCESSION A06968 GI:489053
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synthetic construct
artificial sequence.
1 (bases 1 to 14)
Carr, F.J.
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US-08-653-294-2 x A06966
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US-08-653-294-2 x A06967
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LOCUS A06967
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Quality: 9.00 Length: 4
Ratio: 2.250 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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Percent Similarity: 100.000 Percent Identity: 100.000
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/organism="synthetic construct"
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1 4 c 3 g 6 t
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Patent: EP 0246864-A 21 25-NOV-1987;
IMPERIAL CHEMICAL INDUSTRIES PLC
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Patent: EP 0246864-A 24 25-NOV-1987;
IMPERIAL CHEMICAL INDUSTRIES PLC
LOCATION/QUALIFIERS
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LOCUS A06963
DEFINITION Oligonucleotide CRN4D.
ACCESSION A06963
VREYWORDS
SOURCE Synthetic construct.
                                                                                                     from: 1
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Oligonucleotide CRN3A.
A06966
A06966.1 GI:489051
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synthetic construct
artificial sequence.
1 (bases 1 to 14)
Carr,F.J.
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synthetic construct
artificial sequence.
1 (bases 1 to 14)
Carr, F.J.
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US-08-653-294-2 x A06959
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US-08-653-294-2 x A06963
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3 CTGACTGCCCGT 14
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LOCUS A06966
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unclassified.
1 (bases 1 to 14)
Schlingensiepen, G., Schlingensiepen, R., Schlingensiepen, K. and
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Ratio: 2.250 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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Location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630" 4 t

    1.14
/organism="synthetic construct"
/db_xref="taxon:32630"
a 4 c 5 9 4 t

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Patent: EP 0246864-A 30 25-NOV-1987;
IMPERIAL CHEMICAL INDUSTRIES PLC
LOCATION/QUALIFIERS
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Sequence 9 from Patent W09502051.
A42493
A42493.1 GI:2297942
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synthetic construct
artificial sequence.
1 (bases 1 to 14)
Carr, F.J.
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US-08-653-294-2 x A06970
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US-08-653-294-2 x A06971
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Gaps: 0
Percent Identity: 100.000
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Percent Identity: 100.000
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/db_xref="taxon:32630"
a 5 c 4 9 4 t
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Patent: EP 0246864-A 29 25-NOV-1987;
IMPERIAL CHEMICAL INDUSTRIES PLC
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Patent: EP 0246864-A 28 25-NOV-1987;
IMPERIAL CHEMICAL INDUSTRIES PLC
Location/Qualifiers
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Carr, F.J.
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Carr, F.J.
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Ratio: 2.250
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LOCUS A06970
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Brysch, W.
A PHARMACEUTICAL COMPOSITION COMPRISING ANTISENSE-NUCLEIC ACID FOR PREVENTION AND/OR TREATMENT OF NEURONAL INJURY, DEGENERATION AND CELL DEATH AND FOR THE TREATMENT OF NEOPLASMS PATENT: WO 9502051-A 9 19-JAN-1995; BIGGNOSTIK GES FUER BIOMOLEKUL (DE) Other publication AU 7345694 950206.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schlingensiepen, G., Schlingensiepen, R., Schlingensiepen, K. and Brysch, W. acklingensiepen, G., Schlingensiepen, R., Schlingensiepen, K. and Brysch, W. acklingensiepen, G., Schlingensiepen, R., Schlingensiepen, K. and Brysch, W. are the TREATHEN COMPOSITION COMPRISING ANTISENSE-NUCLEIC ACID FOR PREVENTION AND POR THE TREATHENT OF NEOPLASMS
PATENT AND FOR THE TREATHENT OF NEOPLASMS
PATENT AND FOR THE TREATHENT OF NEOPLASMS
BIOGNOSTIK GES FUER BIOMOLEKUL (DE)
Other publication AU 7345694 950206.
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Sequence 61 from Patent W09502051.
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A42545.1 GI:2297994
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/organism="unidentified"
/db_xref="taxon:32644"
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Deamidating antibody heavy ch
Antisense primer 68 for the h
Oligo 877 for hCG alpha-subun
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20-DEC-1993; U12388.

R 23-DEC-1995; US-12336.

R 37-DEC-1995; US-12336.

R 17-SEP-1995; US-12336.

R 4-DEC-1995; US-12336.

R 57-DEC-1995; US-12336.

R 6GENE-) GENELABS TECHNOLOGIES INC.

Andrews Bw. Cantor CR, Edwards CA, Fry KE, Turin LM;

MP1; 94-244711/28.

PT Andrews Bw. Cantor CR, Edwards CA, Fry KE, Turin LM;

MP1; 94-234711/28.

PT Sequence-directed DNA-binding molecules - useful in

pharmaceuticals and as molecular reagents

Disclosure: Fig 294; 587Pp; English.

PT Disclosure: Fig 294; 587Pp; English.

To bind DNA test sequences on be tested by placing the test sequence

adjacent to a defined protein-binding screening sequence. Binding

to bind DNA test sequences can be tested by placing the test sequence

adjacent to a defined protein-binding screening sequence. Binding

con fmols. to these test sequences changes the binding sequence. Binding

adjacent to a defined protein-binding screening sequence. Binding

con fmols. to these test sequences changes the binding sequence. Binding

adjacturbed, generating changes in the concentration of free DNA:protein complexes

is adjacturbed, generating changes in the concentration of free DNA:protein

factors (e.g. TFIID), where the target region is typically selected

from DNA sequences adjacent to the binding site for the encaryotic

transcription factor. Numerous exemplary test sequences are given:

the sequences may also be randomly generated. DNA:protein interaction may

be used for screening purposes, e.g. the Herspes Simplex Viral genes. The test

sequences may also be randomly generated. DNA:protein interaction may

be used for screening purposes, e.g. the Herspes Simplex Viral genes.

The sequences given in Q69881 and Q69883-85 illustrate sample test

oligionucleotides for use in the polymerase chain reaction based
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149563:
17-MAR-1997 (first entry)
Xbal/Scal primer to generate UL9 binding site screening sequence.
                                                                                                                                                                        XbaI/SacI primer.

DNA protein-binding assay; test sequence; screening sequence; promoter; target; TATA box; Herpes Simplex Virus; HSV; corigin of replication; UL9; transcription factor; TFIID: ds. Synthetic.
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N_Geneseq_36:T00654
N_Geneseq_36:X27470
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c'jun antisense oligonucleotide. Probe for HGBW UTR detection. Prebe Gor HGBW UTR detection. Prebe Gor HGBW UTR detection. Prebe gene antisense oligonucleot plant transforming principle dete HLA allele, HLA-DRB1*08, *12 and Human CETP HH ribozyme target se Human CETP HH ribozyme target se Human CETP HH ribozyme target se Human ICAM hammerhead ribozyme target se Human ICAM hammerhead ribozyme target se Human ICAM hammerhead ribozyme target se Rabbit CETP HH ribozyme target se Human ICAM hammerhead ribozyme target se Human ICAM hammerhead ribozyme target se Rabbit CETP HH ribozyme target se Human ICAM hammerhead ribozyme target se Rabbit CETP HH ribozyme target se Farbet CEAM hammerhead ribozyme target se FODB70 used to identify Probe F67DR70 used to identify HLA-DR beta sub-type tailed probe HLA-DR beta sub-t
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-MODEL-frame+plan.model -DEV=xlp
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-Q-(cgn1_1/USPTO_spool/US08653294/runat_0402000_160701_15807/app_query.fasta.1
-DB-N_Geneseq_36 -QFMT=fastap -SUFFIX=rng -GADOP=12.000
-GAPGXT=4.000 -MINMATCH=0.100 -LOOPEXT=0.000
-QAPGXT=4.000 -MINMATCH=0.100 -LOOPEXT=0.000
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-ALIGN=15 -MODE-LOCAL -OUTFWT=pfs -NORM=ext -MINLEN-0
-MAXLEN=1000000 -USER=US08653294 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
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                                                                                   Copyright (c) 1993-2000 Compugen Ltd
OM of: US-08-653-294-2 to: N_Geneseg_36:*
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Query: US-08-653-294-2
Query length: 10
Database: N_Geneseq_36:*
Database sequences: 311585
Database length: 125096042
Search time (sec): 590.520000
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The primer sequences given in T49562-63 were used to generate the general sequences given in T49564-66. The general formulae represent oligonucleotides containing the UL9 recognition sequence of the invention sequence of the invention. The method of the invention comprises altering the binding characteristics of a DNA-binding protein to duplex DNA. The method comprises contacting the duplex DNA with a small molecule which binds sequence-specifically to a target region, where, when the which binds sequence-specifically to a target region, where, when the contapping by more than 4 bp, a binding site for a DNA-binding protein. The small molecule is added at a concentration effective to alter the binding of the DNA binding site for a DNA-binding protein. The small molecule is added at a concentration effective to alter the binding protein, pref. TFIID or UL9, to its binding of the DNA-binding of the small molecule may inhibit or enhance the binding of the DNA-binding protein to its binding site (see also 763713-4312).
Duplex DNA; target region; binding characteristic; DNA binding protein; TFIID; transcription factor; binding site; inhibition; enhance; cancer; inherited genetic disorder; primer; amplify; ss. Synthetic. US5578444-A.
                                                                                                                                                                                                                                                                                                                                                         Altering binding characteristics of DNA binding proteins to duplex DNA - by attaching specific small cpd. to target region close to the protein's binding site, useful in treatment of viral disease, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human ribozyme target sequence from HLA-A exon 3 #20.
Ribozyme; target; human lymphocyte antigen; HLA-A; MHC allele; major histocompatability complex; cleavage; suppression; transplant; incompatability; autoimmune disease; juvenile diabetes; rheumatoid arthritis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouality: 9.00 Length: 4
Ratio: 2.250 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 I;
                                                                                                                                                                                                                                                                                   (GENE-) GENELABS TECHNOLOGIES INC.
Andrews BM, Cantor CR, Edwards CA, Fry KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 G;
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C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 A;
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                                                                                                                                                     27-JUN-1991; 723618.
27-JUN-1991; US-723618.
23-DEC-1992; US-996783.
17-SEP-1993; US-123936.
20-DEC-1993; US-171389.
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18-JUL-1996; E03173.
18-JUL-1995; EP-111256.
(KRUP/) KRUPP G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: T49563
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US-08-653-294-2 x T49563
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                                                                                                                                                                                                                                                                                                               Andrews BM, Canto
WPI, 97-020402/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 BP;
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                                                                                                                                   26-NOV-1996
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          ID DT CON CONTRACT CO
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PT Ribozyme that cleaves specific MHC allele(s) - used to inhibit graft versus host reactions, to overcome blood incompatibility and to treat auto:immune-disease

Claim 5; Fig II; 76pp; German.

Claim 5; Fig II; 76pp; German.

Claim 5; Fig II; 76pp; German.

V10915-V11123 are target sequences for a novel ribozyme which cleaves specific alleles from the major histocompatability complex (MHC). This cromplementary to all mRNA transcribed from vertebrate genes of a specific complementary to all mRNA transcribed from vertebrate genes of a specific allele, and is able to cleave such mRNA. The mRNA has a target region which in case is essentially conserved in all genes of the family but differs from genes of all other MHC alleles to such a degree that no cleavage of mRNA transcribed from these other alleles occurs. This allows the selective reduction or inhibition of expression of all genes of a family or of a single gene. This ribozyme can be used for permanent or translent suppression of expression of MHC alleles, in vivo or in vitro. Specific applications are to prevent guest vs. host or host vs. guest reactions, to prevent blood incompatibilities (partic. of the ABO, rhesus cand Kell systems) and to treat autoimmune diseases such as juvenile need for immunosuppressants in transplant patients. It provides very specific reduction of particular HLA molecules that cause incompatibility between donor and recipient.

Sequence 13 BP; 4 A; 1 C; 6 G; 2 U;
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06-JUL-1993; E0218.
10-JUL-1993; EP-111059.
18106-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
BIYSCH W. Schlingensiepen G, Schlingensiepen R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Autisense nucleic acid hybridising with an area of the mRNA and/or latejasse nucleic acid hybridising with an area of the mRNA and/or DNA comprising the genes c-jun, jun-B or c-fos, expression of which plays a causal role in neuronal injury, degeneration, cell death and/or neoplasms, can be used to prevent and treat such conditions. c-jun antisense sequences are described in 083267-321 and 08344-45; jun-B antisense sequences are described in 083367-321 and 083446-51. Preferably the antisense sequences are described in 083364-439 and 083446-61; preferably the antisense sequences are phosphorothicate oligonucleotides since these are not destroyed as fast by endogenous factors as naturally occuring molecules.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-SEP-1995 (first entry)
Lubs antisense oligonucloctide.
c-jun; c-fos; jun-B; neuronal injury; cell death; neoplasm; antisense; phosphorothloate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps: 0
Percent Identity: 100.000
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US-08-653-294-2 x V10946/rev
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Ratio: 2.250
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alignment_scores
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                                                                                                                                                        7-FEB-1997
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence
primer; probe; PCR; polymerase chain reaction; Hepatitis GB virus; HGBV; isolation; sequencing; diagnosis; treatment; acute; chronic; hepatitis; blood; organ donation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and/or neoplesms
Claim 2; Page 23; 86pp; English.
Antisense nucleic acid hybridising with an area of the mRNA and/or
NA comprising the genes c-jun, jun-B or c-fos, expression of which
plays a causal role in neuronal injury, degeneration, cell death and/or
reoplasms, can be used to prevent and treat such conditions
or neoplasms, can be used to prevent and treat such conditions
or neoplasms, can be used are described in Q83267-321 and Q83440-43;
jun-B antisense sequences are described in Q83322-63 and Q83444-45;
and c-fos antisense sequences are described in Q83364-439 and Q83446-
51. Preferably the antisense sequences are phosphorothicate
oligonucleotides since these are not destroyed as fast by endogenous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JAN-1995.
06-JUL-1994; E02218.
10-JUL-1993; EP-111059.
(BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
Brysch W. Schlingensiepen G, Schlingensiepen R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of antisense c-jun, c-fos or jun-B nucleic acids - for preventing and treating neuronal injury, degeneration, cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-5EP-1995 (first entry)

c-jun antisense oligonucleotide.

c-jun: c-fos: jun-B: neuronal injury: cell death; neoplasm;

antisense: phosphorothioate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps: 0
Percent Identity: 100.000
                                                                                                 Percent Identity: 100.000
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                                                                                                                                                                                                                                 to reverse of: Q83327 from: 1 to: 14
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                                                                              Gaps:
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                                                   Length:
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Sequence 14 BP; 3 A; 2 C; 5 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
ID T76848 standard; DNA; 14 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        083275 standard; DNA; 14 BP
                                                                                                                                                     alignment_block:
US-08-653-294-2 x Q83327/rev
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US-08-653-294-2 x Q83275/rev
                                                                                                                                                                                                                                                                                                                                                                                         seq_name: N_Geneseq_36:083275
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Ratio: 2.250
Percent Similarity: 100.000
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                                                                         Ratio: 2.250
Percent Similarity: 100.000
                                                   9.00
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                                                                                                                                                                                                                                                                                                                                     12 CTCTCTACACGA 1
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                                                Quality:
                                                                                                                                                                                                                                                                                                                alignment_scores
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Probes and primers for detection of hepatitis GB virus - specific for 5' non-translated region and non-structural region 3 claim 2; Page 44: 56pp; English.

T76826-56 are primers and probes for detection of Hepatitis GB virus.
T56826-56 are primers and probes for detection of Hepatitis GB virus. Isolation and sequencing of the HGBV genome using the primers and probes will allow design of additional probes and polypeptides which will be useful in the diagnosis and/or treatment of HGBV, both as a prophylactic and therapeutic agent. In particular, the probes could greatly enhance the ability to more accurately diagnose acute and/or chronic viral hepatitis and could provide a safer blood and organ supply by detecting non-A, non-B and non-C hepatitis in these blood and organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Preparation of autisense oligo:nucleotide(s) which lack long runs of consecutive guanosine or inosine - and have specific ratio of residues able to form two or three hydrogen bonds, have greater activity and reduced toxicity, used therapeutically or to modulate growth of cells in culture

Glaim 10; Fig 6b; 286pp; English.
V48709-86s represent antisense oilgonucleotides directed against the ErbB-2 gene. Of these, only oligonucleotides V48709-91 resulted in significant redcution in ErbB-2 protein expression, while oligonucleotides V48792-886 had little effect. The oligonucleotides variety the invention. The specification describes oligonucleotides that contain 8-30 nucleotides, which contain at most 8 nucleotides that can each form three hydrogen bonds to cytosine; do not contain four
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ErbB-2 gene antisense oligonucleotide ErbB-2-67.
ErbB-2; antisense oligonucleotide; modulate; gene expression; ss.
Synthetic.
                                                                                                                                                                                                                                                                                                             Marshall RL, Muerhoff AS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps: 0
Percent Identity: 100.000
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31-JAN-1997; EP-101531.
(BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
Brysch W, Schlingenslepen K;
WPI; 98-400910/35.
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G;
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/mod_base= G-carbazole-3'
Location/Qualifiers
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C;
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WPI; 97-165323/15.
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ID V48775 standard; DNA; 14 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 A;
                                                                                                                                                                    14-AGG-1996; U13199.
19-APR-1996; US-635309.
14-AGG-1995; US-002255.
(ABBO ) ABBOTT LAB.
Desal SM, Jou C, Leary
Mushahwar IK, Simons JN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ratio: 2.250
Percent Similarity: 100.000
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US-08-653-294-2 x T76848/rev
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EP-856579-A1.
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              cases
consecutive nucleotides able to form three H-bonds each to four consecutive cytosines; do not contain two sequences of three consecutive uncleotides each able to form three H-bonds to three consecutive cytosines, and the ratio between residues able to form two H-bonds each (2R) or three such bonds (3R) is given by 2R/3R = 0.33-0.72. The oligonucleotides are used to modulate expression of genes, particularly the genes for p53, ErB-2, junB, junD, 7GF-beta 1 or beta 2 to control proliferation of primary cell cultures (e.g. bone marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or keratinocytes). The oligonucleotides can also be used to analyse function of proteins (by altering their expression or activity) and therapeutically, e.g. in cases of cancer or (targeting TGF) for stimulating the immune system.
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junB gene antisense oligonucleotide JunB-16.
junB; junD; antisense oligonucleotide; modulate; gene expression; ss.
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Percent Similarity: 100.000 Percent Identity: 100.000
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31-JAN-1997; EP-101531.
(BIGG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
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US-08-653-294-2 x V48775
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F 31-MAY-1991.

S1-MAY-1991. JP-128924.

A (SHMA) SHIMADZU CORP.

R WPI; 93-030366/04.

R WPI; 93-030366/04.

T Gene coded to DNA of Agrobacterium rhizogenes

Claim 1; Page 2; JOpp; Japanese.

C method for the detection of the plant transforming principle of Agrobacterium rhizogenes. It detects the life plant principle of Agrobacterium rhizogenes it detects the latter half of the TR-DNA ROLB gene. The method provides highly sensitive, easy and highly selective detection of a specific foreign gene from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-DEC-1996 (first entry)
HLA allele, HLA-DRB1*08, *12 and *1404 resolution probe, F67.
HLA allele, HLA-DRB1*08, allele; HLA-DR*08; HLA-DR*12; locus B1;
Polymorphism; amplify; conserved region; detection; primer; probe;
tissue matching; identifying disease susceptibility; ss.
Gaps: 0 Gaps: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                           24-MAY-1993 (first entry)
Plant transforming principle detection PCR primer.
Polymerase chain reaction; TR-DNA ROLB gene;
Agrobacterium rhizogenes; ss.
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C;
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                                                                                                        from: 1
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ID T41816 standard; DNA; 15 BP.
AC T41816;
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                                                                                                                                                                                                                                             035256 standard; DNA; 15
035256;
Quality: 9.00
Ratio: 2.250
Percent Similarity: 100.000
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Ratio: 2.250
Percent Similarity: 100.000
                                                                                                                                                                                                seq_name: N_Geneseq_36:Q35256
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US-08-653-294-2 x Q35256/rev
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US-544218.
US-025038.
                                                                                                        Align seg 1/1 to: V48580
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Sequence 15 BP;
                                                           alignment_block:
US-08-653-294-2 x V48580
                                                                                                                                     7 Leu****** 10
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27-JUN-1990; 5
27-JUN-1990; U
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US5545526-A.
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Human leukocyte antigen typing of tissue samples - using allele-specific amplification to distinguish allele pairs

Example 1: Column 19: 2409; English.

CC The sequences given in 7409; English.

The sequences given in 7409; English.

CC The sequences given in 14081-20 represent probes which were used to resolve the human leukocyte antigen (HLA) DRB1 alleles, DRB1*08, *12

and *1404. This probe sequence Mybridises to the Phe67 conding region of the method of invention which concerns HLA typing of a sample for an unknown pair of alleles. The pair of alleles comprises one of two known types which have the same overall set of polymorphisms but have a different distribution of polymorphisms between their two alleles. The method comprises selectively amplifying the DNA of just one allele of method comprises selectively amplifying the DNA of just one alleles. The method comprises of a locus malaysing the amplified DNA to determine which comprises. The Known type having that allele, and therefore assigning the unknown pair to the known type having that allele. The method comprises to three test stages. The first stage is to establish the number of alleles present in each sample. Primers corresponding to fatily while amplified and potentially detected by hybridisation with a probe. In the second stage, the group or basic type identified of the group identified in the first stage but different from a primers comprises an opt. labeled sequence common to each cother groups identified in stage one. The second primer may be a maximum of different labeled primers, complementary to two or more cother groups identified in stage one. The second primer of different labeled primers, complementary to two or more sequences within the group, or the amplification may be performed with a sequence within the group, or the amplification may be performed of alleles. The method of the propence of a single group of alleles. The method of the propence of a single group of alleles. The method may be used for tissue matching at adiolabeles an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-FEB-1997 (first entry)
Human CETP HH ribozyme target sequence #550.
Human CETP HH ribozyme; cholesterol ester transfer protein; mRNA cleavage; hammerhead ribozyme; cholesterol ester transfer; plasma lipoprotein; afherosolerosis; atherectomy; reverse cholesterol transport; high density lipoprotein; therapy; CETP; familial hypercholesterolaemia; dystlipidaemia; hypolaphalipoproteinemia; peripheral vaccular disease; hyperbetalipoproteinaemia; RCT; inhibitor; angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps: 0
Percent Identity: 100.000
BLOOD CENT RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: T41816 from: 1
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ID T49643 standard; RNA; 15 BP.
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(RIBO-) RIBOZYME PHARM INC.
(WARN ) WARNER LAMBERT CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity: 100.000
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                                  96-383664/38
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Pyror regression to vaccutation to the property of the cleavage site in full length CETP. The ribozyme to the position of the cleavage site in full length CETP. The ribozyme binds to continuous of the cleavage site in full length CETP. The ribozyme binds to mediately upstream. The ribozymes are able to cleave mRNA from the conding CETP, thereby blocking synthesis and/or expression of the mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway can be inhibited (or eliminated) thereby preventing the reduction in size density of the high density lipoproteins (HDL), prolonging HDL half life, and therefore increasing HDL levels. The ribozymes can be used to treat conditions associated with abnormal levels of CETP. Created and sngioplastic restenosis. By inhibiting CETP, the levels of HDL and low density lipoproteinsemia, hypopalphalipoproteinaemia, disease, hyperbetalipoproteinaemia, hypopalphalipoproteinaemia, created and angioplastic restenosis. By inhibiting CETP, the levels of HDL and low density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered (a decrease in LDL levels, and a corresponding configurence in HDL levels). The HH ribozymes can also be used diagnostically to study genetic drift and mutations in diseased cells, and to detect CETP mRNA. As the HH ribozymes target specific regions of the CETP gene, they have low non-specific activity.
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Human CETP HH ribozyme target sequence #525.
Human CETP HH ribozyme target sequence #525.
Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;
neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
reverse cholesterol transport; high density lipoprotein; therapy; CETP;
familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
angloplastic restenosis; low density lipoprotein; diabetes; HDL; human;
Bisgaier C, Couture L, McSwiggen J, Pape M, Stinchcomb D; WPI: 96-321852/32.
New ribozymae(s) for cleaving cholesterol ester transfer protein mRNA - useful for preventing or treating initial development, progression or regression of vascular diseases, esp. familial
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New Tibozyme(s) for cleaving cholesterol ester transfer protein mRNA - useful for preventing or treating initial development, progression or regression of vascular diseases, esp. familial
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Percent Identity: 100.000
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ID T49633 standard; RNA; 15 BP.
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11-DEC-1995; U16000.
23-DEC-1994; US-363240.
(RIBO-) RIBOZYME PHARM INC.
(WARN ) WARNER LAMBERT CO.
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Ratio: 2.250
Percent Similarity: 100.000
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US-08-653-294-2 x T49643
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hypercholesterolaemia

Claim 4, Page 29; 72pp; English.

Tud9608-Tud9608 represent target sequences for the human cholesterol ester

transfer protein (CETP) hammerhead (HH) ribozymes (see Tud9808-T50137).

CETP is a 74 kD glycoprotein; The numbering of the targets refers to the cheven plasma lipoproteins. The numbering of the targets refers to the position of the cleavage site in full length CETP. The ribozyme binds to immediately upstream. The ribozymes and/or expression of the month of the cleavage site in full length CETP. The ribozyme binds to gene encoding CETP, thereby blocking synthesis and/or expression of the mNNA. By inhibiting CETP, the reverse cholesterol transport (RCT)

c pathway can be inhibited (or eliminated) thereby preventing the reduction in size density of the high density lipoproteins (HDL), prolonging HDL half life, and therefore increasing HDL levels. The ribozymes can be used to treat conditions associated with abnormal levels of CETP, specifically familial hypercholesteroleania, atherosclerosis, peripheral vascular complications of diabetes, transplant, catherectomy and angioplastic restencies (LDL), and the HDL:LDL ratio are favourably altered (a decrease in LDL levels, and a corresponding increase in HDL levels). The HH ribozymes can also be used diagnostically to study genetic drift and mutations in diseased cells, the CETP gene, they have low non-specific activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-1997 (first entry)
Human CETP HH ribozyme target sequence #526.
Human CETP HH ribozyme target sequence #526.
Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage; neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy; reverse cholesterol transport; high density lipoprotein; therapy; CETP; familial hyperchelsterolaemia; dyslipidaemia; hypoalphalipoproteinemia; peripheral vascular disease; hyperbetallpoproteinaemia; RCT; inhibitor; angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 29; 72pp; English.
T49608-T49863 represent target sequences for the human cholesterol ester transfer protein (CETP) hammerhead (HH) ribozymes (see T49881-T50137).
CETP is a 74 kD glycoprotein that facilitates neutral lipid transfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA - useful for preventing or treating initial development, progression or regression of vascular diseases, esp. familial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Couture L, McSwiggen J, Pape M, Stinchcomb D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T49635 standard; RNA; 15 BP.
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11-DEC-1995. U16000.
23-DEC-1994; US-361240.
(RIBO-) RIBOZYME PHARM INC.
(WARN.) WARNER LAMBERT CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality: 9.00
Ratio: 2.250
Percent Similarity: 100.000
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WPI; 96-321852/32
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between plasma lipoproteins. The numbering of the targets refers to the position of the cleavage site in full length CETP. The ribozyme binds to constition of the cleavage site in full length CETP. The ribozyme binds to constitute the cleaves mkNA from the immediately upstream. The ribozymes are able to cleave mkNA from the gene encoding CETP, thereby blocking synthesis and/or expression of the mkNA so inhibiting CETP, the reverse cholesterol transport (RCT) pathway can be inhibited (or eliminated) thereby preventing the reduction in size density of the high density lipoproteins (HDL), prolonging HDL in size density of the high density lipoproteins (HDL), prolonging HDL and file, and therefore increasing HDL levels of CETP, specifically familial hypercholesteroleamia, atherosclerosis, peripheral specifically familial hypercholesteroleamia, hypoalphaliopproteinaemia, dyslipidaemia, vascular complications of diabetes, transplant, catherectomy and angioplastic restencies (IDL), and the HDL:LDL ratio are favourably altered (a decrease in LDL levels, and a corresponding increase in HDL levels). The HH ribozymes can also be used diagnostically to study genetic drift and mutations in diseased cells, the CETP gene, they have low non-specific activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human ICAM hamerred and into the cleavage; inhibition; Bnzymatic nucleic acid; ribozyme; trans cleavage; inhibition; Bnzymatic nucleic acid; ribozyme; trans cleavage; inhibition; gene expression; downregulation; interleukin-5; IL-5; ICAM-1; intercellular adhesion molecule; rel #; tumour necrosis factor; TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene; Translocation; chronic myelogenous leukaemia; CML; cancer; Philadelphia chromosome; Inflammation; autoimmune disease; atherosclerosis; myocardial infarction; stroke; restenosis; ransplant rejection; rheumatoid arthritis; psoriasis; myocardial ischaemia; Rawasaki disease; septic shock; HIV; human immunodeficiency virus; acquired immune deficiency syndrome;
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Gaps: 0
Percent Identity: 100.000
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ID T51807 standard; RNA; 15 BP.
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Ratio: 2.250
Percent Similarity: 100.000
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US-22795.
US-224483.
US-228041.
US-227958.
US-245736.
US-245736.
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US-08-653-294-2 x T49635
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23-FEB-1995; IB0156.
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WO9523225-A2.
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7 Leu*****Arg 10
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HHHHMOUDOODOODOODOODOOO
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Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;
Hammerhead ribozyme; cholesterol ester transfer protein; atherosclerosis; atherectomy;
reverse cholesterol transport; high density lipoprotein; therapy; CETP;
familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
peripheral vascular disease, hyperbetalipoproteinaemia; RCT; inhibitor;
angioplastic restenosis; low density lipoprotein; diabetes; HDL; rabbit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents and methods for producing them for use in inhibiting disease related genes

Claim 2. Page 172; 407pp: English.

The present sequence represents a ribozyme) which cleaves ICAM-1

The present sequence represents a ribozyme) which cleaves ICAM-1

The present sequence represents a ribozyme which cleaves ICAM-1

The present sequence represents a ribozyme by the folding

The present sequence in the form secondary folding

The present sequence identified by computer analysis.

Thosymes cleavage sites were identified by computer analysis.

Thosymes directed against these mRNA sequences were designed and synthesised with modifications that improve their nuclease

The ribozymes cleave the ICAM-1 target sequences and thereby inhibit ICAM-1 expression, making them useful for reducing transplant rejection and alleviating symptoms in patients with rehumatorid arthritis, asthma and other inflammatory disorders.
                                                                                                                                                                                                                                                                                                                                                                                   Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW; Grimm S, Karpelsky A, Kisich K, Matulic-Adamic J; KGWiggen JA, Modak A, Pavco P, Beigelman L, Sullivan SW; Sweedler D, Thompson JD, Tracz D, Usman N, Wincott FE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Couture L, McSwiggen J, Pape M, Stinchcomb D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio: 2.250 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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11-DEC-1995; U16000.
23-DEC-1994; US-363240.
(KIBC.) RIBOZYME PHARM INC.
(WARN.) WARNER LAMBERT CO.
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ID T50179 standard; RNA; 15 BP.
AC T50179;
                                                                                                                                                                                                                                                                                                                                                       (RIBO-) RIBOZYME PHARM INC. Stinchcomb DT, Chowrira B,
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US-08-653-294-2 x T51807/rev
                                                                          03-OCT-1994; US-316771.
07-OCT-1994; US-319492.
11-OCT-1994; US-319493.
04-NOV-1994; US-334847.
10-NOV-1994; US-337608.
28-NOV-1994; US-357516.
16-DEC-1994; US-35577.
23-DEC-1994; US-357373.
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Ratio:
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WPI; 96-3;
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AAC DDE TO DDE T
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PT very thosywests of the cleaving cholesterol ester transfer protein mRNA or useful for preventing or treating initial development, progression or vacular diseases, esp. familial protecholesteroleans and account diseases, esp. familial development, progression or vacular diseases, esp. familial development, progression of vacular diseases, esp. familial progression of vacular diseases, esp. familial progression of vacular diseases, esp. familial progression of the disease that family in the target sefers refers to the constition of the cleavage state in full length CETP. The ribozymes then be position of the cleavage state in full length CETP. The ribozyme then consist to and/or expression of the mRNA. By inhibiting CETP, the reverse and/or expression of the mRNA. By inhibiting CETP, the reverse cholesterol transport (RCT) pathway can be inhibited (or aliminated) thereby preventing the reduction in size density of the high density consistenced transport (RCT) pathway can be inhibited (or aliminated) thereby preventing the reduction in size density of the high density in the analysis of CETP, specifically atherosclerosis, familial hyporthelesteroleans, peripheral vacular disease, dislibited managements, peripheral vacular disease, dislibited managements of the HDL:LDL ratio are favourably altered (a decrease in LDL levels, and a corresponding increase in HDL levels). The creases in LDL levels, and a corresponding increase in HDL levels of HDL included disposition and the CETP mRNA. As the HH ribozymes target specific regions of the CETP gene, they have low conspecific activity.

So sequence 15 BP; 4 A; 5 C; 2 G; 4 U;

Alignment_block:

Guality: 100.000 Percent Identity: 100.000

Alignment_block:

Graph or specific foot; 100:000 Percent Identity: 100:000
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A1300663 qo22a04.x1 NCI_CGAP_
A1376705 tc29d03.x1 Soares_to
A1974168 fd23a09.x1 zebrafish
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                                                                                                                                                                            CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Waterston, waterston, waterston, waterston, waterston, waterston, waterston, waterston, washo-HHMM Mouse EST Project
Contact: Marra M/Mouse EST Project
Washu-HHMI Mouse EST Project
Washu-HMI Mou
                                                                                                                      seq_documentation_block:
LOCUS AA921614 25 bp mRNA EST 20-APR-1998
DEFINITION vy21d09.r1 Stratagene mouse macrophage (#937306) Mus musculus of the colone IMAGE:1296113.5' similar to SW:UCP2_MOUSE P70406
MITOCHONDRIAL UNCOUPLING PROTEIN 2;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28mi3 revi Er from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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Gaps: 0
Percent Identity: 100.000
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5e+04
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85.38
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966
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                                                                                    seq_name: gb_est21:AA921614
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US-08-653-294-2 x AA921614
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                                                                                                                                                                                                                                                                                                         house mouse
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gb_est25:AI300663
gb_est26:AI376705
gb_est37:AI974168
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ORIGIN
                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                       SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA7344 CAD7905.31 NCI_CGAP_GC4
AA73948 0912402.51 NCI_CGAP_GC4
AI196654 unf88a04.47 Sugano mouse
AI196654 unf88a04.47 Sugano mouse
AI196659 wh74c03.x1 NCI_CGAP_Ut4
AI806139 gw37c11.x1 NCI_CGAP_LUt4
AA8181661 2255c05.x1 Stratagene NAA73970 zv18911.s1 Scares_NHBMF
AA531819 TGESTZ247602.r1 TGME49
AA673970 zv18911.s1 NCI_CGAP_LCG
AA878823 of87c04.s1 NCI_CGAP_EM
AA67897 nx77a12.s1 NCI_CGAP_EM
AA77939 yf61c12.s1 Scares_NHMF
AI832311 at68b06.x1 Barstead col
A0773796 EP(3)3179 brosophila me
A16840 gy46608.s1 Stratagene ifv
AA14860 mr73e06.r1 Stratagene ifv
AA14860 mr73e06.r1 Stratagene ifv
AA14864 ta74690.x1 NCI_CGAP_Pan
AI1854 ta74690.x1 NCI_CGAP_Pan
AI1854 ta74690.x1 NCI_CGAP_Pan
AI1854 ta74690.x1 NCI_CGAP_HSC
AI785 yf9266.s1 Stratagene liv
T71023 yc50c11.s1 Stratagene liv
T77191 yc64410.s1 Stratagene liv
T77191 yc64410.s1 Stratagene liv
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N94347 zb75g05.sl Soares_senesce
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C01323 HUMG$0006349 Human adult
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zj26e08.sl Soares_fetal
os54g04.sl NCI_CGAP_Br2
                                                                                                                                                                     About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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Database sequences: 4538634
Database length: 1887831982
Search time (sec): 8553.360000
OM of: US-08-653-294-2 to:
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Query length: 10
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gb_est26.Ai36439
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gb_est6:N94347
gb_est20:AA864650
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gb_est10:AA144860
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95_est8:C01323
95_est18:AA508464
95_est12:AA508464
95_est21:AA999748
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gb_est35:AI813858
gb_est35:AI832311
gb_gss8:AQ073796
                                           Date: Feb 8, 2000
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gb_est21:AA921614
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gb_est19:AA796605
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SOURCE ORGANISM

JOURNAL COMMENT

REFERENCE AUTHORS TITLE

ACCESSION VERSION KEYWORDS

DEFINITION

source

FEATURES

BASE COUNT

ORIGIN

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AA86450 EST 13-MAY-1998 oh37b09.s1 NCI_CGAP_Kid6 Homo sapiens CDNA clone IMAGE:1459961 3'similar to SW.ATPQ_BOVIN P13620 ATP SYNTHASE D CHAIN, MITOCHONDRIAL '; MANA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butharia; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 28)

Norl-GGAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
On Jan 17, 1998 this sequence version replaced gi:1900516.
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                          Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: polyT not found
Seq primer: mob.REGA+ET
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Soares_senescent_fibroblasts_NbHSF"
Unpublished (1995)
On May 8, 1995 this sequence version replaced gi:799997
On tact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="senescent fibroblast"
/lab_host="DH10B (ampicillin resistant)"
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Gaps: 0
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                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="GDB:1252878"
/db_xref="taxon:9606"
/clone="IMAGE:309464"
                                                                                                                                                                                                                                                                                                High quality sequence stop: 1. Location/Qualifiers
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LOCUS AA864650
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5 c 6 g 6 t
                                                                                                                                                                                                       western European house mouse.

Buts musculus domesticus
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

I (bases 1 to 27)
Kawamoto,S., Okubo,K., Yoshii,J., Katsuki,M. and Matsubara,K.
Analysis of gene expression in mouse embryogenesis by 3'-directed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2D75905.sl Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:309464 3' similar to gb|M11120|RATRRWX Rat 28S rRNA 3'
                                                                    D18733 27 bp mRNA EST 12-DEC-1995
MUSGS01795 Mouse 3'-directed Mus musculus domesticus cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 28)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kocaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-APR-1996
                                                                                                                                                                                                                                                                                                                                                             cDNA sequencing
Unpublished (1995)
On May 18, 1995 this sequence version replaced gi:811454.
Contact: Kawamoto,S., Okubo,K., Yoshii,J., Katsuki,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matsubara, K.
Institute for Cellular and Molecular Biology
Osaka University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus domesticus"
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/db_xref="taxon:10092"
/clone="md0789"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3-1 Yamada-oka, Suita, Osaka 565, Japan
Insert Length: 978 Std Error: 0.00
High quality sequence stop: 234.
Location/Qualifiers
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                                                                                                                   md0789 3', mRNA sequence
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Percent Similarity: 100.000
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                                              seq_documentation_block:
seq_name: gb_est5:D18733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
LOCUS N94347
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Ratio:
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE

DEFINITION

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Note-Tyctor: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I oligo(dI) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
        DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGPP clone distribution information can be found through the I.M. G.E. Consortium/LLNL at: www-blo.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 28)
Marra,M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Mooris,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block: 28 bp mRNA EST 14-OCT-1998
LOCUS Al196094 12 Sugano mouse liver mlia Mus musculus cDNA clone
DEFINITION u168a04.11 Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1887534 5' similar to TR:099624 099624 TRANSPORTER PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL ; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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/clone="ImAcE:1586115"
/clone=lib="NCI_CGAP_GC4"
/tissue_type="pooled germ cell tumors"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Agaps: 4 Gaps: 0 Percent Identity: 100.000
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                                                                                                                                    Trace considered overall poor quality Insert Length: 790 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 1. Location/Qualifiers
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The WashU-HHMI Mouse EST Project
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A1196054
A1196054.1 GI:3748660
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US-08-653-294-2 x AA973948/rev
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Ratio: 2.250
Percent Similarity: 100.000
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VERSION
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COMMENT
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                        Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael Enmert-Buck, M.D., Ph.D. ChA. Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eukaryota; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 28)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

Tumor Gene Index

Unpublished (1997)

On Sep 12, 1996 this sequence version replaced gi:1407105.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert Strausbergenih.gov
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Ratio: 2.250 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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AA973948
AA973948.1 GI:3149128
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US-08-653-294-2 x AA864650/rev
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LOCUS AA973948
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25 CTCACCTCCAGG 14
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Trace considered overall poor quality
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US-08-653-294-2 x AI364399/rev
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Percent Similarity: 100.000
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                             /note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG); Site_2: DraIII (CACCATGTG); Ist strand cDNA was primed with an oligo(dT) primer (ATGGCCTATTTTTTTTTTTTTT); double-stranded cDNA was lighted to a DraIII adaptor [TGTTGGCTACTGG], digested and cloned into distinct DraIII sites of the MNE18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). MnoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGCCTCAACACCACCA."
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1 (bases 1 to 28)

NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)

On Jan 19, 1998 this sequence version replaced gi:2150844.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@aih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:971858
                                                    Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: custom primer used
High quality sequence stop: 1.
Location/Qualifiers
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                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="taxon:10090"
/clone_lib="Sugano mouse liver mlia"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 4
Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                          /organism="Mus musculus"/strain="C57BL"
                                                                                                                                                                                                                                                                                                                          /dev_stage="adult"
/lab_host="DH10B"
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US-08-653-294-2 x AI196054/rev
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Percent Similarity: 100.000
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LOCUS A1364399
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TITLE
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 28)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

Tumor dene Index

Tumor dene Index

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausbergenih.gov

Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,

M.D., Louls M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Mashington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M. A.G.E. Consortium/LLNL at:

www-blo.llnl.gov/bbrp/image/image.html
              Sequencing Center information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="DH10B"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.48 kb. Life Technologies catalog #:
11542-016"
8 c 10 g 2 t
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LOCUS A1808936 28 bp mRNA EST 07-JUL-1999

LOCUS A1608936 CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2386468 3'

DEFINITION WAY4003.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2386468 3'

SIMILAT TO TR:Q15834 Q15834 HEPATITIS DELTA ANTIGEN INTERACTING ACCESSION A1808936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. 28
//organism="Homo sapiens"
//do.xerf="taxon:9606"
//do.xerf="taxon:9606"
//clone="IMAGE:1993268"

DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 4
Gaps: 0
Percent Identity: 100.000
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2
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                                                                                                                                                                                                                   www-bio.llnl.gov/bbrp/image/image.htm]
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1

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

1 (bases 1 to 31)

8 Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lady,M., Le,N., Lennon,G., Marra,M., Martin,J., Monce,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T. Waterston,R. and Wilson,R. WashU-Merck EST Project 1997

10 Unpublished (1997)

11 On Sep 12, 1996 this sequence version replaced gi:1393169.

12 Contact: Wilson RK Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1800

Fax: 314 286 1810

Email: est@watson,wustl.edu

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered oversall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: -41mi3 fwd. Er from Amersham

High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA479970 31 bp mRNA EST 08-AUG-1997 zv18b11.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:753981 3' similar to SW:CAlH_HUMAN P39060 COLLAGEN ALPHA 1(XVIII) CHAIN ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality: 9.00 Length: 4
Ratio: 2.250 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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/db_xref="GDB:5976854"
/db_xref="taxon:9606"
/clone="IMAGE:753981"
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      1. .31
/organism="Homo
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US-08-653-294-2 x AA181661
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AA479970
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LOCUS AA479970
DEFINITION ZV18b11.s1 So
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                                                                                                                                                                                                                seq_documentation_block: 31 bp mRNA EST 10-MAR-1998
LOCUS AA181661 Stratagene NT2 neuronal precursor 937230 Homo sapiens
cDNA clone IMAGE:613352 5' similar to TR:G1006657 G1006657
CATHERSIN C PRECURSOR; mRNA sequence.
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Hiller, Allan, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theislang, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Washo-NCI human EST Project
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 2069 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2386468"
/clone_lib="NCI_CGAP_CLL1"
/tissue_type="B-cell, chronic lymphotic leukemia"
/lab_host="B-tell, chronic lymphotic leukemia"
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Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Gaps: 0
Percent Identity: 100.000
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Seq primer: -400r 110... Ligh quality sequence stop: 1. Location/Qualifiers
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AA181661.1 GI:1765144
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Ratio: 2.250
Percent Similarity: 100.000
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                                                                                                     /note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI: Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Sarcocystidae; Toxoplasma.

1 (bases I Toxoplasma.

1 (bases I L. Dubugue, T., Sibley, L.D., Hillier, L.,
Allen, M., Bowles, L., Dubugue, T., Geisel, S., Kucaba, T., Lacy, M.,
Le, N., Jost, S., Martin, J., Moore, B., Schellenberg, K., Steptoe, M.,
Tan, F., Theising, B., Bowers, Y., Wylie, T., Ajloka, J.A., Aslett, M.A.,
Wan, K. L., Wilson, R., Waterston, R. and Boothroyd J.C.
Washly-Stanford-PAMF-NIH Toxoplasma EST project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seg_documentation_block:
LOCUS AA531819
AA531819
DEFINITION TGESTZ247e02.r1 TGME49 invivo Bradyzoite cDNA size selected
TOXOPLASTA GONAL CDNA clone tgzz47e02.r1 5' similar to TR:G603568
G603568 HISTONE H3 ;, mRNA sequence.
/clone_lib="Soares_NhHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1397996.
On Sep 12, 1996 this sequence version replaced gi:1397996.
Ontact: Marra M
Washlowersek EST Project
Washlogton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Contact Steve Parmley, PAMF (76424.16@compuserve.com) for
Information on clone and library availability.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
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Percent Identity: 100.000
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/strain="ME49"
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Location/Qualifiers
                                                                                        /lab_host="DH10B"
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US-08-653-294-2 x AA479970/rev
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Fax: 314 286 1810
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Percent Similarity: 100.000
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/de_abbost="DHIO"
/note="Vector: Bluescript II SK-; Site_1: EcoRI; Site_2:
Noti: Mature bradyzoites were obtained from infected mouse
brains by percoll density centrifugation. The original
library was constructed by Steve Parmley, Palo Alto
Medical Foundation. CDNAS were synthesized by priming with
oligo d(T) and directionally cloned into the EcoRI/NotI
sites of lambda gill. Warning: the library contains a
small percentage of host cDNAS derived from mouse cells.
Inserts from this cDNA library were excised with Notl and
ECORI, size selected in a range of 0.7 - 2.0 kb and
subcloned into Bluescript II SK- (Adrian Hehl, Ian Manger
and John Boothhroyd, Stanford University)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D. CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. CDNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-GAP Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
/clone="tgzz47e02.rl"
/clone_llb="TgME49 invivo Bradyzoite cDNA size selected"
/dev_stage="Bradyzoite"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 31)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NATIORAL Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

Unpublished (1997)

On Jan 9, 1998 this sequence version replaced gi:949681.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA744598 31 bp mRNA EST 22-JAN-1998 ny25h10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1272835 similar to SW:GLI4_HUMAN P10075 GLI4 PROTEIN ;, mRNA sequence. AA744598 GI:2783362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 9.00 Length: 4
Ratio: 2.250 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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US-08-653-294-2 x AA531819/rev
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/organism="Homo sapiens"

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/note="vector: pT73D-Pac (Pharmacia) with a modified

/note="vector: pT73D-Pac (Pharmacia) proposed (NCI) propulation of (NCI) propulation of (NCI) propulation of propulation of index proposed (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library vent through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of87cO4.sl NCI_CGAP_Li5 Homo sapiens cDNA clone IMAGE:1437318 3' similar to TR:Q63627 Q63627 CTD-BINDING SR-LIKE PROTEIN RA4 ;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to: 0 31)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index
Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2152184.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 4
Gaps: 0
Percent Identity: 100.000
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Trace considered overall poor quality
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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AA878823.1 GI:2987788
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Ratio: 2.250
Percent Similarity: 100.000
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LOCUS AA878823
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KEYWORDS
SOURCE
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Unpublished (1997)

On Jan 19, 1998 this sequence version replaced gi:2285157.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert-Strausbergenin.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Patima Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CON Gistribution: NGI-GGAP clone distribution information can be found through the I.M. A.G.E. Consortium/LiNT at:

www-bio.llni.gov/bbrp/image/image.html
                                                                                                                           seq_documentation_block:

LOCUS
AA84784
DEFINITION od39a01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1370280
similar to TR:Q92615 Q92615 MYELOBLAST KIAA0217;, mRNA sequence.
ACCESSION AA847844
VERSION AA847844. GI:2934362
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases i to 31)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                             constructed by Bento Soares and M. Fatima Bonaldo." 13\ c \ 10\ g \ 5\ t
     /db_xref="taxon:9606"
/clone="IMAGE:1272835"
/clone_lib="NCI_CGAP_GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH108"
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
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Ratio: 2.250
Percent Similarity: 100.000
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US-08-653-294-2 x AA744598
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ORGANISM

VERSION KEYWORDS SOURCE

AUTHORS TITLE

JOURNAL

COMMENT

FEATURES

REFERENCE

alignment_scores

BASE COUNT ORIGIN

31

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alignment_block:
US-08-653-294-2 x T67801
                                                                                                                                                                      alignment_scores:
                                                         BASE COUNT
ORIGIN
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insert size: 1.1 kb; Uni-ZAP XR Vector; -5' adaptor
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 0.8 kb."
4 c 20 g 1 t
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1 (bases 1 to 33)

11 (bases 1 to 33)

12 (bases 1 to 33)

13 (bases 1 to 32)

14 1114er. L. Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Soares, M. B., Tan, F., Thierry-Meg, J. Trevaskis, E., Underwood, K., Koares, M. B., Tan, F., Thierry-Meg, J. Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T67801 32 bp mRNA EST 22-FEB-1995
3739409:s1 Strategene liver (#937224) Homo sapiens CDNA clone
IMAGE:83032 3' similar to gb:X02162 APOLIPOPROTEIN A-I PRECURSOR
(HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Generation and analysis of 280,000 human expressed sequence tags Genome_Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High qality sequence starts: 1
High qality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality
Seq primer: -21ml3
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="GDB:500089"
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Ratio: 2.250 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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r67801.1 GI:678949
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US-08-653-294-2 x AA878823/rev
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AUTHORS
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sequence: 5' GAATTCGGCACGAG 3' ~3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTTT 3'"
                                                         S
B
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Gaps: 0 Gaps: 0 Percent Identity: 100.000 Quality: 9.00 Ratio: 2.250 Percent Similarity: 100.000

:: 2 from: 1 Align seg 1/1 to: T67801

R CTGAGCACCCGG 19 7 Leu*****Arg 10

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein – protein search, using sw model

February 8, 2000, 01:29:34; Search time 122.56 Seconds (without alignments) 1.933 Million cell updates/sec Run on:

US-08-653-294-3 25 1 REXLRXXXXX 10 Title: Perfect score: Seguence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

188963 Total number of hits satisfying chosen parameters:

188963 seqs, 23686106 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

A_Geneseq_36:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARTES

	Description	• •	LA-B7 CTL		Pentide B7 75-84 t		.84-75-84	B7.84	Peptide B7.84-75/7	44	CIL	ပ	õ	Human MORT-1 prote	acid	MSRV-1 virus clone	Human 5' EST secre	. pneumoniae	S. pneumoniae 50S	iae	Amino acid sequenc	acid s	eic acid	\sim	acid	Human FADD protein	ĸ		calcium	calcium	⊶	a.	Exon 1 prod	MORT-1 modulator o
SUMMAKIES	Œ	R41209	R83061	W0/515	M33796	R92913	R95415	W33790	W33797	R41207	R83073	R95431	R95419	W00210	W85049	W67637	Y12165	Y11295	Y11165	W38577	W87491	W87492	W14700	W03653	W87493	W96154	Y07103	R72605	W63157	R72606	W63158	R39697	R30191	R98346
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Modulator of cellu Human adult brain Fragment of MSRV-1 Multiple solerosis UGTLE Exon 1 produ Cyclin D3 protein. Human cyclin D3. N Brevibacterium fla STR3 (suppressor o Thermopsin. Gene e Thermopsin. Gene e Thermopsin.	human crimeric iuc
W11894 W82005 W36025 W71085 R30190 R44804 R28073 R95602	W14332
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ALIGNMENTS

R41209 standard; peptide; 10 AA. R41209; standard; peptide; 10 AA. 15-WAR-1994 (first entry) Peptide fragment of Class I HLA peptide. Human leukocyte antigen; HLA; peptide; transplantation. Parasitic disease; cytotoxic T lymphocyte; modulation. W09317699-A. 16-SEP-1993. 16-SEP-1993. 16-SEP-1993. 16-SEP-1993. 16-SEP-1993. 16-SEP-1993. 16-SEP-1993. 16-SEP-1993. 17-SA4716. (STRD) UNIV LELAND STANFORD JUNIOR. (STRD) UNIV LELAND STANFORD JUNIOR. (STRD) UNIV LELAND FRANFORD JUNIOR. (STRD) UNIV LELAND FRANFORD TONIOR. (STRD) UNIV LELAND STANFORD TONIOR. (STRD) UNIV LELAND STANFORD JUNIOR. (STRD) UNIV LELAND STANFORD JUNIOR. (STRD) UNIV LELAND TANFORD TONIOR. (STRD) UNIV LELAND TANFORD TONIOR. (STRD) UNIV LELAND TANFORD TONIOR. (STRD) UNIV LELAND TONIOR. (STRD) UNIV LELAND TONIOR. (STRD) UNIV LELAND TONIOR. (STANFILLY OF TONIOR TONI	R41209 standard; peptide; 10 AA. R41209; standard; peptide; 10 AA. 15-MAR-1994 (first entry) Peptide fragment of Class I HLA peptide. Human leukocyte antigen; HLA; peptide; transplantation; neoplasi parasitic disease; cytotoxic T lymphocyte; modulation. W09317699-A. 16-SEP-1993. 16-SEP-1993. 16-SEP-1993. 16-SEP-1993. 10-SAR-1992; US-844716. (STRD) UNIV LELAND STANFORD JUNIOR. (STRD) UNIV LELAND S	12	
15-Mar-1994 (first entry) Peptide fragment of Class I HLA peptide. Human leukocyte antigen; HLA; peptide; transplantation; neoplasi parasitic disease; cytotoxic T lymphocyte; modulation. Synthetic. W09317699-A. 16-SEP-1993. 25-FEB-1993; U01758. 02-MAR-1992; US-844716. (STRD) UNIV LELAND STANFORD JUNIOR. Clayberger CA, Krensky AM; WPI; 93-303134/38. New peptide(s) based on class I HLA antigen domains - used for modulating cytotoxic T-lymphocyte activity towards targets Claim 11; Page 54; 61pp; English. The peptide synthition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CT inhibiting CTL toxicity in transplantations, for inducing CT inhibiting CTL toxicity in transplantations, for inducing cactivity, either by inhibition or stimulation. The peptide can also be used for identifying CTLs who infection. The peptide can also be used for identifying CTLs who infection in parasitic diseases and neophasia and in studies on vinfection. The peptide can also be used for identifying CTLs who bind to it and removing subsets of CTLs from a T-cell composition of the sequence is more commonly found within larger peptide sequence is more than 30 amino acids in length. Sequence 10 AA; 1 REXLR 5 1 REXLR 5 1 RESLR 5 1 RESLR 5 1 RESLR 5 1 RESLR 5 1000	### ### ### ### #### #################		41209 standard; peptide; 10 AA.
15-WAR-1994 (first entry) Peptide fragment of Class I HLA peptide. Human leukocyte antigen; HLA; peptide; transplantation; neoplasi parasitic disease; cytotoxic T lymphocyte; modulation. Syntheric. W09317699-N. 16-SEP-1993. 25-FEB-1993; U01758. 02-WAR-1992; US-844716. (STRD) UNIV LELAND STANFORD JUNIOR. Clayberger CA, Krensky AM; WPI; 93-303134/38. New peptide(s) based on Class I HLA antigen domains - used for modulating cytotoxic T-lymphocyte activity towards targets Claim 11; Page 54; Glap; English. The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CT control or stimulation. The peptide sequence is more commonly found within larger peptide sequence is more commonly found within larger peptide of not more than 30 amino acids in length 10; Sequence 10 AA; 1 REXLR 5 1 REXLR 5 1 REXLR 5 1 REXLR 5 1 RESLR 5 20017 2 20017 2 20017 2 20017 2 20017 2 20017 2 20017 2 20017 2	15-WAR-1994 (first entry) Peptide fragment of Class I HLA peptide. Human leukocyte antigen; HLA; peptide; transplantation; neoplasi parasitic disease; cytotoxic T lymphocyte; modulation. Synthetic. W09317699-A. 16-SEP-1993. 25-FEB-1993; U01758. 02-WAR-1999; U01758. 03-WAR-1999; U01758. 03-WAR-1999; U01758. ClaypercrA, Krensky AM; WPI; 93-303134/38. New peptide(s) based on Class I HLA antigen domains - used for modulating cytotoxic T-lymphocyte activity towards targets Claim 11; Page 54; 61pp; English. The peptide (s) based on Class I HLA antigen domains cytotoxic T-lymphocyte activity in parasitic diseases and neoplasia and in studies on vinfaction. The peptide can also be used for inducing CTL toxicity in transplantations, for inducing CTL toxicity in parasitic diseases and neoplasia and in studies on vinfaction. The peptide can also be used for identifying CTLs which of it and removing subsets of CTLs from a T-cell composition compounds of not more than 30 amino acids in length 10; Sequence 10 AA; 1 REXLR 5 1 RESLR 5 1 RESLR 5 2001.		41209;
Peptide fragment of Class I HLA peptide. Human leukocyte antigen; HLA; peptide; transplantation; neoplasi parasitic disease; cytotoxic T lymphocyte; modulation. Synthetic. Synthetic. Synthetic. Synthetic. 16-SEP-1993; U01758. 02-MAR-1992; US-844716. (STRD) UNIV LELAND STANKORD JUNIOR. Clayberger CA, Krensky AM; WPI; 93-3031343. New peptide(s) based on Class I HLA antigen domains - used for modulating cytotoxic T-lymphocyte activity towards targets Claymil; Page 54; 61pp; English. The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibition or stimulations, for inducing CT inhibition or stimulations, for inducing CT inhibition or stimulations, for inducing CT infection. The peptide can also be used for identifying CTLs who bind to it and removing subsets of CTLs from a T-cell composition of it and removing subsets of CTLs from a T-cell composition of not more than 30 amino acids in length. Sequence 10 AA; I REXLR 5 I REXLR 5 I RESLR 5 I RESLR 5 SUUT 2 SUULT 2 3061	Peptide fragment of Class I HLA peptide. Human leukocyte antigen; HLA peptide; transplantation; neoplasi parasitic disease; cytotoxic T lymphocyte; modulation. Synthetic. 16.5EP-1993; U01758. 25.FEB-1993; U01758. Clayberger CA, Krensky AM; WPI: 93-303134/38. New peptide(s) based on Class I HLA antigen domains - used for modulating cytotoxic T-lymphocyte activity towards targets Claim 11; Page 54; 61pp; English. The peptide(s) based on Class I HLA antigen domains - used for modulating cytotoxic T-lymphocyte activity towards targets Claim 11; Page 54; 61pp; English. The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CT activity; in parasitic diseases and neoplasia and in studies on infection. The peptide can also be used for identifying CTLs whishering to it and removing subsets of CTLs from a T-cell compositio This peptide sequence is more commonly found within larger peptil compounds of not more than 30 amino acids in length. Sequence 10 AA; I REXLR 5 SULT 2 3061		5-MAR-1994 (first entry)
Human leukočyte antigen; HLA; peptide; transplantation; neoplasi parasitic disease; cytotoxic T lymphocyte; modulation. Synthetic. W0317699-A. 16-SEP-1992; US-844716. C1-SEB-1992; US-844716. C2-MAR-1992; US-844716. C1-MAR-1992; US-84716. C1-MAR-1992; US-844716. C1-MAR-1992; US-844716. C1-MAR-1992; US-844716. C1-MAR-1992; US-844716. C1-MAR-1992; US-84716. C1-MAR-1992; US-	Human leukocyte antigen; HLA; peptide; transplantation; neoplassi parasitic disease; cytotoxic T lymphocyte; modulation. Synthetic. W03317699-A. H0-SEP-1993. 25-FEB-1993; U01758. 02-WAR-1992; US-844716. (STRD) UNIV LELAND STANFORD JUNIOR. Clayberger CA, Krensky AM; WPI; 93-303134/38. New peptide(s) based on Class I HLA antigen domains - used for modulating cytotoxic T-lymphocyte activity towards targets Claim 1; Page 54; 61pp; English. The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, in parasitic diseases and neoplasia and in studies on vinfection. The peptide can also be used for inducing CTL can be used for inhibiting CTL toxicity in transplantations, for inducing CTL inhibiting CTL toxicity in transplantations of not more than 30 amino acids in length. This peptide sequence is more commonly found within larger peptil compounds of not more than 30 amino acids in length. Sequence 10 AA; Matches 4; Conservative 0; Mismatches 1; Indels 0; I REXLR 5		eptide fragment of Class I HLA peptide.
parasitic disease; cytotoxic T lymphocyte; modulation. W00317699-A. 16-SEP-1993. 16-SEP-1993. 02-MRAR-1992. US-844716. (STRD) UNIV LELAND STANFORD JUNIOR. Clayberger CA, Krensky AM; WPI; 93-303134/38. New peptide(s) based on Class I HLA antigen domains - used for modulating cytotoxic T-lymphocyte activity towards targets Claim 11: Page 54: 61pp: English. The Peptide is used to modulate cytotoxic T-lymphocyte (CTL) The Peptide is used to modulate cytotoxic T-lymphocyte (CTL) The Peptide is used to modulate cytotoxic T-lymphocyte (CTL) The Peptide is used to modulate cytotoxic T-lymphocyte (CTL) The Peptide is used to modulate cytotoxic T-lymphocyte (CTL) The Peptide is used to modulate cytotoxic T-lymphocyte (CTL) The Peptide is used to modulate cytotoxic T-lymphocyte (CTL) The Peptide is used to modulate cytotoxic T-lymphocyte (CTL) The Peptide sequence is more commonly found within larger peptide sequence is more commonly found within larger peptide compounds of not more than 30 amino acids in length 10; Sequence 10 AA; I REXLR 5 I REXLR 7 I REXLR 5 I REXLR 7 I REXLR	parasitic disease; cytotoxic T lymphocyte; modulation. W09317699-A. 16-SEP-1993. 16-SEP-1993. 02-MAR-1992; US-844716. (STRD) UNIV LELAND STANFORD JUNIOR. Clayberger CA, Krensky AM; WPI; 93-303134/38. New peptide(s) based on Class I HLA antigen domains - used for modulating cytotoxic T-lymphocyte activity towards targets Claim 11; Page 54; 61pp; English. The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting TL Loxidity in transplantations, for inducing CT control or stimulation. To activity in parasitic diseases and neoplasia and in studies on vinfection. The peptide can also be used for identifying CTLs whe bind to it and removing subsets of CTLs from a T-cell composition or peptide sequence is more commonly found within larger peptide sequence is more commonly found within larger peptide sequence 10 AA; Sequence 10 AA; Score 19; DB 1; Length 10; Matches 4; Conservative 0; Mismatches 1; Indels 0; I REXLR 5 I REXLR 5 I RESLR 5 I RESLR 5		ransplantation;
Synthetic. W09317699-A. 16-SEP-1993, U01758. 25-FEB-1993, U01758. (STRD) UNIV LELAND STANFORD JUNIOR. Clayberger CA, Krensky AM; WPI; 93-303134/38. New peptide(s) based on Class I HLA antigen domains - used for modulating cytotoxic T-lymphocyte activity cowards targets Claim 11; Page 54; 61pp; English. The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity; in parasitic diseases and neoplasia and in studies on vinfection. The peptide can also be used for inducing CT activity in parasitic diseases and neoplasia and in studies on vinfection. The peptide can also be used for identifying CTLs which is peptide sequence is more commonly found within larger peptil compounds of not more than 30 amino acids in length. Sequence 10 AA; I REXLR 5 I RESLR 5 SUUT 2 SUUT 2	Synthetic. W09317699-A. 16-SEP-1993; U01758. 25-FEB-1993; U01758. C1-WAR-1992; US-844716. (STRD) UNIV LELAND STANFORD JUNIOR. Clayberger CA, Krensky AM; WPL: 93-303134/38. New peptide(s) based on Class I HLA antigen domains - used for modulating cytoctoxic T-lymphocyte activity towards targets Claim 11; Page 54; 61pp; English. The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CT activity; in parasitic diseases and neoplasia and in studies on vinfection. The peptide can also be used for inducing CTLs in the peptide can also be used for inducing CTLs bind to it and removing subsets of CTLs from a T-cell compositio This peptide sequence is more commonly found within larger peptil compounds of not more than 30 amino acids in length. Sequence 10 AA; Matches 4; Conservative 0; Mismatches 1; Indels 0; I REXLR 5		
MÖ9317699-A. 16-SEP-1993; U01758. 25-FEB-1993; U01758. 02-MAR-1992; US-844716. Clayberger CA, Krensky AM; WPI; 93-303134/38. New peptide(s) based on Class I HLA antigen domains - used for modulating cytotoxic T-lymphocyte activity towards targets Claim 11; Page 54; 61pp; English. The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL foxicity in transplantations, for inducing CT activity in parasitic diseases and neoplasia and in studies on vinfection. The peptide can also be used for identifying CTLs who bind to it and removing subsets of CTLs from a T-cell composition This peptide sequence is more commonly found within larger peptide sequence 10 more than 30 amino acids in length. Sequence 10 AA; I REXLR 5 I RESLR 5 I RESLR 5 SULT 2 SULT 2 SULT 2 SULT 2 SOULT 2	MÖ9317699-A. 16-SEP-1993; U01758. 25-FEB-1993; U01758. 02-WAR-1992; UG-844716. Clayberger CA, Krensky AM; WPI; 93-303134/38. Clayberger CA, Krensky AM; WPI; 93-303134/38. Clayberger CA, Krensky AM; WPI; 93-303134/38. Modulating cytotoxic T-lymphocyte activity towards targets Claim 11; Page 54; 61pp; English. The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, in parasitic diseases and neoplasia and in studies on vinfection. The peptide can also be used for inducing CT activity in parasitic diseases and neoplasia and in studies on vinfection. The peptide can also be used for identifying CTLs which peptide sequence is more commonly found within larger peptil peptide sequence is more commonly found within larger peptil compounds of not more than 30 amino acids in length. 30 Duery Match Atch Atch Atch Atch Atch Atch Atch A		vnthetic
16-SEP-1993. 25-FEB-1993. 02-MAR-1992. (STRD) UNIV LELAND STANFORD JUNIOR. New peptide(s) based on class I HLA antigen domains - used for modulating cytotoxic T-lymphocyte activity towards targets Claim 11: Page 54: 61pp: English. The peptide is used to modulate cytotoxic T-lymphocyte (CTL) The peptide is used to modulate cytotoxic T-lymphocyte (CTL) The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL inhibition CTL toxicity in transplantations, for inducing CTL infection or stimulation. It can be used for informity of the peptide sequence is more commonly found within larger peptide sequence is more commonly found within larger peptide compounds of not more than 30 amino acids in length 10: Sequence 10 AA; Atches 4: Conservative 0: Mismatches 1: Indels 0: I REXLR 5 I REXLR 5 I REXLR 5 I REXLR 5 I RESLR 5 I RESLR 5	16-SEP-1993. 25-FEB-1993. U01758. 02-MAR-1992. US-84416. (STRD) UNIV LELAND STANFORD JUNIOR. (STRD) UNIV LELAND STANFORD JUNIOR. (STRD) UNIV LELAND STANFORD JUNIOR. (SAPPETION TREAST AM; WPI; 93-303134/38. New peptide(s) based on Class I HLA antigen domains - used for modulating cytotoxic T-lymphocyte activity towards targets Claim 11; Page 54; 61pp; English. The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing Tractivity in parasitic diseases and neoplasia and in studies on vinfection. The peptide can also be used for identifying CTLs who bind to it and removing subsets of CTLs from a T-cell composition of the peptide sequence is more commonly found within larger peptide sequence is more commonly found within larger peptide sequence 10 AA; Duery Match Best Local Similarity 80.0%; Score 19; DB 1; Length 10; Matches 4; Conservative 0; Mismatches 1; Indels 0; I REXLR 5 I REXLR 5 I RESLR 5 SULT 2 SULT 2 SOULT 2		Ó9317699-A.
25-FEB-1993; U01758. (STRD) UNIV LELAND STARFORD JUNIOR. Clayberger CA, Krensky AM; WPI: 93-303134/38. New peptide(s) based on Class I HLA antigen domains - used for modulating cytotoxic T-lymphocyte activity towards targets. Claim 11: Page 54: 61pp; English. The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CT activity, in parasitic diseases and neoplasia and in studies on vinfection. The peptide can also be used for identifying CTLs which is peptide sequence is more commonly found within larger peptil compounds of not more than 30 amino acids in length. Sequence 10 AA; I REXLR 5 I REXLR 5 I REXLR 5 I RESLR 5 SULT 2 SULT 2 SULT 2 SULT 2 SOURT 3 SOURT 2	25-FEB-1993; U01758. (STRD) UNIV LELAND STARFORD JUNIOR. (STRD) UNIV LELAND STARFORD JUNIOR. Clayberger CA, Krensky AM; WPI; 93-303134/38. WPI; 93-303134/38. New peptide(s) based on Class I HLA antigen domains - used for modulating cytotoxic T-lymphocyte activity towards targets Claim 11; Page 54; 61pp; English. The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL toxicity in parasitic diseases and neoplasia and in studies or activity; in parasitic diseases and neoplasia and in studies or infection. The peptide can also be used for identifying CTLs when the peptide can also be used for identifying CTLs who in the peptide can also be used for identifying CTLs who in the peptide can also be used for identifying CTLs who in the peptide can also be used for identifying CTLs who in the peptide can also be used for identifying CTLs who in the peptide can also be used for identifying CTLs who is accompanied to a compound of the more than 30 amino acids in length. Sequence 10 AA; Matches 4; Conservative 0; Mismatches 1; Indels 0; IREXLR 5 I REXLR 5	_	6-SEP-1993,
02-MAR-1992; US-844716. ClayDerger CA, Krensky AM; WPI; 93-303134/38. Claim 1: Page 54: 61pp: English. The peptide sused to modulate cytotoxic T-lymphocyte (CTL) activity in parasitic diseases and neophasia and in studies on vinfection. The peptide can also be used for inducing CTLs which in parasitic diseases and neophasia and in studies on vinfection. The peptide can also be used for identifying CTLs which is peptide sequence is more commonly found within larger peptide sequence is more commonly found within larger peptide sequence 10 AA; Duery Match Sequence 10 AA; I REXLR 5 I REXLR 5 I RESLR 7 I RESLR 8	02-MAR-1992; US-844716. ClayAR-1992; US-844716. ClayDerger CA, Krensky AM; WPI; 93-303134/38. WPI; 93-30314/38. WPI; 93-30314/38	CI	
Clayberger CA, Krensky AM; WPI: 93-303134/38. New peptide(s) based on class I HLA antigen domains - used for modulating cytotoxic T-lymphocyte activity towards targets Claim 11; Page 54; 61pp; English. The peptide is used to modulate cytotoxic T-lymphocyte (CIL) activity, either by inhibition or stimulation. It can be used for inhibiting CIL toxicity in transplantations, for inducing CI infection. The peptide can also be used for identifying CILs who bind to it and removing subsets of CILs from a T-cell composition This peptide sequence is more commonly found within larger peptid compounds of not more than 30 amino acids in length. Sequence 10 AA; I REXLE 5 I REXLE 5 I RESLE 5 SULT 2 SULT 2 SULT 2 SOULT 2 SOULT 2 SOULT 2 SOULT 2 SOULT 2 SOUR 3061	Clayberger CA, Krensky AM; WPI; 93-303134/38. New peptide(s) based on Class I HLA antigen domains - used for modulating cytotoxic T-lymphocyte activity towards targets Claim 11; Page 54; 61pp; English. The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CT infection. The peptide can also be used for identifying CTLs who infection. The peptide can also be used for identifying CTLs who bind to it and removing subsets of CTLs from a T-cell composition. This peptide sequence is more commonly found within larger peptid compounds of not more than 30 amino acids in length. Sequence 10 AA; I REXLR 5 I REXLR 5 I REXLR 5 I REXLR 5 I RESLR 5 I RESLR 5 I RESLR 5 I RESLR 5 SOULT 2 SOULT 2 SOULT 2 SOULT 2		
Clayberger CA, Krensky AM; WHI; 93-93134/38. New peptide(s) based on Class I HLA antigen domains - used for modulating cytotoxic T-lymphocyte activity towards targets Claim 11; Page 54; 61pp; English. The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibition grat toxicity in parasitic diseases and neoplasia and in studies on vinfection. The peptide can also be used for identifying CTLs who bind to it and removing subsets of CTLs from a T-cell compositio This peptide sequence is more commonly found within larger peptid sequence 10 and one commonly found within larger peptid sequence 10 AA; Duery Match RESLE 5 1 RESLE 5 1 RESLE 5 1 RESLE 5 1 RESLE 5 10 RA 10 RESLE 5	Clayberger CA, Krensky AM; WHI; 93-303134/38. New peptide(s) based on Class I HLA antigen domains - used for medulating cytotoxic T-lymphocyte activity towards targets Claim 11; Page 54; 61pp; English. The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CT activity in parasitic diseases and neoplasia and in studies on vinfection. The peptide can also be used for identifying CTLs who infection. The peptide can also be used for identifying CTLs who infection in the agequence as more commonly found within larger peptide sequence 1s more commonly found within larger peptil compounds of not more than 30 amino acids in length. Sequence 10 AA; Matches 4; Conservative 0; Mismatches 1; Indels 0; I REXLR 5 I REXLR 5 I REXLR 5 I RESLR 5 I	_	LELAND STANFORD
NPI; 93-303134/38. New Peptide(s) based on Class I HLA antigen domains - used for modulating cytotoxic T-lymphocyte activity towards targets Claim 11; Page 54; 61pp; English. The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CT activity in parasitic diseases and neoplasia and in studies on vinfection. The peptide can also be used for identifying CTLs which peptide sequence is more commonly found within larger peptic compounds of not more than 30 amino acids in length. Sequence 10 AA; Second Similarity 80.0%; Score 19; DB 1; Length 10; Best Local Similarity 80.0%; Pred. No. 23; Watches 4; Conservative 0; Mismatches 1; Indels 0; Illi I REXLR 5 I REXLR 5 I RESLR 5 SULT 2 SULT 2	NPI; 93-303134/38. New peptide(s) based on Class I HLA antigen domains - used for modulating cytotoxic T-lymphocyte activity towards targets Claim 11; Page 54; 61pp; English. Claim 11; Page 54; 61pp; English. The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CT activity, in parasitic diseases and neoplasia and in studies on vinfection. The peptide can also be used for identifying CTLs which to it and removing subsets of CTLs from a T-cell compositio compounds of not more than 30 amino acids in length. Sequence 10 AA; Duery Match 76.0%; Score 19; DB 1; Length 10; Best Local Similarity 80.0%; Pred. No. 23; Matches 4; Conservative 0; Mismatches 1; Indels 0; I REXLR 5 I REXLR 5 I RESLR 5 SULT 2 SOULT 2	.0	Krensky AM;
New peptide(s) based on Class I HLA antigen domains - used for modulating cytotoxic T-lymphocyte activity towards targets Claim 11; Page 54; Glpp; English. The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL coxicity in transplantations, for inducing CTL infection. The peptide can also be used for identifying CTLs who bind to it and removing subsets of CTLs from a T-cell composition This peptide sequence is more commonly found within larger peptid compounds of not more than 30 amino acids in length. Sequence 10 AA; Duery Match REXLE 5 I REXLE 5 I REXLE 5 I RESLE 5 SULT 2 SULT 2 SULT 2 SOULT 3 S	New peptide(s) based on Class I HLA antigen domains - used for modulating cytotoxic T-lymphocyte activity towards targets Claim 11; Page 54; Glpp; English. The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CT infection. The peptide can also be used for identifying CTLs who bind to it and removing subsets of CTLs from a T-cell composition. This peptide sequence is more commonly found within larger peptid compounds of not more than 30 amino acids in length. Sequence 10 AA; Sequence 10 AA; Score 19; DB 1; Length 10; Best Local Similarity 80.0%; Pred. No. 23; Matches 4; Conservative 0; Mismatches 1; Indels 0; I REXLR 5 I REXLR 5 I RESLR 5 SULT 2 SULT 2		٠.
modulating cytotoxic T-lymphocyte activity towards targets Claim lip Page 54; 61pp; English The peptide used to modulate cytotoxic T-lymphocyte (CTL) The peptide used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in ransplantations, for inducing CT activity in parasitic diseases and neoplasia and in studies on valuetion. The peptide can also be used for identifying CTLs who bind to it and removing subsets of CTLs from a T-cell compositio This peptide sequence is more commonly found within larger peptid sequence 10 AA; Sequence 10 AA; Juery Match REXLE 5 I REXLE 5 I REXLE 5 I RESLE 5 SUUT 2	modulating cytotoxic T-lymphocyte activity towards targets Claim 11; Page 54; 61pp; English The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CT activity in parasitic diseases and neoplasia and in studies on v infection. The peptide can also be used for identifying CTLs wh long peptide sequence is more commonly found within larger peptin Compounds of not more than 30 amino acids in length. Sequence 10 AA; Duery Match Sest Local Similarity 80.0%; Score 19; DB 1; Length 10; Best Local Similarity 80.0%; Pred. No. 23; Attches 4; Conservative 0; Mismatches 1; Indels 0; I REXLR 5 I REXLR 5 I RESLR 5 I RESLR 5		based on Class I HLA antigen domains - used
Claim 11; Page 54; 61pp; English. The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CT activity; in parasitic diseases and neoplasia and in studies on vinfection. The peptide can also be used for identifying CTLs who bind to it and removing subsets of CTLs from a T-cell compositio compounds of not more than 30 amino acids in length. Sequence 10 AA; Duery Match REXLE 5 1 RESLE 5 1 RESLE 5 1 RESLE 7 1 RESLE 8	Claim 11; Page 54; 61pp; English. The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CT activity; in parasitic diseases and neoplasia and in studies on vinfection. The peptide can also be used for identifying CTLs why in parasitic diseases and neoplasia and in studies on vinfection. The peptide can also be used for identifying CTLs why in paptide sequence is more commonly found within larger peptil compounds of not more than 30 amino acids in length. Sequence 10 AA; Duery Match 76.0%; Score 19; DB 1; Length 10; Best Local Similarity 80.0%; Pred. No. 23; Matches 4; Conservative 0; Mismatches 1; Indels 0;		odulating cytotoxic T-lymphocyte activity towards targets
The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CT toxicity in transplantations, for inducing CT toxicity in transplantations or inducing CTL forms of infection. The peptide can also be used for identifying CTLs who bind to it and removing subsets of CTLs from a T-cell composition. This peptide sequence is more commonly found within larger peptic compounds of not more than 30 amino acids in length. Sequence 10 AA; Duery Match 76.0%; Score 19; DB 1; Length 10; Sequence 10 AA; I REXLE 5 I REXLE 5 I RESLE 5 SULT 2 SULT 2 3061	The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CT coxicity in transplantations, for inducing CT activity in parasitic diseases and neophasia and in studies on vinfection. The peptide can also be used for identifying CTLs wh bind to it and removing subsets of CTLs from a T-cell composition of not more than 30 amino acids in length. Sequence 10 AA; Duery Match 76.0%; Score 19; DB 1; Length 10; Best Local Similarity 80.0%; Pred. No. 23; Matches 4; Conservative 0; Mismatches 1; Indels 0; I REXLR 5 I REXLR 5 I RESLR 5 SULT 2 3061		laim 11; Page 54; 61pp; English.
activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CT activity in parasitic diseases and neoplasia and in studies on alreation. The pettide can also be used for identifying CTLs who bind to it and removing subsets of CTLs from a T-cell compositio This peptide sequence is more commonly found within larger peptide sequence is more commonly found within larger peptid Sequence 10 AA; Duery Match 76.0%; Score 19; DB 1; Length 10; Best Local Similarity 80.0%; Pred. No. 23; Atches 4; Conservative 0; Mismatches 1; Indels 0;	activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CT activity in parasitic diseases and neoplasia and in studies on vinfection. The peptide can also be used for identifying CTLs wh bind to it and removing subsets of CTLs from a T-cell compositio This peptide sequence is more commonly found within larger peptide compounds of not more than 30 amino acids in length. Sequence 10 AA; Sequence 10 AA; Secore 19; DB 1; Length 10; Best Local Similarity 80.0%; Pred. No. 23; Atches 4; Conservative 0; Mismatches 1; Indels 0; I REXLR 5 I REXLR 5 I REXLR 5 I RESLR 5 SULT 2 SULT 2 3061		he peptide is used to modulate cytotoxic T-lymphocyte (CTL)
for inhibiting CTL toxicity in transplantations, for inducing CT activity in parasitic diseases and neoplasia and in studies on vinfection. The peptide can also be used for identifying CTLs who bind to it and removing subsets of CTLs from a T-cell composition. This peptide sequence is more commonly found within larger peptil compounds of not more than 30 amino acids in length. Sequence 10 AA; Duery Match 76.0%; Score 19; DB 1; Length 10; Best Local Similarity 80.0%; Pred. No. 23; Matches 4; Conservative 0; Mismatches 1; Indels 0; REXLR 5	for inhibiting CTL toxicity in transplantatic activity in parasitic diseases and neoplasia infection. The peptide can also be used for bind to it and removing subsets of CTLs from This peptide sequence is more commonly found compounds of not more than 30 amino acids in Sequence 10 AA; The Match 76.0%; Score 19; DB 1; Best Local Similarity 80.0%; Pred. No. 23; Matches 4; Conservative 0; Mismatches		ctivity, either by inhibition or stimulation. It can be used
activity in parasitic diseases and neoplasia and in studies on valufection. The peptide can also be used for identifying CILS whe bind to it and removing subsets of CILS from a T-cell composition. This peptide sequence is more commonly found within larger pepting compounds of not more than 30 amino acids in length. Sequence 10 AA; Duery Match 76.0%; Score 19; DB 1; Length 10; Best Local Similarity 80.0%; Pred. No. 23; Watches 4; Conservative 0; Mismatches 1; Indels 0; I REXLR 5 1 REXLR 5 1 RESLR 5 SULT 2 SULT 2	activity in parasitic diseases and neophasia and in studies on valuation. The peptide can also be used for identifying cris when to it and removing subsets of CTLS from a T-cell composition of the peptide sequence is more commonly found within larger peptide sequence is more commonly found within larger pepting sequence 10 AA; Sequence 10 AA; Duery Match REXLE Similarity 80.0%; Score 19; DB 1; Length 10; Best Local Similarity 80.0%; Pred. No. 23; Matches 4; Conservative 0; Mismatches 1; Indels 0; I REXLE 5 I REXLE 5 SULT 2 SULT 2 SOGI		or inhibiting CTL toxicity in transplantations, for inducing CTL
Infection. The peptide can also be used for identifying CTLS wh bind to it and removing subsets of CTLs from a T-cell compositio This peptide sequence is more commonly found within larger peptid sequence 10 AA; Sequence 10 AA; Duery Match 76.0%; Score 19; DB 1; Length 10; Astches 4; Conservative 0; Mismatches 1; Indels 0; I REXLR 5 1 REXLR 5 1 RESLR 5 1 RESLR 5 1 RESLR 5 3061	infection. The peptide can also be used for identifying CTLS wh bind to it and removing subsets of CTLS from a T-cell compositio. This peptide sequence is more commonly found within larger peptide sequence is more commonly found within larger peptide sequence 10 AA; Sequence 10 AA; Sequence 10 AA; Score 19; DB 1; Length 10; Best Local Similarity 80.0%; Pred. No. 23; Atches 4; Conservative 0; Mismatches 1; Indels 0; I REXLR 5 I REXLR 5 I RESLR 5 SULT 2 SULT 2 3061		ctivity in parasitic diseases and neoplasia and in studies on viral
bind to it and removing subsets of CTLs from a T-cell compositio This peptide sequence is more commonly found within larger peptil compounds of not more than 30 amino acids in length. Sequence 10 AA; Sequence 10 AA; Sequence 10 AA; Sequence 10 AA; Secre 19; DB 1; Length 10; Best Local Similarity 80.0%; Pred. No. 23; Matches 4; Conservative 0; Mismatches 1; Indels 0; REXLR 5 RESLR 5	bind to it and removing subsets of CTLs from a T-cell composition. This peptide sequence is more commonly found within larger peptid compounds of not more than 30 amino acids in length. Sequence 10 AA; Sequence 10 AA; Ouery Match 76.04; Score 19; DB 1; Length 10; Best Local Similarity 80.04; Pred. No. 23; Matches 4; Conservative 0; Mismatches 1; Indels 0; I REXLR 5 I REXLR 5 I RESLR 5 SULT 2 SULT 2 SOLI 2		
This peptide sequence is more commonly found within larger pepti Compounds of not more than 30 amino acids in length. Sequence 10 AA; Sequence 10 AA; Duery Match 76.0%; Score 19; DB 1; Length 10; Best Local Similarity 80.0%; Pred. No. 23; Matches 4; Conservative 0; Mismatches 1; Indels 0; 1 REXLR 5 1 REXLR 5 SULT 2 SULT 2	This peptide sequence is more commonly found within larger pepting compounds of not more than 30 amino acids in length. Sequence 10 AA; Duery Match Best Local Similarity 80.0%; Score 19; DB 1; Length 10; Best Local Similarity 80.0%; Pred. No. 23; Matches 4; Conservative 0; Mismatches 1; Indels 0; I REXLR 5 I REXLR 5 I RESLR 5 SULT 2 SULT 2 SOGI	-	
compounds of not more than 30 amino acids in length. Sequence 10 AA; Sequence 10 AA; Juery Match 76.08; Score 19; DB 1; Length 10; Best Local Similarity 80.08; Pred. No. 23; Atches 4; Conservative 0; Mismatches 1; Indels 0; I REXLR 5 I REXLR 5 I RESLR 5 SULT 2 3061	compounds of not more than 30 amino acids in length. Sequence 10 AA; Sequence 10 AA; Usery Match 76.0%; Score 19; DB 1; Length 10; Best Local Similarity 80.0%; Pred. No. 23; Matches 4; Conservative 0; Mismatches 1; Indels 0; REXLR 5 RESLR 5 SULT 2 SULT 2 3061	_	
Sequence 10 AA; Query Match 76.0%; Score 19; DB 1; Length 10; Best Local Similarity 80.0%; Pred. No. 23; Matches 4; Conservative 0; Mismatches 1; Indels 0; I REXLR 5 I REXLR 5 I RESLR 5 SULT 2	Sequence 10 AA; Duery Match 76.0%; Score 19; DB 1; Length 10; Best Local Similarity 80.0%; Pred. No. 23; Matches 4; Conservative 0; Mismatches 1; Indels 0; I REXLR 5 I I RESLR 5 SULT 2 SULT 2 3061		
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dest Local Similarity (0.1) Pred. No. 23. Matches 4; Conservative 0; Mismatches 1; Indels 0; I REXLR 5 I RESLR 5 SULT 2 3061	dest Matches 4; Conservative 0; Mismatches 1; Indels 0; Matches 4; Conservative 0; Mismatches 1; Indels 0; I REXLR 5 1 RESLR	Š	. 40 . 01
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R83061	R83061	RESULT	
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Tratment of auto-immune disease by admin. of peptide(s) corresp. to major histocompatibility complex antigens - esp. for delaying onset of cilinical symptoms of insulin dependent diabetes by modulating T cell mediated attack on target cells.

Tratment of the contract on target cells modulating peptides that can be used in the method of the invention. These sequences are based on a portion of the method of the invention. These sequences are based on a portion of the method of the invention. These sequences are based on a portion of the generic peptide corresponding to residues 70-91 of the alphal-domain of the major histocompatability complex (MHC) class I antigen (see NVO510). The method is for affecting the course of an autoimmune disease involving T-cell mediated destruction of tissue in mammals. These peptides are used especially to treat insulin-dependent diabetes mellitus, preferably being administered during the pre-clinical stage to delay onset of the disease. Other diseases that can be treated are multiple sclerosis, rheumatoid arthritis, psoriasis, pemphigus vulgaris, sjoren's disease, thyroid disease, Hashimoto's thyroiditis, myasthenia stayet cells, and may also reduce inflammation, swelling, and release of contact of the disease of contact of anotymes etc. associated with T cell activation.
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                                        Claim 13; Page 66; 80pp; English.

This sequence represents a fragment of a class I major histocompatibility complex (MHC) antigen. This sequence corresponds to residues 75-84 of the albha-1 domain of the class I MHC HLA-B7. This sequence, and the peptide fragments represented by R83062-R83085, R83090-R83096 and P82007-R92913 can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLs) of the patient.
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T-cell modulating peptide #4.
T-cell modulator; autoimmune disease; tissue destruction; alphal-domain;
T-cell modulator; autoimmune disease; tissue destruction; perforin;
mammal; major histocompatability complex; MHC class I; antigen; perforin;
insulin-dependent diabetes mellitus; multiple sclerosis; inflammation;
theumatoid arthritis; psoriasis; pemphigus vulgaris; Sjoyren's disease;
thyroid disease; Hashimoto's thyroiditis; myasthenia gravis; granzyme;
autologous target cell; cytokine release; T cell activation; therapy.
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donor hosts - using Class I B75-84 MHC antigen of the recipient
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0; Mismatches
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12-MAY-1995; US-440504.
(SANG-) SANGSTAT MEDICAL CORP.
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Best Local Similarity
Matches 4; Conserv
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1 RESLR 5
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With a proposition of transplants or treating autoriments of transplants or treating autochmeute diseases.

For treating autochmeute diseases.

Example 1; Page 19; 41pp; English.

Peptides Wi3784-98 and Wi3778-9 were assayed for their immunomodulating compound or variant is claimed which has activity. A peptide-type compound or variant is claimed which has climunomodulating activity, including the N-terminal acylated and/or creminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B = CC (terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B = CC (R aa87-771) [aa79-484] or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = CC Small amino acid; aa82 = R or L; aa83 = G or R; and as represents amino acid; aa82 = R or L; aa83 = G or R; and as represents amino acid sequences related to a Class I HLA-B alphal domain (positions or any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a Class I HLA-B alphal domain (positions or 19-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the proliferation of T cells in a combination of treating autoimmune diseases, e.g. diabetes, and also be also the companiant of the peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, and described the products can also be also the companiant of the peptide can be used for preventing can also be also the companiant of the 
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                  W33786;
19-JUN-1998 (first entry)
19-ptide Br.75-84 tested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
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19-JUN-1998 (first entry)
Peptide B7.75-84 tested for immunomodulating activity.
Immunomodulating dimer. Immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
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(STRD ) UNIV LELAND STANFORD JUNIOR.
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22-NAY-1997.
24-NAY-1995. US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                         Beulow R, Clayberger C, Krensky AM;
WPI; 98-086530/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          used for detection and diagnosis
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W33786 standard; peptide; 10
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22-MAY-1997; U08689.
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WO9744351-A1.
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WO9744351-A1.
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Gaps

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DB 1; Length 10; 1; Indels

Score 19; DB Pred. No. 23; 0; Mismatches

76.0%; ilarity 80.0%; Conservative

Query Match Best Local Similarity Matches 4; Conserv

400

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treating autoimmune diseases

Example 1: Page 19: 41pp: English.

Peptides W33784-98 and W33778-9 were assayed for their immunomodulating crivity. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or crivity. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or cretified forms of up to 60 anino acids, where the peptide-type compound comprises the formula; A-B, where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = (D, Sor N; aa79 = R or E, aa80 = I or N; aa10 = E or V; aa77 = (D, Sor N; aa79 = R or E, aa80 = I or N; aa10 = E or V; aa77 = (D, Sor N; aa79 = R or E, aa80 = I or N; aa10 = E or V; aa77 = (D, Sor N; aa79 = R or E, aa80 = I or N; aa10 = E or V; aa77 = (D, Sor N; aa79 = R or E, aa80 = I or N; aa10 = E or V; aa77 = (D, Sor N; aa79 = R or E, aa80 = I or N; aa10 = E or V; aa77 = (D, Sor N; aa79 = R or E, aa80 = I or N; aa10 = E or V; aa77 = (D, Sor N; aa70 = R or E, E or E
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R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B7. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjuction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLs)
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Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HLA-B7.
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Beulow R, Clayberger C, Krensky AM; WPI: 98-086530/008.
New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Extension of acceptance period of transplants from MHC unmatched donor hosts – using Class I B75-84 MHC antigen of the recipient
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05-ARR-1995; U04349.
05-ARR-1994; US-222851.
CTRD ) UNIV LELAND STANFORD JUNIOR.
CLAYDEFGER C, KERNSKY AM, Parham F
WPI; 95-358582/46.
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Matches 4; Conserv
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WO9526979-A1.
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Nat: 95-194027/25.

Nat: 95-194027/25.

National States of Companion of Class                                          ö
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HIA-B7.84-75-84 Palindrome.
HIA-B7.84-75-84 healindrome.
HIA-1974: alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic I lymphocyte; CTL; differentiation;
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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19-JUN-1998 (first entry)
19-Dine B7.84-75/75-84 tested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-I domain;
rejection.
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                                             Indels
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                                         Ξ;
80.0%; Pred. No. 46; ive 0; Mismatches
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80.0%; Pred. No. 46;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytolysis; antigen presenting cell.
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                                                                                                                                                                                                                                                                                                                                                                     R95415 standard; peptide; 20 AA.
R95415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W33790 standard; peptide; 20 AA.
    Best Local Similarity 80.0
Matches 4; Conservative
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10-NOV-1994; U12985.
10-NOV-1993; US-150493.
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Best Local Similarity
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|1 RESLR 15
                                                                                                                    1 REXLR 5
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WO9744351-A1
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R95415
                                                                                                                                                                                                                                                                                                                                                                                                                                            NE HOLD DAY KEE HO
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crivity. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or c-terminal amdated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B = (C-terminal amdated compound comprises the formula; A-B, where A, B = (C-terminal amino acids, and a and a 27 - (C-terminal amino acids aa81 - R or L; aa83 - G or R; and a represents amino acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a Class I HiA-B alphal domain (positions 79-84). They can be used to inhibit cyctoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the proliferation of T cells in response to anti-C2B. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, consulting and lupus erythematosis. The products can also be consulted and also be consulted and also the products can also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New immunomodulating dimer peptide(s) - based on a class I HLA-B alpha-1 domain, used for preventing rejection of transplants or trating autoimmune diseases.

Example 1: Page 19: 41pp: English.

Example 1: Page 19: 41pp: English.

Example 1: Page 19: 42pp: English.

Example 19: 42pp: 42pp: English.

Example 19: 42pp: 42p
                                                                                                                                                                                   New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or treating autoimmune diseases.

Example 1: Page 19: 41pp; English.

Peptides W33784-98 and W33778-9 were assayed for their immunomodulating
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Peptide B7.84-75/75-84 tested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CTL activation; transplantation; autohamune disease; Class I HLA-B alpha-1 domain;
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(STRD ) UNIV LELAND, STANFORD JUNIOR.
Beulow R. Clayberger C, Krensky AM:
WPI; 98-086530/08.
                                                                                       (STRD ) UNIV LELAND STANFORD JUNIOR. Beulow R, Clayberger C, Krensky AM; WPI; 98-086530/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     used for detection and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W33797 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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80.0%;
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27-NOV-1997.
22-MAY-1997; U08689.
24-MAY-1996; US-653294.
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22-MAY-1997; U08689.
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Best Local Similarity
Matches 4; Conserv
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WO9744351-A1.
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     (positions
TL) from
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25-FEB-1993; U01758.

26-MRR-1992; UG-844716.

27-MRR-1992; UG-844716.

28-MRR-1992; UG-844716.

21-MRR-1992; UG-844716.

21-MRR-1993; UNIV LELAND STANFORD JUNIOR.

21-MRR-1993; US-844716.

21-MRR-19
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Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation: therapy;
class I MHC; HLA-Bw62.
amino acid sequences related to a class I HLA-B alphal domain (position 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from undesitably attacking cells in a host or in vitto. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLS. They can also inhibit the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosis. The products can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R41207;
15-MAR-1994 (first entry)
Peptide fragment of Class I HLA peptide.
Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
parasitic disease; cytotoxic T lymphocyte; modulation.
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                                                                                                                                                                                                                                                                                                                      Length 20;
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                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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0; Mismatches
                                                                                                                                                                                                                                                                                                                           Score 19;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R41207 standard; peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                      76.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.0%;
80.0%;
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                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 80.v
Local 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 80.0
Matches 4; Conservative
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05-APR-1995; U04349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 RESLR 15
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WO9526979-A1.
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Will 9194940.720.

While of the comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLS.

Example 12. 29pp. English.

Example 12. 29pp. English.

R65413, and R65415.R95431 represent palindromes and fragments of R65413. And R65415.R95431 represent by R65416. And R65415. And R65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                        HIA-Bw62. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MFC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I imphocytes (CILS) of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLA-B7.60-84.
HLA-B7.60-84.
HLA: p74: alphal-helix; human-leucocyte-associated antigen; inhibitor;
HLA: p74: alphal-helix; human-leucocyte-associated antigen; HSC70; APC;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
R cell: calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
                                                                                                                                                                                                                                               This sequence
                                                                                                                                                                                   Example 13; Page 32; 80pp; English.
R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
class I major histocompetallity complex (MHC) antigens. This sequence
corresponds to residues 60-84 of the alpha-1 domain of the class I MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                     Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 19; DB 1; Length 25;
Pred, No. 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                       Krensky AM, Parham P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-MAY-1995.
10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIY LELAND STANFORD JUNIOR.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytolysis; antigen presenting cell. Synthetic.
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R95431;
12-NOV-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clayberger C, Krensky AM; WPI; 95-194027/25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 4; Conserv
                                                         Clayberger C, Krer
WPI; 95-358582/46.
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16 RESLR 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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Name 1 leucocyte associated antiquenes and radgments on the man-leucocyte associated antiquenes. This sequence represents the HLA-Bw62.60-84. These sequences can be used to isolate the protein from a T-cell lysate. P74 is a T-cell surface membrane protein of sesociated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein HSC70. P74 is found in a limited number of cell types, but is particularly expressed on a and T cells. P74 can be isolated by lysis of a suitable cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HLA-B3702 palindromic peptide.

Containing a covalently bound HLA-B3702 palindromic peptide.

Containing a covalently bound HLA-B3702 palindromic peptide.

Containing a covalently for their effect on the cytolytic activity of T-cells, by combining them with the extracellular portion of p74 and determining the amount of binding between the candidate compound and p74.

Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCS), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete with the present of the p74 in an amount sufficient to compete with the process.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                       HIA; p74; alphal-helix; human-leucocyte-associated antigen; inhibitor; real lysate; membrane protein; mammal; heat shock protein; Hsc70; APC; B cell; calcium influx; cytotoxic I lymphocyte; CTL; differentiation; cytolysis; antigen presenting cell.
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Compsos. comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLs. Example, Page 9, 29pp, English. R95413, and R95415-R95431 represent palindromes and fragments of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-APR-1997 (first entry)

Human MORN-1 protein death domain motif.

Death domain; regulatory protein, NGF-R; nerve growth receptor;

FAS-R; Fas ligand acceptor; ARS-APO1; ankyrin 1; p55 TNF-R;

tumour necrosis factor receptor; MORT1; cell cytotoxicity; HIV;

human immunodeficiency virus; cancer; neoplasia; disease.
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  Length 25;
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                                          Indels
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Score 19; DB 1
Pred. No. 56;
0; Mismatches
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Pred. No. 56;
0; Mismatches
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                                                                                                                                                                                                                          R95419 standard; peptide; 25 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W00210 standard; peptide; 62 AA.
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                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clayberger C, Krensky AM;
WPI; 95-194027/25.
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Best Local Similarity 80.0
Matches 4; Conservative
                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                18-MAY-1995.
10-NOV-1994; U12985.
Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                    HLA-Bw62.60-84
                                                                                                                      16 RESLR 20
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                                                                              1 REXLR 5
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                                                                                                                                                                                    RESULT
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WO0210
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Wallacto D:

Warlactor of regulatory cellular events mediated by "death domain"

Words regulatory proteins - useful for modulating functions

PT contg. regulatory proteins - useful for modulating functions

PT mediated in cells by proteins contg the death domain

Claim 9: Fig 1: Napp: English.

W00210 shows the death domain of the WRT-1, which binds to the

CC intracellular portion of the human Fas-ligand receptor (FAS-R). The

CC intracellular portion of the human Fas-ligand receptor (FAS-R). The cath domain (DD) of FAS-R, p55 tumour necrosis factor receptor

CC qiven (see W00206 and W00208 w00210). These DDs are used to identify

CC qiven (see W00206 and W00208 w00210). These DDs are used to identify

CC qiven (see W00206 and W00208 w00210). These DDs are used to identify

CC such modulators which may be antibodies, antisense sequences or

Inboxymes (which can affect the cellular mRAA sequences or other

CC such modulators which may be antibodies, antisense sequences or other

CC such modulators within the cell. Tumour cells, HV-infected cells or other

CC diseased cells can be treated by targeting the cells with animal viral

CC diseased cells can be treated by targeting the cells with animal viral

CC diseased cells can be treated by targeting the ASP, Glu, Thr, Arg and

The common amino acid residues Trp, Ala, ASP, Glu, Thr, Arg and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptides reactive with multiple sclerosis antibodies - useful for diagnosis or vaccine preparation.

Example 4, Fig 4, 43pp; French.

The present sequence is encoded by clone GM3 and represents a region from a protein of multiple sclerosis-associated retrovirus MSRV-1.

Peptides that specifically react with antibodies from multiple sclerosis (MS) patients can be derived from the sequence. The peptides can be used to diagnose or monitor multiple sclerosis, and to detect the multiple sclerosis and to detect the autiple sclerosis exection in untitiple sclerosis or MSRV-1. The peptides can also be used for "fixation" of multiple sclerosis or MSRV-1 antibodies in blological samples, especially serum, cerebrospinal fluid or urine. Vaccines can also be prepared from the peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                      Mett I, Pancer 2, Varfolomeev EE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               roups of common amino acid residues Trp, Ala, Asp, Glu, Try within locations that can be aligned to show homology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-FEB-1999 (first entry)
Multiple sclerosis; MS; antibody fixation;
multiple sclerosis; MS; antibody fixation;
multiple sclerosis-associated retrovirus; MSRV-1; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.0%; Score 19; DB 1; Length 62;
80.0%; Pred. No. 1.4e+02;
ive 0; Mismatches 1; Indels
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Jolivet RC, Mandrand B, Perron H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W85049 standard; Protein; 95 AA.
                                                                                                               13-SEP-1995; IL-115289.
(WEIN,) WEINWIZEL H
(YEDA ) YEDA RES & DEV CO LTD.
Boldin MP, Goncharov TM, Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 76.0
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-APR-1997; FR-005679.
                                                                                            2-FEB-1995; IL-112742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-DEC-1997; 016870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 98-586098/50.
N-PSDB; V63612.
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W85049
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Query Match
Best Local Similarity 80.0%; Score 19; DB 1; Length 95;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 1; Indels
Qy 1 REXLR 5
|| || ||
Db 16 REALR 20
Search completed: February 8, 2000, 01:29:35
Job time: 1747 sec
```

95 AA;

Sequence

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Gaps

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

February 7, 2000, 11:54:11; Search time 117.7 Seconds (without alignments) 4.008 Million cell updates/sec Run on:

US-08-653-294-3 25 1 REXLRXXXXX 10 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

142080 segs, 47169319 residues Searched:

142080 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

PIR_62:* Database :

pirl:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	stic	pepsin (EC 3.4.23.	probable ribosomal	2K112.4 protein -	hypothetical prote		듺	hoxL protein - Azo	hypothetical prote		ն	w	ribosomal protein	somal pr	class	ss I hist	class I	class I	н	hypothetical prote	Ω	o	_	_	hypothetical prote	n tyrosin			othetical prot	MHC CEIT SULIACE G
SOMMAKIES	ţ	OT .	D69330	S01800	064	S44892	S19733	C75046	S26322	B44915	S74019	C24733	C72247	JQ0370	S78260	5xm1	138875	180176	138876	I38860	I38874	E69359	F69130	B69696	F64000	S40999	S75758	C75157	A37815	B70760	F72600	129188
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hypothetical 20.3	RNA polymerase ECF	hypothetical prote	RAG-1 protein - go	conserved hypothet	nifQ protein - Azo	hypothetical prote	probable regulator	ruvA protein - Esc	hypothetical prote	netical	yagK protein - Esc	orotein -	receptor-induced t	probable transcrip
E65105	H69706	069867	150123	H70375	E27733	669459	G70752	BVECRV	C36795	T02685	E64753	A56912	138041	C70652
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186	187	191	192	192	195	197	202	203	202	202	208	208	208	209
76.0	76.0	76.0	76.0	76.0	76.0	76.0	76.0	76.0	76.0	76.0	76.0	76.0	76.0	0.94
19	13	61	19	19	19	19	19	19	19	19	19	19	19	19
31	32	ED :	34	32	36	37	38	36	40	41	42	43	44	45

ALIGNMENTS

Popsin (EC 3.4.23.-) 3 precursor - North Pacific bluefin tuna (fragment)
pepsin (EC 3.4.23.-) 3 precursor - North Pacific bluefin tuna)
C;Species: Thunnus thynnus orientalis (North Pacific bluefin tuna)
C;Species: Thunnus 1990 #sequence_revision 07-Jun-1990 #text_change 08-Nov-1996
C;Accession: S01800
R;Tanji, M.; Kageyama, T.; Takahashi, K.
Eur. J. Blochem. 177, 251-259, 1988
Eur. J. Blochem. 177, 251-259, 1988
A;Title: Tuna pepsinogens and pepsins. Purification, characterization and amino-termi A;Reference number: S01798; MUID:89052692
A;Accession: S01800
A;Accession: S01800
A;Molecule type: protein
A;Residues: 1-60 cTAN>
C;Superfamily: pepsin
C;Superfamily: pepsin
F;1-35/Domain: propeptide #status experimental <AMI>
F;36-60/Product: pepsin (fragment) #status experimental <AMI> RESULT S01800

Gaps ; 0 Ouery Match 76.0%; Score 19; DB 2; Length 60; Best Local Similarity 80.0%; Pred. No. 85; Matches 4; Conservative 0; Mismatches 1; Indels

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Gaps

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Indels

Length 102;

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A;Molecule type: DNA
A;Residues: 1-104 <KAM>
A;Cross-references: GB:AJZ48287; GB:AL096836; NID:g5458657; PIDN:CAB50264.1; PID:e151
A;Experimental source: strain Orsay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Species: Pyrococcus abyssi
C; Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C; Accession: C75046
R; anonymous, Genoscope
Submitted to the EMBL Data Library, July 1999
A; Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Species: Mus musculus (house mouse)
C; Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 17-Apr-1998
C; Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 17-Apr-1998
R; Stark, S. E.; Caton, A.J.
Fxp. Med: 174, 613-624, 1991
A; Title: Antibodies that are specific for a single amino acid interchange in A; Reference number: $26309; MUID::91341421
A; Accession: $26322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-106 <STRA-
A; Cross-references: EMBL:X59182
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein PAB0900 - Pyrococcus abyssi (strain Orsay)
                                                                                                                   A; Cross-references: GB: M58001; NID: g154632; PID: g154636
                                                                                                                                                                                      Score 19; DB 2; Le
Pred. No. 1.5e+02;
0; Mismatches 1;
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Pred. No. 1.5e+02;
0; Mismatches 1;
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A; Reference number: S19730; MUID:92111471
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80.0%;
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Best Local Similarity 80.0%;
Matches 4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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A, Accession: C75046
A, Status: preliminary
                         A; Accession: S19733
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-102 < UBB>
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95 REALR 9
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                                                                                                                                                        probable ribosomal protein L30 rpmD - Mycobacterium tuberculosis (strain H37RV)

C.Species: Mycobacterium tuberculosis

C.Species: Mycobacterium tuberculosis

C.Spate: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 24-Sep-1999

C.Accession: E70644

R.Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S. Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamilin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Atile: Deciphering the biology of Mycobacterium tuberculosis from the complete genome, A;Accession: E70644
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R;Ubbink, M.; van Kleef, M.A.G.; Kleinjan, D.J.; Hoitink, C.W.G.; Huitema, F.; Beintema, Eur. J. Biochem. 202, 1003-1012, 1991
Eur. J. Biochem. 202, 1003-1012, 1991
A;Title: Cloning, sequencing and expression studies of the genes encoding amicyanin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A:Cross-references: GB:284395, GB:AL123456; NID:g3261698; PIDN:CAB06446.1; PID:e293132; A:Experimental source: strain H37Rv C;Genetics: C;Genetics: A;Gene: IpmD C;Superfamily: Escherichia coli ribosomal protein L30
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A;Residues: 1-65 <COL>
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Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 09-Sep-1997
Accession: S44892
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Pred. No. 1.4e+02;
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A;Residues: 1-100 <DU2>
A;Cross-references: EMBL:L14324; NID:9289740; PID:9289747
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Submitted to the EMBL Data Library, May 1993
A;Description: Sequence of the C. elegans cosmid ZK112.
A;Accession: $44892
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0; Mismatches
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Matches 4; Conserv
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20 RESLR 24
1 REXLR 5
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photosystem I 11K protein precursor - Chlamydomonas reinhardtii
photosystem I 11K protein precursor - Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 26-Aug-1999
C;Accession: J00370; 806063
R;Franzen, L.G; Frank, G; Zuber, H.; Rochaix, J.D.
Mol. Gen. Genet. 219, 137-144, 1989
A;Title: Isolation and characterization of cDNA clones encoding photosystem I subunit
A;Reference number: J00370; MUID:90136501
A;Molecule type: MRNA
A;Residues: 1-130 <FRA>
A;Cross-references: EMBL:X15164; NID:918191; PIDN:CAA33256.1; PID:918192
C;Comment: Photosystem I catalyzes the light-driven electron transfer from plastocyan
C;Comment: This protein is an extrinsic membrane protein.
C;Superfamily: photosystem I protein psaH
C;Superfamily: photosystem I protein psaH
C;Superfamily: photosystem I llK protein #status predicted <NAP>
F;31-130/Pondain: transit peptide (chloroplast) #status predicted <NAT>
                                                                                                                                                                                                                ribosomal protein SII - Thermotoga maritima (strain MSB8)
C;Species. Thermotoga maritima
C;Species. In-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 23-Jul-1999
C;Accession: C72247
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                              Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome A; Reference number: A72200; MUID:99287316
A; Accession: C72247
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-130 < ARN>
A; Cross-references: GB:AE001798; GB:AE000512; NID:94982033; PID:94982040; TIGR:TM1474
A; Experimental source: strain MSB8
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llarity 80.0%; Pred. No. 1.9e+02;
Conservative 0; Mismatches 1; Indels
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C;Superfamily: Escherichia coli ribosomal protein Sl1
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Pred. No. 1.9e+02;
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  4; Conservative
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Best Local Similarity
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J. Bacteriol. 174, 4549-4557, 1992
J. Bacteriol. 174, 4549-4557, 1992
Aritile: Nucleotide sequences and genetic analysis of hydrogen oxidation (hox) genes in A; Reference number: A4915; MUID:92325046
A; Reference number: preliminary
A; Status: preliminary
A; Molecule type: DMA
A; Residues: 1-106 <MEN>
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Proc. Natl. Acad. Sci. U.S.A. 82, 7183-7187, 1985
A;Reference number: A94066; MUID:86042630
A;Accession: C24733
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A;Title: Organizational characteristics and information content of an archaeal genome: A;Reference number: S73076; MUID:97055432
A;Reference number: S73076; MUID:97055432
A;Sterus: nucleic acid sequence not shown; translation not shown
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A;Cross-references: BMBL:V08256; NID:g1707679; PID:e284023; PID:g1707713
A;Experimental source: strain P2
A;Experimental source: strain P2
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1996
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                        noxL protein - Azotobacter vinelandii
C;Species: Azotobacter vinelandii
C;Date: 01-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 13-Sep-1998
C;Accession: B44915
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C:Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 17-Mar-1999
C:Accession: S74019
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C:Date: 24-Jun-1987 #sequence_revision 24-Jun-1987 #text_change 13-Feb-1998
C;Accession: C24733
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C;Superfamily: hydrogenase related protein
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A; Residues: 1-124 <NEXP.
C; Superfamily: myosin heavy chain; myosin motor domain homology
C; Keywords: ATP; cardiac muscle; heart; muscle
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Pred. No. 1.5e+02;
0; Mismatches 1; Indels
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Pred. No. 1.5e+02;
0; Mismatches 1; Indels
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Length 137 1; Indels

Score 19; DB 2; Pred. No. 2e+02; 0; Mismatches

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C;Species: Homo sapiens (man)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
C;Accession: 138875
C;Accession: 138860; MUID:95317819
A;Title: HLA-B alleles of the Cayapa of Ecuador: new B39 and B15 alleles.
A;Reference number: 138860; MUID:95317819
A;Accession: 138875
                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-137 < RES.>
A; Cross-references: EMBL:U15639; NID:9930332; PIDN:AAA74046.1; PID:9930333
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
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Matches 4: Conservative
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ribosomal protein L18, chloroplast - Odontella sinensis chloroplast
C; Species: chloroplast Odontella sinensis
C; Date: 17-Feb-1998 #Sequence_revision 26-Feb-1998 #text_change 13-Aug-1999
C; Accession: 57826
R; Kowallik, K.V.; Stoebe, B.; Schaffran, I.; Kroth-Pancic, P.; Freier, U.
Plant Mol. Biol. Rep. 13, 336-342, 1995
A; Title: The Chloroplast Genome of a chlorophyll a+c- containing Alga, Odontella sinensi
A; Reference number: 57828
A; Accession: 57826
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-135 < KOW>
A; Residues: 1-135 < KOW>
A; Residues: 1-135 < KOW>
A; Rosidues: L135 < KOW>
A; Residues: L135 < KOW>
A; Rosidues: L135 < KOW>
A; Residues: L135 < Kowentics: C; Superfamily: Bscherichia coli ribosomal protein L18
C; Keywords: chloroplast; protein biosynthesis; ribosome
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A; Residues: 1-137 <OHK>
A; Cross-references: EMBL:X06414; NID:g44207; PIDN:CAA29711.1; PID:g44216
A; Cross-references: EMBL:X06414; NID:g44207; PIDN:CAA29711.1; PID:g44216
A; Experimental source: ATCC 27343
R; Bork, P.; Ouzounis, C.; Casari, G.; Schneider, R.; Sander, C.; Dolan, M.; Gilbert, W.; Mol. Microbiol. 16, 955-967, 1995
Mol. Microbiol. 16, 955-967, 1995
A; Title: Exploring the Mycoplasma capricolum genome: a minimal cell reveals its physiolo A; Reference number: S77739; MUID:96059641
A; Accession: S77860
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A:Experimental source: ATCC 27343
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
C; Genetics:
A; Genetics:
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C;Species: Mycoplasma capricolum
C;Date: 28-May-1986 #sequence_revision 31-Dec-1990 #text_change 22-Jun-1999
C;Accession: S02838; S77860: A02797; S48576
R;Ohkubo, S.; Muto, A.; Kawauchi, Y.; Yamao, F.; Osawa, S.
Mol. Gen. Genet. 210, 314-322, 1987
A;Title: The ribosomal protein gene cluster of Mycoplasma capricolum.
A;Reference number: S02830; MUID:88142549
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Pred. No. 2e+02;
0; Mismatches 1; Indels
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Pred. No. 2e+02;
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C;Superfamily: Escherichia coli ribosomal protein L16
C;Keywords: protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - Mycoplasma capricolum (SGC3)
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80.0%;
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Best Local Similarity 80.0%;
Matches 4; Conservative (
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Best Local Similarity 80.0
Matches 4; Conservative
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28 RESLR 32
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streptomyce corynebacte sulfolobus

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homo sapien mus musculu bradyrhizob

thermus agu

P37641 P19844 P06150

mycobacter1 emericella

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Perfect score:

Seguence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database :

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STRAIN=H37RV;
MEDLINE; 98295987.
COLE S.T., BROSCH R., PARKHILL J., GARNIER T., CHURCHER C., HARRIS D.,
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REL30_MYCTU STANDARD; PRT; 65 AA.

LD PS5070;
DT 15-DEC-1999 (Rel. 39, Created)
DT 15-DEC-1999 (Rel. 39, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DF 50S RIBOSOWAL PROTEIN L30.
GN RPMD OR RV0722 OR MYCV210.41.
GN RPMD OR RV0712 OR MYCV210.41.
GS Mycobacterium tuberculosis.
CS Bacteria; Firmicutes; Actinobacteriaes; Mycobacterium.

OC Actinomycetales; Corynebacterineae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                       01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-RD-1995 (Rel. 32, Last annotation update)
PEPSINOGEN 3 (EC 3.4.23.-) (FRAGMENT).
Thunnus thynnus orientalis (North Pacific bluefin tuna).
Eukaryota, Metazoa, Chordata, Craniata; Vertebrata; Actinopterygii;
Perciformes; Scombroidei; Scombridae; Thunnus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EUI. J. Blochem. 177:251-259(1988).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1; ALSO KNOWN AS THE EUKARYOTIC ASPARTYL PROTEASES FAMILY.
BISSP: P56272; JAM5.
HSSP: P56272; JAM5.
PROSITE; P800141; ASP_PROTEASE; PARTIAL.
Hydrolase; Aspartyl protease; 2ymogen.
PROPEP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE.
MEDLINE: 89052692.
TANJI M., KAGETAMA I., TAKAHASHI K.;
TANJI M., KAGETAMA I., TAKAHASHI K.;
"Tuna pepsinogens and pepsins. Purification, characterization and amino-terminal sequences.";
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ACTIVATION PEPTIDE.
PEPSIN 3.
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Pred. No. 47;
0; Mismatches
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YHJC_ECOLI
NOSF_PSEST
DHGA_EMENI
HEM2_MYCLE
HEM2_STRCO
BIOB_CORGL
THPS_SULAC
1B24_HUMAN
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CPXU_BRAJA
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P34011
P34011
P405501
P405611
P40592
P403352
P403354
P10452
P10452
P1068
P106
                     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                           82229 seqs, 29864866 residues
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YAGK_ECOLI
IFE4_CAEEL
ET3_MOUSE
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HOXL_AZOVI
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Listing first 45 summaries
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    protein search, using sw model

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GORDON S.V., EIGLMEIER K., GAS S., BARRY C.E. III, TEKAIA F.,
BADCCCK K., BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R.,
BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R.,
HORNES R., DEVLIN K., FELTWELL T., GENTLES S., HAMLIN N., HOLNOY S.,
HORNEST T., JAGELS K., KROGH A., MCLEAN J., MOULE S., MURPHY L.,
OLIVER S., OSBORNE J., QUAIL M.A., RAJANDREAM M.A., ROGERS J.,
ROTTER S., SEGEBER K., SKELTON S., SQUARES S., SQARES R., SULSTON J.E.,
TAXLOR K., WHITEHEAD S., BARRELL B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium leprae.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                           Nature 393:337-544(1998).
-!- SIMILARITY: BELONGS TO THE L30P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COLE S.T., FLESSELLES B., HONORE N.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE L30P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 65,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
508 RIBOSOMAL PROTEIN L30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9253D057 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             779051E0 CRC32;
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Pred. No. 56;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00634; RIBOSOMAL_L30; FALSE_NEG.
PFAM; PF00327; Ribosomal_L30; 1.
Ribosomal protein 7346 MW; 9253D057 CRC32
SEQUENCE 65 AA; 7346 MW; 9253D057 CRC32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS00634; RIBOSOMAL_L30; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 19;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00327; Ribosomal_L30; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1998 (Rel. 36, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.0%;
80.0%;
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z84395; CAB06446.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; 298756; CAB11454.1; -
                                                                                                                                                                                                         complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 76.0
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RPMD OR MLCB2492.22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ribosomal protein.
SEQUENCE 71 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESLR 24
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033001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RL30_MYCLE
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                                                                                                                                                                                                                                                                                                                                                                    WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., COULSON A., BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A., ERAZIELD J., BURTON J., CONNELL M., COPER T., COOPER J., COLLSON A., COLLSON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FRASER A., JOHNSTON L., JONES M., KERSHEN P., HILLIER L., JIER M., JOHNSTON L., JONES M., KERSHEN J., LAISSTER N., LAIGHTNING J., LLOYD C., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C., RIFEN L., ROOPRA A., SAUNDERS D., SHOWNKEN R., SULSTON J., PERCY C., RIFEN L., ROOPRA A., SAUNDERS D., SHOWNKEN R., SULSTON J., THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WAITSON J., WAITSON A., WAITSON A., WAITSON A., WILKINSON-SPROAT J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         '2.2 Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Azotobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                    01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-TUN-1994 (Rel. 29, Last annotation update)
HYPOTHETICAL 11.2 KD PROTEIN ZK112.4 IN CHROMOSOME III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            il protein.
100 AA; 11248 MW; 52F18207 CRC32;
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01-FEB-1995 (Rel. 31, Last annotation update)
HYDROGENASE EXPRESSION/FORMATION PROTEIN HOXL
100 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 81;
0; Mismatches
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Pred. No. 6
  PRT;
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(Rel. 31, Last sequ
(Rel. 31, Last anno
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80.0%;
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WORMPEP; ZK112.4; CE00375.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
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  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 368:32-38(1994).
                                                                                                                                                                                       Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Azotobacter vinelandii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                     STRAIN-BRISTOL N2;
MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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01-FEB-1995 (
01-FEB-1995 (
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SEQUENCE 10
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P40592;
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YOG4_CAEEL
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31 1
130 AA:
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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80 RESLR 84
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                                              SEQUENCE
  TRANSIT
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MEDLINE: 90136501.
FRANZEN L.-G., FRANK G., ZUBER H., ROCHAIX J.-D.;
"ISOLAtion and characterization of cDNA clones encoding photosystem I subunits with molecular masses 11.0, 10.0 and 8.4 kDa from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-FB-1996 (Rel. 33, Last annotation update)
PHOTOGYSTEM I REACTION CHENTE SUBUNIT VI PRECURSOR (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlamydomonas reinhardtii.
Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
Chlamydomonadaceae, Chlamydomonas.
                                                                                          Nucleotide sequences and genetic analysis of hydrogen oxidation
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Photosynthesis; Photosystem I; Chloroplast; Transit peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                (hox) genes in Azotobacter vinelandii.";
J. Bacteriol. 174:4549-4557(1992).
-!- SIMILARITY: BELONGS TO THE HUPF/HYPC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 19; DB 1;
Pred. No. 86;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM; PF01455; HupF_HypC; 1.
SEQUENCE 106 AA; 11436 MW; 3113532D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 AA.
                                                                      ., MORTENSON L.E., ROBSON R.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M80522; AAA22127.1; -.
EMBL; L23970; AAA19502.1; -.
PPR; B44915; B44915;
PROSITE; PS01097; HUPF_HYPC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X15164; CAA33256.1; -. PIR; S06063; S06063.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 76.0%;
Similarity 80.0%;
4; Conservative
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Best Local Similarity
Matches 4; Conserv
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  SEQUENCE FROM N.A.
                                            MEDLINE; 92325046
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P13352;
                                                                    MENON A.
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CHLOROPLAST.
PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI.
                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

KOWALLIK K.V., STOEBE B., SCHAFFRAN I., KROTH-PANCIC P., FREIER U.;

The chloroplast genome of a chlorophyll a+c-containing alga,
oddontella sinensis.";

Plant Mol. Biol. Rep. 13:336-342(1995).

-! SIMILARITY: BELONGS TO THE LIBP FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, stramenopiles, Bacillariophyta, Coscinodiscophyceae;
Biddulphlophycidae, Eupodiscales; Eupodiscaceae, Odontella.
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Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
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                                                                                                           RESULT 8
RL16_MYCCA STANDARD; PRT; 137 AA.

ID RL16_MYCCA STANDARD; PRT; 137 AA.

AC P02415;
DT 21-4U1-1986 (Rel. 01, Created)
DT 01-MAR-1989 (Rel. 33, Last annotation update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DF NS RIBOSOMAL PROTEIN L16.
GN RRDP.
OS Mycoplasma capricolum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
CC Capricolum group.
RP SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; 267753; CAA91633.1; -.
MENDEL; 9483; ODOSi;rpl18;1.
PFOWS61; Ribosomal_L18p; 1.
SEQUENCE 135 AA; 15417 MW; 524017AC CRC32;
                                                  37EAE662 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
CHLOROPLAST 50S RIBOSOMAL PROTEIN L18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       135 AA.
                                                                                                                                                                                               0; Mismatches
                                                        14151 MW;
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80.0%;
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SIMILARITY)
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                                                                                                                                                                                                             YAMAO F., MUTO A., KAWAUCHI Y., IWAMI M., IWAGAMI S., AZUMI Y., OSAWA S.;
"UGA is read as tryptophan in Mycoplasma capricolum.";
Proc. Natl. Acad. Sci. US.A. 82:2306-2309(1985).
-i- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AND IS LOCATED AT THE A SITE OF THE PEPTIDYLITRANSFERASE CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=ATCC 27556 / R8A2;
LE DANTEC L., SAILLARD C., BOVE J.M.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: THIS PROFER BINDS DIRECTLY TO 23S RIBGSOMAL RNA AND IS
LOCATED AT THE A SITE OF THE PEPTIDYLTRANSFERASE CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                      SEQUENCE FROM N.A.
STRAIN-ATCC 27343 / KID;
MEDLINE; 96059641.
BORK P., OUZOUNIS C., CASARI G., SCHNEIDER R., SANDER C., DOLAN M.,
GILBERT W., GILLEVET P.M.;
"Exploring the Mycoplasma capricolum genome: a minimal cell reveals
                                                                                                                                                                                                                                                                                       (BY SIMILARITY).
SIMILARITY: BELONGS TO THE LIGP FAMILY OF RIBOSOMAL PROTEINS.
STRAIN-ATCC 27343 / KID;
MEDLINE; 88142549.
OKRUBO S., MUTO A., KAWAUCHI Y., YAWAO F., OSAWA S.;
"The ribosomal protein gene cluster of Mycoplasma capricolum.";
MOI. Gen. Genet. 210:314-322(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes; Spiroplasmataceae; Spiroplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76.0%; Score 19; DB 1; Length 137; 80.0%; Pred. No. 1.1e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68B1D725 CRC32;
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
50S RIBOSOWAL PROTEIN L16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137 AA
                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, X06414; CAA29711.1; -.
EMBL, 233011; CAA88693.1; -.
EMBL, KO2973; AAA25439.1; -.
PIR; SO2888; R5YML,
PROSITE; PS00586; RIBOSOWAL_L16_1; 1.
PROSITE: PS00251; RiboSOWAL_L16_2; 1.
PFAM; PP00252; RiboSOWAL_L16_2; 1.
RLDOSOMAL Proctein; TRNA binding.
SEQUENCE 137 AA; 15799 MW; 68BID725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                 its physiology.";
Mol. Microbiol. 16:955-967(1995).
                                                                                                                                                                                    SEQUENCE OF 1-117 FROM N.A. MEDLINE; 85190486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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Best Local Similarity
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031162;
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STAIN-DELTA H;

A MEDLINE; 98037514.

A ALDREDGE T., BASHIRADEH R., BLAKELY D., COOK R., GILBERT K.,

ALDREDGE T., BASHIRADEH R., BLAKELY D., COOK R., GILBERT K.,

A ALDREDGE T., BASHIRADEH R., BLAKELY D., COOK R., GILBERT K.,

A HARRISON D., HOANG L., KEAGLE P., LUMM W., POTHIER B., OUT D.,

SPADAFORA R., VICARE R., WANG Y., WIERZBOWSKI J., GIBSON R.,

JUMNI N., CARUSO A., BUSH D., SAFER H., PATWELL D., PRABHAKA S.,

A MCDOUGALL S., SHIMER G., GOYAL A., PIETROVSKI S., CHURCH G.M.,

DANIELS C.J., MAO J.-I., RICE P., NOLLING J., REEVE J.N.;

"Complete genome sequence of Methanobacterium thermoautotrophicum
deltah: functional analysis and comparative genomics.";

J. Bacteriol. 179:7135-7155(1997).

C. -! CATALYTIC ACTIVITY: S-PHOSPHOPORMIMINO)-1-(5-PHOSPHO-RIBOSYL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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SIMILARITY: BELONGS TO THE LI6P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 137;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 19; DB 1; Length 137 Pred. No. 1.1e+02; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
PHOSPHORIBOSYL-AMP CYCLOHYDROLASE (EC 3.5.4.19).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PSUV/U1; ALCOSOMELLIG; 1.
PFAM; PF00252; Ribosomel rRNA-Dinding.
Ribosomel protectin; 7RNA-Dinding.
15742 MW; 971D639D CRC32;
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PFAM; PF01502; PRA-CH; 1.
Attidine biosynthesis; Hydrolase.
SEQUENCE 138 AA; 15458 MW; BAEB24D6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 AA.
                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF031160; AAC35871.1; -. PROSITE; PS00586; RIBOSOMAL_L16_1; 1. PROSITE; PS00701; RIBOSOMAL_L16_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Methanobacterium thermoautotrophicum
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80.0%;
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Best Local Similarity 80.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             spc-alpha region.";
Gene 169:17-23(1996).
-!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AND IS
-!- COATED AT THE A SITE OF THE PEPTIDYLIRANSFERASE CENTER.
-!- SIMILARITY: BELONGS TO THE L16P FAMILY OF RIBOSOMAL PROTEINS.
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                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 96186897.
SUH J.W., BOYLAN S.A., OH S.H., PRICE C.W.;
"Genetic and transcriptional organization of the Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDILINE; 90016806.
HENKIN T.M., MOON S.H., MATTHEAKIS L.C., NOMURA M.;
"Cloning and analysis of the spc ribosomal protein operon of Bac
subtilis: comparison with the spc operon of Escherichia coll.";
Nucleic Acids Res. 17:7469-7486(1989).
                                                                                        ö
                         Length 138;
Score 19; DB 1; Lengtn 100
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-SG38;
LI X., LINDAHL L., ZENGEL J.M.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YOSHIKAWA H., YASUMOTO K., TAKAHASHI H.;
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ribosomal protein; rRNA-binding.
SEQUENCE 144 AA; 16190 MW; 8580A491 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                     144 AA.
                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                            76.0%;
80.0%;
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                                                                                        4; Conservative
                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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01-NOV-1995 (Rel. 32,
15-JUL-1999 (Rel. 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / MARBURG;
                         Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                   RESULT 11
RL16_BACSU
ID RL16_BACSU
AC P14577;
                                                                                                                                              1 REXLR
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STEAIN=RD / KW20;
BUDGE STATE 
                                                                                 Gaps
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Eukaryota; Metazoa; Arthropoda; Crustacea; Branchiopoda; Anostraca;
                                                                                 ;
0
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0
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Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Whole-genome random sequencing and assembly of Haemophilus influenzae \mbox{Rd}.";
                          Length 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 19; DB 1; Length 146;
Pred. No. 1.2e+02;
0; Mismatches 1; Indels
                    Score 19; DB 1; Length 144
Pred. No. 1.2e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGR; HI0074; -.
Hypothetical protein.
SEQUENCE 146 AA; 17127 MW; A139C9F4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
HYPOTHETICAL PROTEIN HI0074.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
GLOBIN E7, EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                     146 AA
                                                                                                                                                                                                                                                                                                                                     PRT;
                    76.0%;
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80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 269:496-512(1995).
Query Match
Best Local Similarity 80..
Loc 4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haemophilus influenzae.
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                                                                                                                                                                                 115 REALR 119
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YO74_HAEIN
ID YO74_HAEIN
AC P43934;
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GLB7_ARTSX
ID GLB7_ARTSX
AC P19364;
                                                                                                                                  1 REXLR
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156 AA; 16998 MW; 488642E3 CRC32;
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Best Local Similarity
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                                                                                                                                                                            1 REXLR 5
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                                                                                                                                                                                                                                                                                                                                                  YK12_MYCTU
Q10845;
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  SEQUENCE
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YK12_MYCTU
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                                                                                               MOENS L., YAN HAUWARET M.-L., DE SMET K., VER DONCK K.,
WAN DE PEER Y., VAN BEEUMEN J., WODAK S., ALARD P., TROTMAN C.;
"Structural interpretation of the amino acid sequence of a second
domain from the Artemia covalent polymer globin.";
J. Biol. Chem. 26:14285-14281(1990).
-!- SUBUNIT: ARTEMIA HEMOGLOBIN IS A DIMER OF TWO SIMILAR SIZED
SUBUNITS: EACH SUBUNIT REPRESENTS A GLOBIN CHAIN WHICH EXISTS IN
TWO FORMS (ALPHA AND BETA), THUS MAKING POSSIBLE THREE DIFFERENT
PHENOTYPES (HBI, ALPHA(2), HB2, ALPHA/BETA, HB3, BETA(2)). THE
GLOBIN CHAIN IS A POLYMER OF EIGHT HEME-BINDING COVALENTLY LINNED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-ATC 15697 / PAO1;
LIAO X., HANCOCK R.E.W.;
SUBMITTED (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ACTIVATES THE TRANSCRIPTION OF THE SOXS GENE WHICH
ITSELF CONTROL THE SUPEROXIDE RESPONSE REGULON. SOXR CONTAINS A
ZPE-2S IRON-SOLIEUR CLUSTER THAT MAY ACT AS A REDOX SENSOR SYSTEM
THAT RECOGNIZES SUPEROXIDE. THE VARIABLE REDOX STATE OF THE FE-S
CLUSTER MAY THUS BE EMPLOYED IN VIVO TO MODULATE THE
TRANSCRIPTIONAL ACTIVITY OF SOXR IN RESPONSE TO SPECIFIC TYPES OF
OXIDATIVE STRESS (BY SIMILARITY).
-!- SUBUNIT: HOWODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
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12 31 H-T-H MOTIF (POTENTIAL).
117 128 MIGHT BE PART OF A SENSOR REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.0%; Score 19; DB 1; Length 1>z
80.0%; Pred. No. 1.3e+02;
1; Indels
                                                                                                                                                                                                                                                                                                                                                                         PIR; A37815; A37815.
PROSITE; PS01033; GLOBIN; 1.
PFAM; PF00042; globin; 1.
SEQUENCE 152 AA; 17074 MW; 6058429B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
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PROSITE; PS00552; HTH_MERR_FAMILY; 1.
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Best Local Similarity 80.0
Matches 4; Conservative
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DNA-binding; Transcrip
DNA_BIND 12 31
DOMAIN 117 128
       Artemiidae; Artemia
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                                                   SEQUENCE.
MEDLINE; 90354411
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Q51506;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COLE S.T., BROSCH R., PARKHILL J., GARNIER T., CHURCHER C., HARRIS D., GORDON S.V., EIGLMEIER K., GAS S., BARRY C.E. III, TEKAIA F., BADCOCK K., BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R., DAVIES R., DEVLIN K., FELTWELL T., CENTLES S., HAMLIN N., HOLROYD S., HORNSBY T., JAGELS K., KROGH A., MCLEAN J., MOULE S., MURPHY L., OLIVER S., OSBORNE J., QUAIL M.A., RAJANDREAM M.A., ROGERS J., RUTTER S., SEGER K., SKELTON S., SQUARES S., SOARES R., SULSTON J.E., TAYLOR K., WHITEHEAD S., BARRELL B.G.;
"Deciphering the blology of Mycobacterium tuberculosis from the complete genome sequence.";
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                                                                     Gaps
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   Length 156;
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                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Score 19; DB 1; I
Pred. No. 1.3e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                     01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
HYPOTHETICAL 18.2 KD PROTEIN RV2012.
                                                                                                                                                                                                                                                                                                                                                         164 AA
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164 AA; 18202 MW;
      76.0%;
80.0%;
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Best Local Similarity 80.0
Matches 4; Conservative
                                                                     Conservative
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sapien sapien sapien sapien sapien sapien sapien sapien

Perfect score: Sequence: Scoring table:

OM protein

Run on:

Minimum DB s Maximum DB s

Database

Searched:

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019638 homo sapien
P79487 homo sapien
019567 homo sapien
019575 homo sapien
019581 homo sapien
019583 homo sapien
019583 homo sapien
086794 streptomyce
056376 escherichia
P90836 caenorhabdi
077729 ovis aries
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Q56375 escherichia
Q87365 staphylococ
Q82684 infectious
Q89837 infectious
Q89871 infectious
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STRAIN-VC-16 / DSM 4304 / ATCC 49558;

STRAIN-VC-16 / DSM 4304 / ATCC 49558;

MEDLINE; 98049343.

KLENK H.-P., CLAXTON R.A., TOMB J.-F., WHITE O., NELSON K.E.,

KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,

KICHARDSON D.L., KERLAYAGE A.R., GRAHAM D.E., KYRRIDES N.C.,

FLEISCHMANN R.D., OUACKENBURE A.R., MCKENNEY K., ADAMS M.D., LOFFUGS B.,

KIRKNESS E.R., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFFUGS B.,

PETERSON S., REICH C.I., MONEIL L.K., BADGER J.H., GLODEK A., ZHOU L.,

OVERBEER R., GOCAYNE J.D., WEIDMAN J.F., MCHONALD L., UTTERBACK T.,

COTTON M.D., SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M.,

SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,

MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus.";
Rature 390:364-370(1997).
EMBL; AE001060; AAB90607.1; -
                                                                           078077
078174
                               019640
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Archaea: Buryarchaeota; Archaeoglobales; Archaeoglobaceae;
Archaeoglobus.
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Last annotation update)
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35 AA; 4056 MW; 9F03E370 CRC32;
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01-JAN-1998 (TrEMBLrel. 05, C
01-JAN-1998 (TrEMBLrel. 05, I
01-AUG-1998 (TrEMBLrel. 07, I
HYPOTHETICAL 4.1 KD PROTEIN.
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Best Local Similarity
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RETLR 33
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3.317 Million cell updates/sec
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                                                                                                          8, 2000, 13:17:26; Search time 209.03 Seconds
              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                225878 seqs, 69334122 residues
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Listing first 45 summaries
                                                                           protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
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sp_human:*
sp_invertebrate:*
sp_mammal:*
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sp_virus:*
sp_vertebrate:*
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sp_phage:*
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Match 1
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Score

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Result

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019787; 019787

RESULT 019787

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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK
RUNGROUNG E., BEJCHANDRA S.;
SUDMILTEG (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF011769; AAB67807.1; -
PFAM; PF00129; MHC_I; 1.
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                                                                                                                                              Last sequence update)
Last annotation update)
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Pred. No. 3.4e+02;
0; Mismatches 1;
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NON_TER 81 81
SEQUENCE 81 AA; 9405 MW; 073087CE CRC32;
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NON_TER 81 81
SEQUENCE. 81 AA; 9405 MW; 073087CE CRC32;
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01-JAN-1998 (TrEMBLrel: 05, Last seq
01-JNV-1998 (TrEMBLrel: 08, Last ann
MHC CLASS I ANTIGEN HLA-B (FRAGMENT)
                                                            PRT;
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80.0%;
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80.0%;
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|66 RESLR 70
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Proc. Natl. Acad. Sci. U.S.A. 93:9687-9692(1996).
EMBL: D84438; BAA12664.1; -...
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Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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MEDLINE; 96382528.
ITO H., FUJITANI K., USUI K., SHIMIZU-NISHIKAWA K., TANAKA S.
YAMAMOTO D.;
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE; 94090601.
YOSHIDA N. KIMURA A., KATSURAGI K., NUMANO F., SASAZUKI T.;
"DNA typing of HLA-B gene in Takayasu's arteritis.";
Tissue Antiqens 42:87-90(1993).
FIBMEL; S67638; AMB23305-1;
PFAM; PF00129; MHC_I; 1.
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                                                                                                             01-JAN'1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JNOV-1998 (TrEMBLrel. 08, Last annotation update)
HLA CLASS I ANTIGEN (FRAGMENT).
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Last annotation update)
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                                                            47 AA
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Best Local Similarity 80.0
Matches 4; Conservative
                                                         PRELIMINARY;
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CHANDANAINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
RUNGKOUNG E., BEJCHANDRA S.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF014771; AAB67809.1; -.
PFAM; PF00129; MHC_I; 1.
                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 81;
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01-JAN-1998 (TIEMBLTEL 05, Created)
01-JAN-1998 (TIEMBLTEL 05, Last sequence update)
01-NO-1998 (TIEMBLTEL 08, Last annotation update)
MHC CLASS I ANTIGEN HIA-B (FRAGMENT).
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Pred. No. 3.4e+02;
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               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HLA-B.
HOMO sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SEQUENCE FROM N.A. SIRIKONG M., LUANGTRAKOOL K., SRINAK
RUNGROUNG E., BEJCHANDRA S.;
SUBMITHEA (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF01477; AAB67B15.1; -.
PFAM; PF00129; MHC_I: 1.
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CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK
RUNGROUNG E., BEJCHANDRA S.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF014779; AAB67817.1; -.
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76.0%; Score 19; DB 7; Length 81; 80.0%; Pred. No. 3.4e+02; 1ve 0; Mismatches 1; Indels
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Pred. No. 3.4e+02;
0; Mismatches 1; Indels
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
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(TrEMBLrel. 05, Last sequence update)
(TrEMBLrel. 08, Last annotation update)
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NON_TER 81 81
SEQUENCE 81 AA; 9405 MW; 073087CE CRC32;
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                                                                                                                                                                                             81 AA; 9405 MW;
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Best Local Similarity 80.0%;
Matches 4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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66 RESLR 70
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CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
RUNGROUNG E., BEJCHANDRA S.;
Submitted (JUL.1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AF014775; AAB67813.1;
PFAM; PF00129; MHC_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                    CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D., CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D., RUNGROUNG B., BEJCHANDRA S.; Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases. EMBL: AF014773; AAB67811.1; -. PFRAM: PF00129; MHC_I: 1.
                                                                                                                                                                                                                                                                                                      Score 19; DB 7; Length 81; Pred. No. 3.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 19; DB 7; Length 81; Pred. No. 3.4e+02;
                                                                                                                                                                                                                                                                                                                                  1; Indels
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019527;
01-JAN-1998 (TIEMBLIEL. 05, Created)
01-JAN-1998 (TIEMBLIEL. 05, Last sequence update)
MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
HLA-B.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
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80.0%;
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Best Local Similarity 80.0
Matches 4; Conservative
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                                                                                   Homo sapiens (Human).
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Best Local Similarity
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SEQUENCE FROM N.A.
CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
RUNGKOUNG E., BEJCHANDRA S.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF014787; AAB67825.1;
PFAM; PF00129; MHC_I: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
CHANDANATINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
RUNGROUNG E., BEJCHANDRA S.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF014789; AAB67827.1;
PFAM; PF00129; MHC_I: 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                               Length 83;
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Pred. No. 3.5e+02;
0; Mismatches 1; Indels
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
HHCA-B.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
                                                                                                                                          Score 19; DB 7;
Pred. No. 3.5e+02;
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83 83
83 AA, 9731 MW; 24B8D666 CRC32;
                                                                                  24B8D666 CRC32;
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83 AA; 9731 MW; 24B8D666 CRC32;
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PFAM; PF00129; MHC_I; 1. MHC.
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83 AA;
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68 RESLR 72
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  SEQUENCE FROM N.A.
CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
RUNGKOUNG E., BEJCHANDRA S.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF014781; AAB67819.1; -.
PFAM; PF00129; MHC_I; 1.
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CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
RUNGROUNG E., BEJCHANDRA S.;
SUBMITTER (JUL.1997) to the EMBL/GenBank/DDBJ databases'
EMBL; AF014783; AAB67821.1;
PFAM; PF00129; MHC_1; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 3.4e+02;
0; Mismatches 1; Indels
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
HLA-B.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I ANTIGEN HIA-B (FRAGMENT).
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81 AA; 9405 MW; 073087CE CRC32;
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Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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BIRD T., DUNN P.P., BUNCE M.;
BIRD T., DUNN P.P., BUNCE M.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
SUBMIT AJ13471; CAB37940.1; -.
NON_TER 1 1
NON_TER 89 A9; 10568 MW; 531E6106 CRC32;
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01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
HUMAN LEUCOCYTE ANTIGEN B (FRAGMENT).
HIA-B.
HEA-B.
EUKARYOta: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
Ouery Match

76.0%; Score 19; DB 7; Length 83;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 1; Indels
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DT 01-MAY-
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Search completed: February 8, 2000, 13:17:28 Job time: 32477 sec

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Sequence 29 from pate
H.sapiens CpG island
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                                                                                                                                                         unidentified.

ISM unidentified.

NCE 1 (bases 1 to 15)

ORS Andrien, W. Dupont, E., Rossau, R. and De, C.I.

ORS TOTION, W. Dupont, E., B. USING SPECIFIC PRIMERS AND PROBES SETS

NENAL Patent: WO 9421818-A 51 29-SEP-1994;

INNGENETICS NV (BE.)

Other publication CA 2158578 940929

Other publication AU 6258594 941011.

Location/Qualifiers

15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Andrien, Dupont, E., Rossau, R. and De, C.I.
Andrien, M., Dupont, E., Rossau, R. and De, C.I.
PROCESS FOR TYPING HLA-B USING SPECIFIC PRIMERS AND PROBES SETS
PACHAT: WO 9421818-A.52 29-SEP-1994;
INNOGENETICS NV (BE)
Other publication CA 2158578 940929
Other publication AU 6258954 941011.
196192 8
255580 H
K03213 H
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Gaps: 0
Percent Identity: 100.000
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/organism="unidentified"
/db_xref="taxon:32644"
a 4 c 7 g 1
                                                                                                      A40090 15 bp DNA
Sequence 51 from Patent W09421818.
A40090.1 GI:2296255
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Sequence 52 from Patent W09421818.
A40091
A40091.1 GI:2296256
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Ratio: 3.800
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US-08-653-294-3 x A40090
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LOCUS A40090
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LOCUS A40091
                                                           seq_name: gb_pat:A40090
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gb_pat:196192
gb_pr1:HS50D4R
gb_pr1:HUMSRC06
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AUTHORS
TITLE
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JOURNAL
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-Q-/cgnl_1/USPTO_spool/US08653294/runat_04022000_160701_15779/app_query.fasta.1
-DB-Genembl -OFMT=fastap -SUFFTX=rge -GAPOP=12.000 -GAPEXT=4.000
-QGAPEXT=0.000 -LOOPCL=0.000 -LOOPEXT=0.000 -GAPOP=6.000
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-NCPU=6 -ICPU=3 -NO_XLPXY -WAIT -THREADS=1
                                                        Results were produced by the GenCore software, version Copyright (c) 1993-2000 Compugen Ltd.
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Database length: -1518192014
Search time (sec): 11370.480000
                             Date: Feb 8, 2000 4:37 PM
                                                                                                                                                                                                                                                                                    Search information block:
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Query length: 10
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gb_prc:MUSMYOCB
gb_prl:HS165G8F
gb_prz:HNSCG13
gb_rc:S72924
gb_bal:PH1P30149M
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9b_pr1:HSSRCE7

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9b_pat:AR054638

9b_pr1:HS30D1F

9b_ba1:EVM16RNA7

9b_sts:HUMSWX1283

9b_pr1:HSSVX22
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Sequence
Sequence
Gb_pat:A40090
gb_pat:A40064
gb_pr:A40064
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gb_pat:E08878
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gb_pat:E08878
gb_pat:E08978
gb_pat:E186379
gb_pat:I65794
gb_pat:I65794
gb_pat:I67936
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gb_ov:AB031373
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to reverse of: HUMTH06
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US-08-653-294-3 x HUMTH06/rev
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Ratio: 3.800
Percent Similarity: 100.000
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Ratio: 3.800
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                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 18)
Andrien,, Dupont, E., Rossau, R. and De, C.I.
PROCESS FOR IYPING HA.B USING SPECIFIC PRIMERS AND PROBES SETS
Patent: WO 9421818-A 25 29-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMTHOG 19 bp DNA PRI 11-MAR-1998 Homo saplens gene for tyrosine hydroxylase, exon 6, partial sequence.
                                                                                                                                                                                                                     05-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 19)
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Gaps: 0
Percent Identity: 100.000
 Percent Identity: 100.000
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Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                     INNOGENETICS NV (BE)
Other publication CA 2158578 940929
Other publication AU 6558594 941011.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Biochem. 103 (6), 907-912 (1988)
89008200
                                                                                                                                                                                                        A40064 18 bp DNA
Sequence 25 from Patent W09421818.
A40064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="unidentified"
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D00274.1 GI:220104
TH: tyrosine hydroxylase.
6 of 24
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Ratio: 3.800
Percent Similarity: 100.000
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                                                                                                        3 CGAGAGAGCCTGCGG 17
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                                                                         Align seg 1/1 to: A40091
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unidentified
unclassified.
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US-08-653-294-3 x A40064
                            alignment_block:
US-08-653-294-3 x A40091
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Blochchaftsry 26, 6910-6914 (1987)
In [1], they determined the nucleotide sequences of all exons and their surrounding regions of human TH gene, and the exon/intron boundaries are shown. The boundaries were determined by comparing the genomic DNA sequence with the cDNA sequence. The human TH gene is split into 14 exons. In [1], they concluded that the four types of human TH mRNA are produced through alternative splicing from a
2 (sites)
O'Malley,K.L., Anhalt,M.J., Martin,B.M., Kelsoe,J.R., Winfield,S.L.
and Ginns,B.I.
Isolation and characterization of the human tyrosine hydroxylase
gene: identification of 5' alternative splice sites responsible for
multiple mRNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-SEP-1999
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Svendsen,A., Patkar,S.Anant, Gormsen,E., Okkels,J.Sigurd and
Thellersen,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps: 0
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Percent Identity: 100.000
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/db_xref="taxon:9606"
/tissue_type="placenta"
/note="157 bp after segment 5"
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Patent: US 5869438-A 5 09-FEB-1999;
Location/Qualiflers
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Sequence 5 from patent US 5869438.
AR034425
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/note="AA 224 at 11"
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DEFINITION ACCESSION VERSION KEYWORDS

ORGANISM

SOURCE

REFERENCE AUTHORS source

BASE COUNT

ORIGIN

TITLE JOURNAL FEATURES

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Unknown.
Unclassified.
Unclassified.
Unclassified.
Unclassified.
Dubersky.T.W. Jr., Polo,J.M., Jolly,D.J. and Driver,D.A.
Eukaryotic layered vector initiation systems
Patent: US 5814482-A 50 29-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 41)
Dubensky,T.W. Jr., Polo,J.M., Ibanez,C.E., Chang,S.M.W.,
Jolly,D.J., Driver,D.A. and Belli,B.A.
Alphavirus vector constructs
Patent: US 843723-A 50 01-DEC-1998;
Location/Qualifiers
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Gaps: 0
Percent Identity: 100.000
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Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                        AR043432 41 bp DNA
Sequence 50 from patent US 5814482.
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                                              to: 41
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17 a 6 c 5 g
                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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a 6 c 5 g
                                               from: 1
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ARO43432.1 GI:5964440
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Ratio: 3.800
Percent Similarity: 100.000
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Percent Similarity: 100.000
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US-08-653-294-3 x AR021017
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US-08-653-294-3 x AR043432
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Unclassified.
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Locus AR043432
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LOCUS AR062347
                                                                                                                                                                                                                                                                   Unknown.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
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                                              Align seg 1/1
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ACCESSION
VERSION
KEYWORDS
SOURCE
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ORIGIN
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 41)
Dubensky, T.W. Jr., Polo, J.M., Ibanez, C.E., Chang, S.M.W., Jolly, D.J. and Driver, D.A.
Alphavirus structural protein expression cassettes
Patent: US 5789245-A 50 04-AUG-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-DEC-1998
                                                                                                                                                                                                                                                                                  Unknown.
Unclassified.
Unclassified.
Jarrell,K.A.
Intron-mediated recombinant techniques and reagents
Patent: US 5780272-A 27 14-JUL-1998;
                                              24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality: 19.00 Length: 5
Ratio: 3.800 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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Percent Identity: 100.000
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t
                                              from: 1
                                                                                                                                                                          аки17933 30 bp DNA
Sequence 27 from patent US 5780272.
AR017933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AR021017 41 bp DNA
Sequence 50 from patent US 5789245.
AR021017
AR021017.1 GI:3975632
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2
                                              Align seg 1/1 to reverse of: AR034425
                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                             /organism="unknown"
8 c 8 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="unknown"
6 c 5 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from: 1
                                                                                                                                                                                                                                      AR017933.1 GI:3973536
alignment_block:
US-08-653-294-3 x AR034425/rev
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Ratio: 3.800
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-08-653-294-3 x AR017933
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                                                                                                                                        seq_name: gb_pat:AR017933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unknown.
Unclassified.
                                                                                                                                                                       seq_documentation_block:
LOCUS AR017933
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Locus AR021017
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29-SEP-1999

DEFINITION ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

source

FEATURES

TITLE JOURNAL

BASE COUNT ORIGIN

DEFINITION ACCESSION

ORGANISM

VERSION KEYWORDS SOURCE

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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TCR V alpha 8 (V alpha 8HAP50)-T-cell receptor alpha chain variable region [human, peripheral blood lymphocytes, bullous pemphigoid syllent, Genomic, 48 nt].
                                  26-AUG-1992 JP 1992227507
HARADA YASUHIRO, NAKANO EIICHI, TATSUMI HIROKI, UMETSU MOTOAKI
C12N15/18,C12P21/02,(C12P21/02,C12R1:865);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product-"T-cell receptor alpha chain variable region"
/protein_id="ARA30638.1"
/db_xref="G1.639538"
/translation="CAENLYGGGSEKLVPG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GenBank staff at the National Library of Medicine created this entry [NOBI glbbsq 154951] from the original journal article. This sequence comes from Fig. 3C.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 numan bullous pemphigoid patient peripheral blood lymphocytes
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1 (bases 1 to 48)

Michalaki, H., Roman-Roman, S., Nicolas, J.F., Mackensen, A., Thivolet, J., Triebel, F., Hercend, T. and Ferradini, L.

In-Situ preferential usage of V alpha 8 T-cell receptor gene segments in a patient with bullous pemphigoid

J. Autoimmun. 6 (6), 827-839 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="TCR V&agr;8"
/note="T-cell receptor alpha chain variable region"
/allele="V&agr;8HAP50"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="TCR V<alpha>8"
/note="This sequence comes from Fig. 3C."
                                                                                                                                                                                                                                                                                                                                     Quality: 19.00 Length: 5
Ratio: 3.800 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47
                                                                                                                                                                                                     /organism="synthetic c/db_xref="taxon:32630"
                                                                                                                                                                    Location/Qualifiers
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;
                                                                                              strandedness: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from: 1
                                                                                                                  topology: Linear;
hypothetical: No;
1994070776-A/7
                                                                                                                                                   anti-sense: No;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S73031.1 GI:639537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: E06878
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LOCUS S73031
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                                                                                                                                                                      FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  artificial sequence.
1 (bases 1 to 47)
Harada,Y., Nakano,E., Tatsumi,H. and Umetsu,M..
NEW RECOMBINANT DNA, PRODUCTION OF MINK GROWTH HORMONE AND DNA FRAGMENT FOR GENE SECRETION MANIFESTATION
PATENT: JP 1994070776-A 7 15-MAR-1994;
                                                                                                                                                                                                                            29-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 45)
Hayashi,T., Yoshida,M. and Terada,K...
PROBE FOR DETECTING LISTERIA AND METHOD FOR DETECTION
PATCH: JP 199319997-A 4 31-AUG-1993;
TOAGOSEI CHEM IND CO LTD
PN JP 1993219997-A/4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-AUG-1993
04-FEB-1992 JP 1992047959
HAYASHI TAKAKO, YOSHIDA MASAO, TERADA KENJI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E06878 47 bp DNA PAT
Synthetic DNA related to mink growth hormone.
E06878 1 GI:2175043
JP 1994070776-A/7.
Synthetic construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 5
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                            PAT
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E05342
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                                                            to: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="unidentified"
/db_xref="taxon:32644"
15 c 10 g 1
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OS Artificial gene
OC Artificial sequence; Genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                          from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              strandedness: Single;
topology: Linear;
                                                                                                                                                                                                                                                                             E05342.1 GI:2173531
JP 1993219997-A/4.
unidentified.
unidentified
                                                                                                                                                                                                                            45 bp
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Ratio: 3.800
Percent Similarity: 100.000
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US-08-653-294-3 x E05342/rev
                                                        Align seg 1/1 to: AR062347
 alignment_block:
US-08-653-294-3 x AR062347
                                                                                                              10 CGAGAAGCTCTAAGG 24
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                                                                                                                                                                                                         seq_documentation_block:
LOCUS E05342
                                                                                                                                                                                                                                                                                                                                                          unclassified
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BASE COUNT

ORIGIN

FEATURES

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE

JOURNAL

COMMENT

DEFINITION

26-JAN-1995

BASE COUNT

ORIGIN

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OS None
OC Artificial sequences.
PN J997220094-A/11
PD 26-AUG-1997
PF 12-DEC-1995 JP 996 331843
PR 13-DEC-1995 JP 95P 324778
PI KOLZUMI MAKOTO, OZAWA YUJI, NISHIGAKI TAKASHI PC
C12N15/09,C07H21/C02,C07H21/C04,C12N5/10,C12N9/00,(C12N15/09, PC
C12N15/2);
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key Location/Qualifiers
FH Source 1. 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   $4017752 84 bp DNA PRI 08-MAY-1993 pancreatic cholesterol esterase, [5' region, exon 1, exon 10] [human, PWE 15, PTCF, Genomic, 84 nt, segment 2 of 2]. $40178 $40178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human PTCF pWE 15.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhin; Hominidae; Homo.
                                                                                                                 E13623 63 bp RNA PAT 27-APR-19
Polyribonucleotide with ribozyme activity which has a tRNA
anti-codon stem loop.

    63
/organism='Artificial sequences' FT

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Ratio: 3.800 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 63)
Koizumi,M., Ozawa,Y. and Nishigaki,T. .
RIBOZYME HAVING TRNA ANTICODON STEM LOOP
PATENT: JP 1997220094-A 26-AUG-1997;
SANKYO CO LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17
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/organism="unidentified"
/db_xref="taxon:32644"
a 13 c 12 g 1
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                                                                                                                                                                                                                                      E13623.1 G1:5708669 JP 1997220094-A/11. unidentified. unidentified
  19 AGAGAACACTCAGA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 AGAGAACACTCAGA 35
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US-08-653-294-3 x El3623
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                                                                                                         seq_documentation_block:
LOCUS
E13623
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LOCUS S40177S2
                                                        seq_name: gb_pat:E13623
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ORIGIN
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AUTHORS
TITLE
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OC Artificial sequences.

PN 1997220094-A/2

PD 26-AUG-1997

PF 12-DEC-1995 JP 995 324778

PR 13-DEC-1995 JP 995 324778

PI KOLZUMI MAKOTO, OZAMA YUJI, NISHIGAKI TAKASHI PC

C12N15/09, C07H21/02, C07H21/04, C12N5/10, C12N9/00, (C12N15/09, PC

C12N15/09, C07H21/02, C07H21/04, C12N5/10, C12N15/09, PC

C12N15/09, C07H21/09, C07H21/09, C12N15/09, PC

C12N15/09, C07H21/09, C07H21/09, C12N15/09, PC

C12N15/09, C07H21/09, C07H21/09, PC

C12N15/09, PC

C1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E13614 61 bp RNA 27-APR-19
Polyribonucleotide with ribozyme activity which has a tRNA
anti-codon stem loop.
                                                                                                                                  Length: 5 Gaps: 0
Percent Identity: 100.000
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Ratio: 3.800 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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Koizumi,M., Ozawa,Y. and Nishigaki,T.
RIBOZYWE HAVING TRNA AWTICODON STEM LOOP
Patent: JP 1997220094-A 26-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 t
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/organism="unidentified"
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. 13 c 11 g 1:
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Ratio: 3.800
Percent Similarity: 100.000
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US-08-653-294-3 x S73031
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US-08-653-294-3 x E13614
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LOCUS E13614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: gb_pat:E13614
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VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL

COMMENT

REFERENCE AUTHORS

BASE COUNT

ORIGIN

FEATURES

DEFINITION

ACCESSION

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E 1 (bases 1 to 84)
S Kumar.B.V., Aleman-Gomez.J.A., Colwell,N., Lopez-Candales,A.,
Bosner.M.S., Spilburg.C.A., Lowe,M. and Lange,L.G.
Structure of the human pancreatic cholesterol esterase gene
Structure of the human pancreatic cholesterol esterase gene
E 92324425
E 92324425
GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 109184] from the original journal article.
This sequence comes from Table II.
Cocation/Qualifiers
1. 84
//Organism="Homo sapiens"
//Dxref="taxon:9606"
| Partial
//partial
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/gene="pancreatic cholesterol esterase, CEase"
/otee="precursor. This sequence comes from Table II;
CEase"
                                                                                                                                                                                                                                                                                                        /gene-"pancreatic cholesterol esterase, CEase"
1. .84
                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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a 29 c 20 g 15 t
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Gaps: 0
Percent Identity: 100.000
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Ouality: 19.00
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US-08-653-294-3 x S40177S2
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                                                                                                                                                                                    FEATURES
Source
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ORIGIN
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JOURNAL
MEDLINE
REMARK
        REFERENCE
AUTHORS
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human

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Human brain Expressed Sequen
CDNA encoding protein homolo
Arabidopsis lysine ketogluta
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PR 18-WAR-1993; EP-400700.

PR 18-WAR-1993; EP-400700.

PI (ANGENETICS NV SA.)

Andrien M. De Canck I, Dupont E, Rossau R;

Andrien M. De Canck I, Dupont E, Rossau R;

But typing using primers and probes enabling discrimination of the Balleles - esp. where difficult to discriminate by serological means.

PT HA-B alleles - esp. where difficult to discriminate by serological means.

PT Glaim 17; Page 50; 66pp; English.

PT Glaim 17; Page 50; 66pp; English.

CC The sequences given in Q72630-55 are probes which were used to discriminate HIA-B alleles which are characterised by having the sequences for these sequences which may also be used are given in Q72656-CC Variants of these sequences which may also be used to distinguish to Filmers given in Q72630-35. These primers may be used to distinguish between HIA-B types which are serologically difficult to discriminate, eg. B54(22), B78(17). Using this method, HIA-B compatibility CC between donors and recipients of organ transplants can be increased, thereby having a beneficial impact on success-rate of organ and bone-comparrow transplants. HIA-B typing may be used to improve or facilitate CC disease susceptibility studies and forensic investigations.

Sequence 15 BP; 3 A; 4 C; 7 G; 1 T;
        Expressed Sequence Tag
                                                                                                                                                                                                                                                                          2.2.30.7

2.2.30.7

Probe S19 for distinguishing HLA-B alleles.

Probe S19 for distinguishing HLA-B alleles.

Polymerase chair reaction; PCR; primer; amplify; detection; HLA-B;

human leukocyte antiqen; B55P; allele; exon 2; B54(22); B52(5); B701;

B62(15); B75(15); B71(70); B46; B79; B53; B5102; B5103; B58(17);

compatibility; donor; recipient; organ transplant; success-rate;

bone-marrow transplant; disease susceptibility study; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probe 519(2) for distinguishing HLA-B alleles.
Probe 519(2) for distinguishing HLA-B alleles.
Polymerase chain reaction; PCR; primer; amplify; detection; HLA-B;
human leukocyte antigen; B25F; allele; exon 2; B54(22); B52(5); B7801;
B62(15); B75(15); B71(70); B46; B53; B5102; B5103; B58(17);
compatibility; donor; recipient; organ transplant; success_rate;
bone-marrow transplant; disease susceptibility study; probe;
forensic investigation; ss.
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Gaps: 0
Percent Identity: 100.000
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Q72680 standard; DNA; 15 BP.
Q72680;
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ID Q72681 standard; DNA; 16 BP.

AC Q72681;

DT 22-MAY-1995 (first entry)
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Ratio: 3.800
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US-08-653-294-3 x Q72680
                          N_Geneseq_36:059303
N_Geneseq_36:V35857
N_Geneseq_36:V99554
        N_Geneseq_36:Q39891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WÓ9421818-A.
29-SEP-1994.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                  Documentation ...
Probe S19 for distinguishing HLA Probe S19(2) for distinguishing Probe 19, anneals to bases 220-2 TPA PCR primer. New intron-media PCR primer used to amplify human pETPFR tissue plasminogen actival Isolate OC9a phosphatase (27A3A) Antisense PCR primer XSVSD4647F (Forward p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Listeria monocytogenes DNA detect Listeria monocytogenes DNA detect Listeria monocytogenes DNA detect Listeria monocytogenes DNA detect Ribozyme (2) to specifically clear Ribozyme (1) to specifically clear Platelet derived growth factor Platelet derived growth factor Human corrected protein tyrosine kinas Receptor protein tyrosine kinas Receptor protein tyrosine kinas Receptor protein tyrosine kinas Human secreted protein 5 to 35 to 1 actobacillus delbrueckii ssp. Lactobacillus delbrueckii ssp. Human secreted protein 5 to 35 thuman secreted protein 5 to 35 thuman brain Expressed Sequence Arabidopsis thaliana antifungal Nucleotide sequence of clone GM Nucleotide sequence of clone GM Nucleotide sequence of clone GM SNV-1 virus clone GM3. Peptide EST clone GM3. Peptide
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EST clone FX536. New polynucled
                                                                                                                                                                                                                   -MODEL-frame-pan.model -DEV-xlp

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-GAPEXT=4,000 -QGAPEXT=0.000 -XGAPOP=10.000 -XGAPEXT=0.500

-FGAPOP=6.000 -FGERYT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500

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-MAXLEN=1000000 -USER=US08653294 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
                                                                                                              About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
  out_format :
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OM of: US-08-653-294-3 to: N_Geneseq_36:*
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Database sequences: 311585
Database length: 125096042
Search time (sec): 590.520000
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                                                                                                                                                                                               Command line parameters:
                                                       Date: Feb 8, 2000 1:27
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Ouery length: 10
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N_Geneseq_36:v97317
N_Geneseq_36:v66869
N_Geneseq_36:v063294
N_Geneseq_36:v82702
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N_Genesed_36:056719
N_Genesed_36:V55893
N_Genesed_36:V55893
N_Genesed_36:V55815
N_Genesed_36:V57371
N_Genesed_36:077371
N_Genesed_36:070371
N_Genesed_36:059367
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N_Geneseq_36:X51592
N_Geneseq_36:Q61237
N_Geneseq_36:V27265
N_Geneseq_36:V27265
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N_Geneseq_36:Q63760
N_Geneseq_36:T92326
N_Geneseq_36:T92335
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N_Geneseq_36:V70724
N_Geneseq_36:Q48012
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N_Geneseq_36:T61622
N_Geneseq_36:X39550
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N_Geneseq_36:V81378
N_Geneseq_36:V89988
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N_Geneseq_36:072654
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N_Geneseq_36:V88322
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                                                                                                                                                                                                                               serological means.
Claim 7; Page 42; 66pp: English.
The sequences given in Q72636-55 are probes which were used to discriminate HLA-B alleles which are characterised by having the sequence 5'-GCCA-3' at position 30-33 of exon 2 of the HLA-B allele. Variants of these sequences which may also be used are given in 072656-81. These probes are used to identify the amplification products of the prèmers given in Q72630-35. These primers may be used to distinguish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U.750.4.
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                                                                                                    (INNO-) INNOGENETICS NV SA.
Andrien M. De Canck I, Dupont E, Rossau R;
WPI; 94-317037/39.
DNA typing using primers and probes enabling discrimination of
HLA-B alleles - esp. where difficult to discriminate by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA typing using primers and probes enabling discrimination of HLA-B alkeles – esp. where difficult to discriminate by
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Ratio: 3.800 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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07-MAR-1994; E00654.
18-MAR-1993; EP-400700.
(INNO-) INNOGENTICS NV SA.
WPI: 94-317037/39.
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ID Q72654 standard; DNA; 18 BP.
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                                                           07-MAR-1994; E00654.
18-MAR-1993; EP-400700.
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                                                                                                                                                                                                                        serological means.
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                                         29-SEP-1994
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between HLA-B types which are serologically difficult to discriminate, eg. B54(22), B55(5), B7801, B62(15), B75(15), B71(70), B46, B59, B53, B5102, B5103 and B58(17). Using this method, HLA-B compatibility between donors and recipients of organ transplants can be increased, thereby having a beneficial impact on success-rate of organ and bonemarrow transplants. HLA-B typing may be used to improve or facilitate disease succeptibility studies and forensic investigations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TPA PCR primer.
Intron; recombination; combinatorial gene; trans-splicing;
gene therapy; polymerase chain reaction; PCR; primer: amplification;
tissue plasminogen activator; tPA; plasmid TPA-KS+; thrombolytic;
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A cDNA clone of human tissue plasminogen activator (tPA) was simplified by PCR using the primers given in 087368-69. The amplified tPA DNA (08770) was ligated into vector KS+ to obtain plasmid TPA-KS+. The construct was used in combinatorial methods involving RNA splicing-mediated shuffling of tPA domains improved thrombolytic properties.

Sequence 30 BP; 8 A; 8 C; 6 T;
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New intron-mediated recombinant techniques - used for the
generation and selection of novel genes and gene prods. for use
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Gaps: 0
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W09507351-A.
16-WAR-1995.
12-SEP-1994; U10146.
10-SEP-1993; US-119512.
(HARD ) HARVARD COLLEGE.
Jarrell KA:
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Ratio: 3.800
Percent Similarity: 100.000
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Percent Similarity: 100.000
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US-08-653-294-3 x Q87369
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US-08-653-294-3 x Q72654
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22-JUN-1998 (first entry)
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11-MAR-1997; US-814412.
(UYBO-) UNIV BOSTON.
Jarrell KA;
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  Example 4: Column 42: 56pp; English.

PCR primers V37316-17 were used to amplify the human tissue plasminogen activator gene. The PCR product was used to construct plansid TPA-KS+, which is used in the course of the invention. The specification describes a purified reverse-splicing intron which comprises a segment comprising a 5-part of a group II intron, including an exon binding site not naturally present in the intron and a second segment comprising a 3'-part of a group II intron, including a domain V motif, a branch as teceptor, and a nucleophilic group for transesterifying a phosphodiester bond of an RNA. Together the two segments form an autocatalytic Y-branched intron which catalyses integration of at least the reverse-splicing introns are used, by specific cleavage and ligation of discontinuous nucleic acid, to generate new genes and gene products, and anipulation, e.g. replacements for restriction enzymes) or anipulation, e.g. replacements for restriction enzymes) or anipulation, e.g. replacements for restriction enzymes) or antibody and orders.
                                                    10-SEP-1998 (first entry)
PCR primer used to amplify human tissue plasminogen activator gene. Plasmid pINVI; reverse-splicing intron; group II intron; exon binding site; domain V motif; branch site acceptor; nucleophilic group; transesterification; phosphodiester bond; autocatalytic Y-branched intron; reverse splicing reaction;
                                                                                                                                                                                                                                                                                                                           Jarrell KA; WPI; 98-413060/35. Reverse splicing construct containing fragments of autocatalytic introns - able to cleave and ligate discontinuous nucleic acid for generating new genes and e.g. ribozymes, libraries of enzymes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JAN-1999 (first entry)
pETPFR tissue plasminogen activator cDNA region PCR primer t-PA2.
Human; tissue plasminogen activator; t-PA; chimeric gene assembly;
manipulation; ribozyme; incron-mediated recombinant technique;
cleavage; ligation; trans-splicing; PCR primer; ss.
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Gaps: 0
Percent Identity: 100.000
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                    V37317 standard; DNA; 30 BP.
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ID V66869 standard; DNA; 30 BP.
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Ratio: 3.800
Percent Similarity: 100.000
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07-JUN-1995; 488015.
10-SEP-1993; US-119512.
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11-MAR-1998; U04881.
  seg_documentation_block:
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                                                                                                                                                                         PCR primer; ss.
                                                                                                                                                                                                              Homo sapiens.
US5780272-A.
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WO9840519-A1.
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Alkaline phosphatase; thermostable enzyme; thermophilic bacterium;
food; detergent; baking; PCR; primer; ss.
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Ratio: 3.800 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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Wed Feb

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A TOTAKTISTS US-WOOLD.

A LOFARATISTS US-WOOLD.

A CHIRD VIAGENE INC.

Belli BA, Chang SMW, Driver DA, Dubensky TW, Ibanez CE;

Belli BA, Chang SMW, Driver DA, Dubensky TW, Ibanez CE;

Jolly DJ, Polo JM;

WPI; 96-277785/28.

New recombinant alpha-virus vectors - used to develop prods and methods for use in gene therapy and in the prodn. of vaccines

Example 3: Page 92: 256pp; English.

Primer XSVSD4647F (T30827) contains a buffer sequence allowing enzyme digestion, a XhoI site, and nucleotides 4647-4675 of SV40.

CI twas used with reverse primer XSVSA4562R (T30828) to insert an XboI site into the SV40 small t antigen intron to site into the SV40 small t antigen intron to be inserted into eukaryotic layered vector initiation systems (ELVIS) (see also T30787) at a unique XhoI site immediately downstream of 5' sindbis sequences. Recombinant alphavirus expression vectors contg.

Che SV40 promoter are useful in methods of gene therapy and for vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-0cT-1998 (first entry)
Forward PCR primer XSVSD4647F.
DNA alphavirus; structural protein expression; inhibit; pathogen; immune response; stimulate; PCR primer; ss.
                                                                                                                              12-0827-1996 (first entry)
XhoI insertion primer XSVSD4647F.
Alpharirus; Sindbis virus; vector; gene therapy; vaccine;
primer; polymerase chain reaction; ELVIS; PCR; XhoI; SV40; ss.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-AUG-1998.
30-0CT-1996; 741881.
15-MAR-1995; US-404796.
15-SEP-1993; US-122791.
18-FEB-1994; US-198450.
30-NOV-1995; US-376184.
30-0CT-1996; US-376184.
CHIR ) CHIRON CORP.
Chang SMW, Driver DA, Dubensky TW, Ibanez CE, Jolly DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 5
Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: T30827 from: 1
                                                                 seq_documentation_block:
ID T30827 standard; DNA; 41 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
ID V42404 standard; DNA; 41 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: 19.00
Ratio: 3.800
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: N_Geneseq_36:V42404
                        seq_name: N_Geneseq_36:T30827
                                                                                                                                                                                                                                                     W09617072-A2.
06-JUN-1996.
30-NOV-1995; U15490.
30-NOV-1994; US-348472.
18-JAN-1995; US-376184.
15-MAR-1995; US-405827.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 CGAGAAGCICIAAGG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-08-653-294-3 x T30827
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
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US5789245-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                            WELL SOURCE TO SPECIFIC TO SPECIFIC TO SPECIFIC CARMON NAME A SPECIFIC SPECIFIC NEW hepatitis B virus nucleic acid with combination of specific New hepatitis B virus nucleic acid binding interactions are useful for. e.g. detection of binding interactions specification and HBV nucleic card sequences proceed from fulminant hepatitis B virus (FHBV) variants, in the course of the invention. The specification describes Hepatitis B virus (HBV) can card that has a mutation (i.e. alteration from the normal conclected in any of the genotypes A to F) in at least two of the chancer I region, the negative regulatory element region, the enhancer CC in/core upstream regulatory sequence/ basal core promoter region, or a mutation which leads to an X-peptide amino acid change to Cys or Met. CC II/ core upstream regulatory sequence/ basal core promoter region, or a mutation which leads to an X-peptide amino acid change to Cys or Met. CC The HBV variants of the invention are used to detect binding interactions considered disease, especially fullminant infection, but also severe chronic infection or serologically fullminant infections are used to detect of the expecified mutations are associated with fullminant infections in extensions are associated with fullminant infections in extensions are associated with fullminant infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the specified mutations are associated with fulminant infections, probably because they reduce the ability to bind inhibitory proteins in the host cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antisense PCR primer C27 used amplify nucleic acid from FHBV variants. Fulminant hepatitis B virus; variant; FHBV; HBV; binding interaction; HBV-related disease; PCR primer; ss.
utilised in the pharmaceutical, food, detergent, and baking industries.
                                                                                                                                                                                    Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps: 0
Percent Identity: 100.000
                                              6 T;
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                                                                                                                                                                                                                                                                                                    Align seg 1/1 to reverse of: V03294 from: 1 to:
                                                                                                                                     Length:
                                                                                                                                                                Gaps:
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G;
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                                              13 G;
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                                              7
C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V82702 standard; DNA; 34 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-FEB-1999 (first entry)
                                              5 A;
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Ratio: 3.800
Percent Similarity: 100.000
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Percent Similarity: 100.000
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US-08-653-294-3 x V03294/rev
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US-08-653-294-3 x V82702/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: N_Geneseq_36:V82702
                                                                                                                                     19.00
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08-APR-1998; E02048.
09-APR-1997; GB-007221.
(UNIU ) UNIV GLASGOW.
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                                                                                                                                                                                                                                                                                                                                               1 ArgGlu***LeuArg 5
                                                                                                                                                                                                                                                                                                                                                                                                23 CGAGAAGCCTTAAGG 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ArgGlu***LeuArg 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis B virus.
                                           34 BP;
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                                                                                                             alignment_scores:
Quality:
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                                           Sequence
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Eukaryotic layered vector initiation system - containing eukaryotic parameter and heterologous antigen coding sequence, useful for stimulating immune response

Pratimulating immune response

Example 3: Column 77: 144pp; English.

Example 3: Column 77: 144pp; English.

Crample 3: Column 77: 14pp; English.

Crample 3: Column 77: 14pp; English.

Crample 4: Column 77: 14pp; English.

Crample 4: Column 77: 14pp; English.

Crample 4: Column 77: 14pp; English.

Crample 7: 14pp; English.

Crample 7: 14
WPI; 98-446089/38.

WPI; 98-446089/38.

The Alpha retrouble of the structural protein expression cassettes - for producing recombinant alpha:virus particles

Example 3; Column 73; 140pp; English.

Example 3; Column 73; 140pp; English.

POR primers V42367-420 and V4242-54 are used in the course of the protein expression cassette which comprises an inducible promoter and an alphavirus structural protein gene, where the promoter and capression of the alphavirus structural protein gene upon induction of the promoter within a cell, and where prior to induction within the cell; the expression cassette does not express sufficient quantities of structural proteins to be cytotoxic to a BHK cell containing the structural protein gene upon induction of structural protein gene upon induction of cell; the expression cassette does not express sufficient quantities of structural protein gene upon induction of structural protein general p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rorward primer XSVSD4647F used to amplify SV40 small t antigen introns. Eukaryotic layered vector initiation system; stimulate; immune response; Sindbis; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps: 0
Percent Identity: 100,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 T;
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(POLO/) POLO J M.
Driver DA. Dubensky TW, Jolly DJ, Polo JM;
WPI; 98-541753/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: 41
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9
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ID V60164 standard; DNA; 41 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-DEC-1998 (first entry)
Forward primer XSVSD4647F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity: 100.000
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29-SEP-1998.
30-OCT-1996; 739158.
15-SEP-1994; US-122791.
18-FEB-1994; US-198450.
14-SEP-1994; US-198450.
30-NOV-1994; US-348472.
18-JAN-1995; US-378184.
CRIV/) DRIVER D A.
(DUBE/) DUBLIKE D A.
(JOLL/) JOLLY D J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: N_Geneseq_36:V60164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ArgGlu***LeuArg 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
Quality:
Ratio:
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Alphavirus vectors constructs containing a 5' promoter of viral cDNA by in vitro transcription - used in gene therapy

Example 3; Column 73; 140pp; English.

Correct primers V70724-25 are used to amplify the SV40 small t antigen intron sequences. The amplified product is used in the production of the alphavirus vector constructs of the invention. These constructs comprises a promoter 5' of viral cDNA which initiates the synthesis of RNA from the viral cDNA by in vitro transcription, followed by a complex tanscription of alphavirus RNA.

Collowed by a nucleotide sequence encoding alphavirus nonstructural proteins, a viral junction of a subgenomic fragment is prevented, an theraal ribosome entry site or a sequence which promotes ribosome crash those entry site or a sequence which promotes ribosome entry site or a sequence which promotes ribosome crash those and alphavirus sequence. The recombinant alphavirus

Contors can be used for gene therapy.

Sequence 41 BP; 17 A; 6 C; 5 G; 13 T;
                                                                                                                                                                                                                                                                                                                                                                                                                  V70724;
02-FBB-1999 (first entry)
Forward primer XSVSD4647F used to amplify SV40 samm t antigen introns.
Alphavirus vector construct; gene therapy; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
N USS843723-A.
USS843723-A.
USS843723-A.
USS843723-A.
USS843723-A.
USS843723-A.
USS843723-A.
USSEP-1995; US-104796.
R 15-ERP-1994; US-104791.
R 18-ERB-1994; US-108472.
R 20-DAN-1995; US-376184.
R 30-OCT-1996; US-739167.
A (CHIR ) CHIRON CORP.
I Belli Ba. Chang SWW, Driver Da, Dubensky TW, Ibanez CE, UJOlly DJ, Polo JM;
WPPI; 99-044581/04.
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                                                                                                                              Percent Identity: 100.000
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Percent Identity: 100.000
                   13
                                                                                                                Gaps:
                   6
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II-restricted immune response. Sequence 41 BP; 17 A;
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ID V70724 standard; DNA; 41 BP.
                                                                                           Quality: 19.00
Ratio: 3.800
Percent Similarity: 100.000
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Ratio: 3.800
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                           seq_name: N_Geneseq_36:V70724
                                                                                                                                                                                                                                                                                                   10 CGAGAAGCTCTAAGG 24
                                                                                                                                                                                                                            Align seg 1/1 to: V60164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 CGAGAAGCTCTAAGG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: V70724
                                                                                                                                                                                                                                                                   1 ArgGlu***LeuArg 5
                                                                                                                                                                    alignment_block:
US-08-653-294-3 x V60164
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US-08-653-294-3 x V70724
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                                                                           alignment_scores:
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us-08-653-294-3.rng

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4 CGGGAATCTCTTAGA 18
                                                                                                                                                              Listeria monocytogenes detecting probe for testing foodstuffs or patients - comprises DNA or RNA nucleic acid probe in which probe is hybridised with nucleic acid of strain to be detected claim 1; Page 2; 7pp; Japanese.

This DNA sequence, its corresponding RNA version or complementary sequence is claimed for detection of L.monocytogenes. The probes can rapidly and sensitively detect the microrganism in food samples and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1: Page 2: 7pp; Japanese.
This RNA sequence, its corresponding DNA version or complementary sequence is claimed for detection of L.monocytogenes. The probes can rapidly and sensitively detect the microrganism in food samples and in patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-APR-1994 (first entry)
Listeria monocytogenes RNA detection probe 4.
Nucleic acid hybridisation assay; probe; food poisoning; detection;
16S ribosomal RNA; ss.
                                                              13-APR-1994 (first entry)
Listeria monocytogenes DNA detection probe 4.
Nucleic acid hybridisation assay; probe; food poisoning; detection;
16s ribosomal RNA; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Listeria monocytogenes detecting probe for testing foodstuffs or patients - comprises DNA or RNA nucleic acid probe in which probe is hybridised with nucleic acid of strain to be detected Claim 1: Page 2; 7pp; Japanese.
This RNA sequence, its corresponding DNA version or complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saps: 0 0 Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                        10 G;
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                                                                                                                                                                                                                                                                                                                        15 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 C;
                                                                                                                                            31-AUG-1993.
04-FEB-1992; 04-047959.
04-FEB-1992; JP-047959.
(TOAG ) TOA GOSEI CHEM IND LTD.
WPI; 93-308349/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-AUG-1993.
04-FEB-1992. 047859.
04-FEB-1992. JP-047959.
(TOAG ) TOA GOSEI CHEM IND LTD.
WPI: 93-308349/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
ID Q58576 standard; RNA; 45 BP.
                                       Q48012 standard; DNA; 45 BP
                                                                                                                                                                                                                                                                                                                        8 A;
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seq_name: N_Geneseq_36:Q48012
                                                                                                                                                                                                                                                                                                                                                                          Quality: 19.00
Ratio: 3.800
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-08-653-294-3 x Q48012/rev
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Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ArgGlu***LeuArg 5
                         seg_documentation_block:
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Ratio:
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                                                                                                                                  J05219997-A.
                                                                                                                                                                                                                                                                                                            patients
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                                                                                                                                                                                                                                                                                                                         Sequence
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Example; Page 24; 32pp; English.

The sequences given in Q63756-60 are synthetic oligomers which were used in the construction of a DNA fragment encoding the mature mink growth hormone (MGH) to which has been added the pre-sequence of the neutral protease of Aspergillus oryzae and a Kex 2 recognition sequence. The mature mink growth hormone (MGH) coding sequence was isolated using the probe given in Q63754. This probe was based on the sequence of rat growth hormone and lead to the isolation of a 700 bp fragment. Replacement of the mink growth hormone pre-sequence by the pre-sequence derived from the neutral protease of Aspergillus oryzae allows effective production of MGH by recombant microorganisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mink growth hormone/A. Oryzae neutral protease pre-sequence oligomer. Probe; isolation; mink growth hormone; MGH; rat growth hormone; pre-sequence; neutral protease; Aspergillus oryzae; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-AUG-1993; 103623.
26-AUG-1993; JP-227507.
26-AUG-1992; JP-227507.
Harada Y, Nakano E, Tatsumi H, Umezu M;
WPI; 94-159680/20.
Wescombinant prodn of mink growth hormone - using a synthetic DNA fragment pre-sequence for efficient prodn. of the growth hormone in Saccharomyces
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Percent Similarity: 100.000 Percent Identity: 100.000
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ID Q63760 standard; cDNA to mRNA; 47 BP.
AC Q63760;
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                                                                                  Align seg 1/1 to reverse of: Q58576
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alignment_block:
US-08-653-294-3 x Q58576/rev
                                                                                                                                                                                                                                                                seq_name: N_Geneseq_36:Q63760
                                                                                                                                                                                                      26 CGTGAAGCACTAAGG 12
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US-08-653-294-3 x Q63760
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us-08-653-294-3.rst

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D69141 CELK065C8F Yuji Kohar
AA680032 a952e10.sl Gessler
AV199574 AV199574 Yuji Kohar
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information can be
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                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 40)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                    AA811948 40 bp mRNA EST 13-FEB-1998 ob74e04.sl NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1337118 similar to SW:2133_HUMAN P52736 ZINC FINGER PROTEIN 133. [1] ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumor Gene Index
Unpublished (1997)
On Sep 12, 1995 this sequence version replaced gi:1400907.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LENL at:www-bio.llnl.gov/bbrp/image/image.html
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Gaps: 0
Percent Identity: 100.000
    120
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
  4.4e+03
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4.4e+03
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104.96
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AA811948
AA811948.1 GI:2881559
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US-08-653-294-3 x AA811948
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LOCUS AA811948
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gb_est5:D69141
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gb_est36:AV199574
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | MA948106 on51a04.51 NORLCGAP_COR |
| AA008561 mg86d11.r1 Soares mouse |
| AA018655 oi11e09.51 NCI_CGAP_COR |
| AA072180 a165510.s1 NCI_CGAP_COR |
| AA072180 a165510.s1 NCI_CGAP_Kid |
| AA072180 a165510.s1 NCI_CGAP_Kid |
| AA072180 a165510.s1 NCI_CGAP_Kid |
| AA073130 A5027930 A5027930 Nouse oDNA (S. AA073132 a199401.r1 Barstead mou |
| AA073328 vi99401.r1 Barstead mou |
| AA073328 vi99401.r1 Barstead mou |
| AA07330 A5027930 A502790 A502790 A502790 A502790 A502790 A50270 A502790 A502790 A50270 A502
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AQ420129 RPCI-11-203L8.TV RPCI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Documentation ...
AA811948 0574604.51 NCI_CGAP_GCF
AA8164874 nJOLD02.51 NCI_CGAP_FT;
W89758 mf66c12.r1 Soares mouse e
                                                                                                                                                                         -MODEL-frame+_p2n.model -DEV-x1p
-O-/cgnl_1/USFPLO_2spoal/VOS08653294/runat_04022000_160700_15770/app_query.fasta.1
-DB=EST -OFRT=fastap -SUFFIX-rst -GADOP=12.000 -GAPOP=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -QGAPOP=4.500
-GGAPEXXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPOP=6.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-LIST=45 -DOCALIGN=200 -THR_SCORE=PCt -ALIGN=15 -MODE=LOCAL
-OUTPWT=Pfs -NORM=ext -MINEN=0 -MAXIEN=1000000 -USER=US08653294
-NCPU=6 -ICPU=3 -NO_XLPXY -WAIT -THREADS=1
                                                                                      About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6e+03
6e+03
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Database sequences: 4538634
Database length: 1887831982
Search time (sec): 8553.360000
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Query: US-08-653-294-3
Query length: 10
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gb_est2:A1088953
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gb_est7:W85542
gb_est7:A151325
gb_est23:A1151325
gb_est23:B13805
gb_est19:AA798893
gb_est10:AA798833
gb_est11:AA319533
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gb_est17:AA621180
gb_est26:AI352574
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gb_est18:AA701141
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gb_est12:AA292083
gb_est14:AA396862
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gb_est25:AI263925
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 49)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schallenberg,K., Steptco,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                      W89758 49 bp mRNA EST 12-SEP-1996 mf66c12.rl Soares mouse embryo NDME13.5 14.5 Mus musculus CDNA clone IMAGE:419254 5' similar to TR:G881954 G881954 RNPL.;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1405065.
Contact: Marra M/Mouse EST Project
WashIngton University School of MedicineP
H44 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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The WashU-HHMI Mouse EST Project
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AUTHORS
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Mammalia;

Eutheria: Frimates: Catarrhini: Hominidae: Homo.

Eutheria: primates: Catarrhini: Hominidae: Homo.

Eutheria: primates: Catarrhini: Hominidae: Homo.

I (Dases 1 to 43)

NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.

NATIONAI Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

On Sep 12, 1996 this sequence version replaced gi:1332888.

L Unpublished (1997)

On Sep 12, 1996 this sequence version replaced gi:1332888.

Tel: (301) 496-1550

Email: Robert-Strausberg@nih.gov

Tissue Procurement: Michael J. Brownstein, M.D., Ph:D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CON Gistribution: NCI-CGAP clone distribution information can be found through the I.M. N.G. E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viote="Organ: prostate; Vector: pr713D-Pac (Pharmacia)
with a modified polylinker: 1st strand cDNA was prepared
from normal prostate bulk tissue, and was then primed with
a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pr773 vector. Library is not normalized. Library
was constructed by Bento Scares and M. Fatima Bonaldo. "

1 G 9 10 1
                                                                                                                                                                                           Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trace considered overall poor quality Insert Length: 772 Std Error: 0.00 Seq primer: -40m13 fwd. Er from Amersham High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="normal prostate"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:985035"
/clone_lib="NCI_CGAP_Pr21"
  to: 40
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                                                                                                                                                                                                                                                                                                                                             AA564874.1 GI:2336513
Align seg 1/1 to: AA811948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.00
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Percent Similarity: 100.000
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US-08-653-294-3 x AA564874
                                                                                                   7 CGAGAAGCCCTACGT 21
                                                                                                                                                  seq_name: gb_est16:AA564874
                                                1 ArgGlu***LeuArg 5
                                                                                                                                                                                                                                                                                                 sequence.
AA564874
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1. .49
/organism="Mus musculus"
/strain="C57BL/65"
/db_xrson:10090"
/clone="IMAGE:419254"
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/dev_stage="13.5-14.5dpc total fetus"
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                                                                                                                                                                                                                                                                                                          Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                  Gaps:
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50

to:

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 61)
Marray M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                         seq_documentation_block:
LOCUS AA008561 61 bp mRNA EST 25-JUL-1996
LOCUS AA008611.rl Soares mouse embryo NbME13.5 14.5 Mus musculus CDNA
Clone IMAGE:439893 5' similar to PIR:S52089 S52089 hypothetical
protein - chinook salmon ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortlum (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Jan 25, 1995 this sequence version replaced gi:637806.
Contact: Marram Afwouse EST project
WashIngton University School of MedicineP
WashIngton University School of MedicineP
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism-"Mus musculus"
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/db_xref="taxon:10090"
/clone="IMAGE:439893"
/clone=lib="Soares mouse embryo NbME13.5 14.5"
/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: Erprimer
High quality sequence stop: 1.
Location/Qualifiers
     from: 1
     Align seg 1/1 to reverse of: AA948106
                                                                                                                                                                                                                                                                                             AA008561
AA008561.1 GI:1464528
EST.
                                                                                                 29 CGAGAAGCCCTTCGC 15
                                                   Ŋ
                                                                                                                                                seq_name: gb_est8:AA008561
                                                   1 ArgGlu***LeuArg
                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                 house mouse
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Ratio:
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I Unpublished (1997)
On Jan 19, 1998 this sequence version replaced g1:2150604.
Contact: Robert Strausberg, Ph.D.
Tal: (301) 496-11550
Email: Robert_Strausberg@hh.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1560174"
/clone="IMAGE:1560174"
/clone_lib="NoI_CGAB_CO8"
/tissue_type="adenocarcinoma"
/lab_host="Blubs"
/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from colon adenocarcinoma, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                          AA948I06 50 bp mRNA EST 23-JUN-1998 on51a04.sl NCI_CGAP_CO8 Homo sapiens CDNA clone IMAGE:1560174 3' similar to 9b:M58297 ZINC FINGER PROTEIN 42 (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo. 1 (bases 1 to 50) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 5
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Insert Length: 1844 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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t
                                                                        from: 1
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AA948106
AA948106.1 GI:3109359
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Percent Similarity: 100.000
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                                                                                                                                                                       13 AGGGAAACTCTTCGT 27
                                                                                                                                                                                                                        seq_name: gb_est21:AA948106
                                                                        Align seg 1/1 to: W89758
                                                                                                                      1 ArgGlu***LeuArg 5
alignment_block:
US-08-653-294-3 x W89758
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LOCUS AA948106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human.
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FEATURES

REFERENCE AUTHORS

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Ratio: 3.800
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                     24 CGCGAATCNTTGCGC 38
                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: gb_est20:AA872655
                                                                                                                                                                                                                                                           to: H63854
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US-08-653-294-3 x H63854
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                                                                                               Quality:
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                                                                      alignment_scores
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/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: p1713D (Pharmacia)
with a moddlied pollinker: Site_1: Pac I; Site_2: Eco RI;
lst strand cDNA was primed with a Pac I - oligo(dT) primer
[5' AACTGGAAGAATTAAAGATCTTTTTTTTTTTTTTT 3'],
                                                                                                                                                                                                                                                                                                                H63854 68 bp mRNA EST 11-OCT-1995
yu47cil.ri Soares fetal liver spleen INFLS Homo sapiens cDNA clone
IMAGE:229268 5' similar to gb:L05093 60S RIBOSOMAL PROTEIN L18A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 6)

1 Hillier,L. Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Mardis,E., Morre,B., Morris,M., Parsons,J., Prange,C., Rikhin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LINL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 699 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On May 8, 1995 this sequence version replaced g1:800181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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/db_xref="Axxon:9606"
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/clone_lib="Soares fetal liver spleen INFLS"
Percent Identity: 100.000
                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 1. Location/Qualifiers
                                                                                                                Align seg 1/1 to reverse of: AA008561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
Insert Size: 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                       H63854,1 GI:1018655
                                           alignment_block:
US-08-653-294-3 x AA008561/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: M13RP1
Percent Similarity: 100.000
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                                                                                                                                                                                                          57 CGAGAAACCCTCAGA 43
                                                                                                                                                              1 ArgGlu***LeuArg 5
                                                                                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS H63854
                                                                                                                                                                                                                                                        seq_name: gb_est5:H63854
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alignment_Scores:

Dercent Stalinativ: 19:00 Gaps: 0

Percent Stalinativ: 19:00 Percent Identity: 100:000

alignment_block: 10:000 
alignment_
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Percent Identity: 100.000

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Percent Similarity: 100.000
                                                                                                                                                                                        seq_name: gb_est17:AA621180
                                                                                                                                                        36 CGAGAAGCCCTACGC 22
                                                                                                                      1 ArgGlu***LeuArg 5
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Eutheria: Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 72)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

I (1997)

L (Dhublished (1997)

L (Dhublished (1997)

L (Dhublished (1997)

L (Dhublished (1997)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@ih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DAS Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 5
Gaps: 0
Percent Identity: 100.000
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2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ww-bio.lln1.gov/bbrp/image/image.htm1
                                                                                                                                        from: 1
                                                                                                                                    to reverse of: AA872655
                                                                                                                                                                                                                                                                                                                                                            AA995195
AA995195.1 GI:3181684
                                                                                    alignment_block:
US-08-653-294-3 x AA872655/rev
              Quality: 19.00
Ratio: 3.800
Percent Similarity: 100.000
                                                                                                                                                                                      36 AGAGAAGCCCTACGC 22
                                                                                                                                                                                                                                         seq_name: gb_est21:AA995195
                                                                                                                                                                        1 ArgGlu***LeuArg 5
alignment_scores:
Quality:
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                                                                                                                                    Align seg 1/1
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ر 0 م

Length: Gaps:

Quality: Ratio:

us-08-653-294-3.rst

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alignment_block:
US-08-653-294-3 x W96900
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eutherials Finants: Craniata; Vertebrata; Mammalla;
Eutherials Primates; Catarrhin; Hominidae; Homo.

Eutherials Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 80)

National Caneer Institute, Cancer Genome Anatomy Project (CGAP),

National Caneer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

On Jan 17, 1998 this sequence version replaced g1:1900526.

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg@nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

Email: Robert_Strausberg@nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D.,

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Prayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jote-Totoctor: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled polylinker; 1st strand cDNA was prepared from 3 pooled geam cell tumors, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was lighted to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                               AL352574 80 bp mRNA EST 30-DEC-1998
RIJ9cO7.x1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1948044 3',
AI352574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1948044"
/clone=lib="NC1_CGAP_GC4"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps: 0 Gaps: 0 Percent Identity: 100.000
                                                                           <u>:</u>
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                                                                   Align seg 1/1 to reverse of: AA621180 from: 1
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High quality sequence stop: 56.
Location/Qualifiers
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alignment_block:
US-08-653-294-3 x AA621180/rev
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Percent Similarity: 100.000
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US-08-653-294-3 x AI352574
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LOCUS AI352574
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The WashD-HHMI Mouse EST Project
Unpublished (1996)
On May 18, 1995 this sequence version replaced gi:811252.
On May 18, 1995 this sequence version replaced gi:811252.
On Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty.free through LLNL; contact the IMAS Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                           Mus musculus

Mus musculus

Bucharyota, Metazoa, Chordata; Craniata; Muridae; Musinae; Mus.

Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

(Abases 1 to 89)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                             seq_documentation_block:

LOCUS W96900
W96900 Soares mouse embryo NbME13.5 14.5 Mus musculus CDNA
DEFINITION mf88a09.1 Soares mouse embryo NbME13.5 14.5 Mus musculus CDNA
clone IMAGE:421336 5' similar to gb:L35249 VACUCLAR ATP SYNTHASE
SUBUNIT B, BRAIN ISOFORM (HUMAN); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Soares mouse embryo NbME13.5 14.5"
/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 5
Gaps: 0
Percent Identity: 100.000
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Seq primer: ETPINEE.
High quality sequence stop: 1.
Location/Qualifiers
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:421336"
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39 AGAGAAGCCCTTAGA 53
                                                                           seq_name: gb_est7:W96900
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The Washu-HHMI Mouse EST Project
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US-08-653-294-3 x AA701141/rev
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Ratio: 3.800
Percent Similarity: 100.000
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LOCUS AA611878
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Mus musculus
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                                                                                                                                                                                                                                                                                       Eukaryota: Manmalia;
Eukaryota: Metazoa: Chordata: Craniata; Vertebrata: Mammalia;
Eukaryota: Metazoa: Chordata: Craniata; Vertebrata: Mammalia;
Eutheria: Rodontia: Sciurognathi; Muridae: Murinae: Mus.
E (bases 1 to 8);
S Herblot,S., Chastagner,P., Samady,L., Moreau,J.-L., Froussard,P.,
Bonnet,J. and Theze,J.
mRNA level analysis of IL-2-induced genes selected by cDNA
representational difference analysis in mouse T cells
Unpublished (1998)
C on Jan 19, 1998 this sequence version replaced gi:2282087.
Contact: Herblot, Sabine
Immunogenetique Cellulaire
Institut Pasteur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
LOCUS
AA701141
DEFINITION zg56f04.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNa clone
DEFINITION zg56f04.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNa clone
ACCESSION AA701141.
VERSION AA701141. GI:2704306
                                                                                                                                ArU27930 89 bp mRNA EST 29-SEP-1998
#F027930 Mouse cDNA (S.Herblot) Mus musculus cDNA clone C30.1.62,
AF027930
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 91)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
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/clone="C30.1.62"
/clone_lib="Mouse cDNA (S.Herblot)"
24 c 31 g 13 t
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Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 rue du Dr. Roux, Paris 75 724, France
Email: sabine.herblot@immol.u-bordeaux2.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83
83
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US-08-653-294-3 x AF027930
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                                                                                                       seq_name: gb_est23:AF027930
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to: W96900
                                  1 ArgGlu***LeuArg 5
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LOCUS AF027930
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vo90a03.rl Barstead mouse irradiated colon MPLRB7 Mus musculus cDNA clone IMAGE:1066348 5' similar to gb:M37761 Mouse calcyclin mRNA, Accomplete cds (MOUSE);, mRNA sequence.
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Marian, Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality Possible reversed clone: similarity on wrong strand seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 1. Location/Qualifiers
       Schellenberg,K., Steptoe,M., Tan,F.,
., Wylie,T., Waterston,R. and Wilson,R.
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-MCI human EST Project
Unpublished (1997)
Con Sep 12, 1996 this sequence version replaced gi:1404908.
Washington University School of Medicine
Washington University School of Medicine
Washington University School of Medicine
Tel: 314 286 1800
Eax: 314 286 1800
Email: est@watson.wustl.edu
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Gaps: 0
Percent Identity: 100.000
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WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
        TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1402225.
Contact: Marra MyMouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HMI Mouse EST Project
WashIngton University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:588708
Trace considered overall poor quality
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 93)
Marra,M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schallenberg,K., Steptce,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vi19q10.rl Barstead mouse proximal colon MPLRB6 Mus musculus cDNA clone IMAGE:904290 5' similar to gb:X79535 TUBULIN BETA-2 CHAIN (HUMAN); gb:M28732 Mouse beta-tubulin gene M-beta-5, 3' end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-0CT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
%train="reyb."
/db_xref="taxon:10090"
/clone="IMAGE:1066348"
/clone=lib="Barstead mouse irradiated colon MPLRB7"
/dev_stage="8 weeks"
/lab_nost="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vector, Library constructed by Bob Barstead.
20 c 24 g 25 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S Gaps: 0 Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA623328
AA623328.1 GI:2527204
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US-08-653-294-3 x AA611878/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 19.00
Ratio: 3.800
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: gb_est17:AA623328
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LOCUS AA623328
DEFINITION vi19910.rl Ba
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    JOURNAL
COMMENT
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ORIGIN
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VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                      FEATURES
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3'); double-stranded cDNA was ligated to Eco RI adaptors [AATTCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead. "
11 c 34 g 11 t
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On Nov 29, 1993 this sequence version replaced gi:636298.

Contact: Marsa M/Mouse Est Project
Washbrithm Mouse Est Project
Washb
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/clone_lib="Barstead mouse proximal colon MPLRB6"
/de_stage="." day juvenile"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S Gaps: 0 Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trace considered overall poor quality
Seq primer: -28mil rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'organism-"Mus musculus"
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/db_xref="taxon:10090"
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Ratio: 3.800
Percent Similarity: 100.000
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US-08-653-294-3 x AA623328
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

February 8, 2000, 01:29:35 ; Search time 122.56 Seconds
(without alignments)
1.160 Million cell updates/sec

US-08-653-294-4 29 1 RIALRY 6

Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

188963 seqs, 23686106 residues Searched: 188963 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

A_Geneseq_36:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	odul	nseq	agme.	GIL	HLA-B2702 CTL modu	Alphal-helix of HL	4	-cell modul	T-cell modulating	Immunomodulatory p	Immunomodulatory p	Pept1de B2702.75-8	Peptide B2702.75-8	HLA-B2702 84-79-84	Peptide B2702.84-7	Immunomodulating d	HLA-B2702 CTL modu	Peptide B2702.70-8	CTL	L mod	84-72-8	odulating	B2702.8			HLA-B2702 CTL modu	HLAB38 CTL modulat	HLA-B2702.60-84. C	HLAB38.6084. Comps	B2702	Seg	of HLA-B	e of HLA	HLA-Bw53 exon. HLA
SUMMARIES	Ü	W47261	\sim	\sim	R83062	R83094	R95413	R95425	W07512	W07513	W47265	W47269	W33784	W33787	R95429	W33798	W33799	R92912	W33795	R92907	R92908	R95428	W33778	W33791	R41205	R48286	R83090	R83093	R95416	R95422	W33794	Y06801	314	R03144	R12463
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d	Query	00	90	00	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	8	8	100.0	8	8	8	100.0	8	100.0	100.0	8	100.0	8	8	100.0	8	8
	Score	29	59	29	29	59	29	29	29	29	58	53	58	53	53	58	59	53	53	29	29	29	29	29	29	29	29	29	29	29	29	29	29	29	29
	Result No.	1	~	m	4	S	ø	7	ω	σ,	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34

Human amine recept S.antibioticus ole	Rice RSW1-like cel Arabidopsis cellul	S. pneumoniae PTS	eryA region polype	pJH1 gene product	Yeast MSH1 protein	Yeast MSH1 protein	Arabidopsis cellul	Arabidopsis cellul
W09110 W99399	W46202 W33819	W38564	R44431	R04104	R7,6066	R76070	W33817	W33820
нн		Н	Н	1	Н	Н	-	
337	547 1065	141	3567	939	959	971	1081	1081
96.6	93.1 93.1	89.7	89.7	86.2	86.2	86.2	86.2	86.2
28	27	56	56	25	52	25	22	22
35 36	37 38	39	40	41	42	43	44	45

ALIGNMENTS

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-
CC donor, 1.e. to inhibit transplant rejection. It can also be used i
CC the treatment of autoimmune diseases.
CC Peptides using the D-form amino acids are more effective
CC immunomodulators than their diastereomers or enantiomers
2 Sequence 6 AA;

ô Indels ö 0; Mismatches 6; Conservative Matches

ö

Gaps

1 RIALRY 6 |||||| 1 RIALRY 6 ò 셤

RESULT W33780

W33780 standard; peptide; 6 AA.
W33780;
W3801 in immunomodulating dimer peptide.
Immunomodulating dimer; immunosuppressant drug; CTL activation; transplantation; autoimmune disease; Class I HLA-B alpha-1 domain; transplantation.
Synthetic.
Homo sapiens.
W09744351-A1.

I DA GENERAL DE LA CONTRA CONT

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Matches
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R83094
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                                                                                                                                                                                                                                          R83062
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                                                                                                                                                                                                                                                                                                                    of the immunomodulating dimer peptides of the invention. A peptide-type compound or variant is claimed which has immunomodulating dimer peptides of the invention. A peptide-type compound or variant is claimed which has immunomodulating activity.

Including the N-terminal actimed which has immunomodulating activity,

can be comprises the formula; A-B, where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84= a hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to class I HLA-B alphal domain (positions 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CT) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune considers.
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The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL activity in parasitic diseases and neoplasha and in studies on viral infection. The peptide can also be used for identifying CTLs which bind to it and removing subsets of CTLs from a T-cell composition. This peptide sequence is more commonly found within larger peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                   treating autoimmune diseases
Claim 15; Page 35; 41pp; English.
This sequence represents a specifically claimed peptide which forms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-MAR-1994. (first entry)
peptide fragment of class I HLA peptide.
Humen leukocyte antigen: HLA: peptide: transplantation; neoplasia;
parasitic disease; cytotoxic T lymphocyte; modulation.
                                              24-MAY 1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
(STRD ) UNIV LELAND STANFORD JUNIOR.
WPI: 98-086530/08.
New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The products can also be used for detection and diagnosis Sequence 6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 29; DB 1; I
100.0%; Pred. No. 1.5e+05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-FEB-1993; U01758.
02-MAR-1992; US-844716.
(STRD) UNIV LELAND STANFORD JUNIOR.
CLAYDERGER CA, KRENSKY AM;
WPI; 93-303134/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R41208 standard; peptide; 10 AA.
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6; Conserv
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| RIALRY 6
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Best Local S
Matches 6
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DB 1; Length 10; 0.23;

Score 29; Pred. No.

100.0%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of R83061-R83086, R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 75-84 of the alpha-1 domain of the class I MHC HLA-B3702. These sequences can be used to extend the period of The Peptides are administered to a patient from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLS)
                                                                                                                                                                                                                                                            16-MAY-1996 (first entry)
HIA-B2702 CTL modulating peptide (B2702.75-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HIA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIA-B2702 CTL modulating peptide (B2702.75-84(D)). Cytocoxic T lymphocyte; CTL: major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 14; Page 34; 80pp; English.
R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               12-OCT-1995.
05-APR-1995; U04349.
05-APR-1995; UG-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
(STRD ) 95-35982/APA, Parham P;
WPI: 95-35882/APA acceptance period of transplants from MHC unmatched
donor hosts - using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Extension of acceptance period of transplants from MHC unmatched donor hosts – using Class I B75-84 MHC antigen of the recipient
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  Indels
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  Mismatches
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                                                                                                                                                                                                               R83062 standard; peptide; 10 AA.
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R83094;
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  Conservative
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WPI; 95-358582/46.
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                                                                       of the patient
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5 RIALRY 10
                                              1 RIALRY 6
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WO9526979-A1.
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WO9526979-A1.
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HLA-B2702.75-84(D).
HLA, p74; alphal-helix; human-leucocyte-associated antigen; inhibitor; T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC; B cell; calcium influx; cytotoxic I lymphocyte; CTL; differentiation;

R95425 standard; peptide; 10 AA. R95425; (first entry)

12-NOV-1996

/note= "N3D mutation"

Location/Qualifiers

misc_difference 3

WO9513288-A1

cytolysis; antigen presenting cell. Synthetic.

10-NOV-1994; U12985. 10-NOV-1993; US-150493. (STRD) UNIV LELAND STANFORD JUNIOR.

Krensky AM;

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This sequence represents the alphal-helix of the human sequence, represents the alphal-helix of the human-leucocyte-associated antigen B2702 (HLA-B2702). This sequence, represents the alphal-helix of the human-leucocyte-associated antigen B2702 (HLA-B2702). This sequence, protein protein palantanes of it (such as R95428) can be used to isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane protein p74 from a T-cell lysate. p74 is a T-cells, and is also immunologically cross reactive with the heat shock protein Hsc70. p74 is found in a limited number of cell types, but its particularly expressed on B and T cells. p74 can be isolated by lysis of a suitable cell with an amphoteric detergent, and then passed through an affinity expressed on B and T cells. p74 can be isolated by lysis of a suitable coll with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HLA-B2702 palindromic peptide. Compositions comprising the extracellular fragment of p74 combined with HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits compositions can be screened for their effect on the cytolysis cardidate compounds can be screened for their effect on the cytolysis activity of T-cells, by combining them with the extracellular portion of p74 and determining the amount of binding between the candidate composition containing T-cells and antigen presenting cells (APCS), by adding to the candidate to composition of p74, in an amount sufficient to compete canner.
                                                                                                                             S
class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 75-84 of the alpha-1 domain of the class I MHC HLA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CILs)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIA: p74: alphal helix: human-leucocyte-associated antigen; inhibitor; T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC; B cell; calcium influx; cytotoxic I lymphocyte; CTL; differentiation; cytolysis; antigen presenting cell.
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10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R95413 standard; peptide; 10 AA. R95413;
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Best Local Similarity
Matches 6; Conserv
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WPI; 95-194027/25
                                                                                                                                                                                                                       of the patient
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5 RIALRY 10
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R95413
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Whise strategies are secured membrane proteins - which may half solidate activity and differentiation of CTLS.

Tomposins. comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLS.

Example: Page 11: 29pp: English.

R95413, and R95415-R95431 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the cumanical properties of the page of a sultable cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HLA-B2702 palindromic peptide.

Compositions comprising the extracellular fragment of p74 combined with the the page of the cytolysis.

Compositions comprising the extracellular fragment of p74 combined with the extracellular portion of p74 and cetermining the amount of binding between the candidate compound and p74.

CT-cells, by combining them with the extracellular portion of p74 and determining the amount of binding between the candidate compound and p74.

CM Modifiation of CTL activity can be inhibited in a cellular composition composition of mix the extracellular portion of p74, in an amount sufficient to compete componed.
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T-cell modulating peptide #1.
T-cell modulator; autoimmune disease; tissue destruction; alphal-domain;
T-cell modulator; autoimmune disease; tissue destruction; alphal-domain;
mammal; major histocompatability complex; MHC class I; antigen; perforin;
insulin-dependent diabetes mellitus; multiple sclerosis; inflammation;
thenmatoid arthritis; psortasis; pemphigus vulgaris; Sjogren's disease;
thyroid disease; Hashimoto's thyroiditis; myasthenia gravis; granzyme;
autologous target cell; cytokine release; T cell activation; therapy.
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Best Local Similarity
Matches 6; Conserv
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WPI; 95-194027/25.
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WO9635443-A1.
14-NOV-1996.
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Gaps

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100.0%; Score 29; DB 1; Length 10; 100.0%; Pred. No. 0.23; ive 0; Mismatches 0; Indels

Conservative

1 RIALRY 6

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Query Match Best Local Similarity Matches 6; Conserv

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WPI: 90-218410/51.

W PPI: 90-20: 24pp: English.

Claim 7: Page 20: 24pp: English.

W PPI: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20: 90-20:
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Claim 7: Page 20; 24pp; English.

WOY512-WOY518 represent T-cell modulating peptides that can be used in the method of the invention. These sequences are based on a portion of the major histocompatability complex (MHC) class I antigen (see the major histocompatability complex (MHC) class I antigen (see WOY510). The method is for affecting the course of an autoimmune disease involving T-cell mediated destruction of tissue in mammals. These peptides are used especially to treat insulin-dependent diabetes mellitus, preferably being administered during the pre-clinical stage to delay onset of the disease. Other diseases that can be treated are delay onset of the disease. Other diseases that can be treated are multiple sclerosis, rheumatoid arthritis, psoriasis, pemphigus vulgaris, Sjogren's disease, thyroid disease, Hashinoto's thyroiditis, mysathenia gravis, etc. The peptides modulate T-cell mediated attack on autologous
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T-cell modulating peptide #2.
T-cell modulator; autoimmune disease; tissue destruction; alphal-domain;
T-cell modulator; autoimmune disease; tissue destruction; alphal-domain;
mammal; major histocompatability complex; MHC class I; antigen; perforin;
insulin-dependent diabetes mellitus; multiple sclerosis; inflammation;
theumatoid arthritis; psoriasis; pemphigus vulgaris; Sjogren's disease;
thyroid disease; Hashimoto's thyroiditis; myasthenia gravis; granzyme;
autologous target cell; cytokine release; T cell activation; therapy.
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                                                                                                SANGSTAT MEDICAL CORP.
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05-APR-1996; U04710,
12-MAY-1995; US-440504,
                                             12-MAY-1995; US-440504
05-APR-1996; U04710
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RIALRY 10
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04-AUG-1997
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target cells, and may also reduce inflammation, swelling, and release of cytokines, perforins, granzymes etc. associated with T cell activation. Sequence \sim 10\ AA;
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The present sequence is an immunomodulatory peptide, which comprises a Class I HIA-B alpha-1 domain sequence. It can be used in a pharmaceutical composition together with a subtherapeutic dose of an immunosuppressant, to extend the period of acceptance of a transplant from a major histocompatibility complex (MHC) unmatched donor, i.e. to inhibit transplant rejection. It can also be used in the treatment of autoimmune diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunomodulatory peptide.
Immunomodulator; Class I HLA-B alpha-1 domain; inhibition;
transplant rejection; treatment; autoimmune disease.
Homo sapiens.
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Immunomodulatory peptide.
Immunomodulator; Class I HLA-B alpha-1 domain; inhibition;
transplant rejection; treatment; autoimmune disease.
                                                                                                                                                                         Length 10
                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                   Score 29; DB 1;
Pred. No. 0.23;
Mismatches 0
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23-ARR-1997; U06705.
22-MAY-1996; UG-651650.
2STRD ) UNIV LELAND STANFORD JUNIOR.
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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WPI; 98-018220/02.
                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transplant rejection
                                                                                                                                                                         Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptides using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc_difference 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc_difference 1
                                                                                                                                                                                                                                                                                                                                                  5 RIALRY 10
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5 RIALRY 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-MAY-1998
                                                                                                                                                                                                                                                                                         1 RIALRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RIALRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
W47265
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ID W4
AC W4
AC W4
DT 222
DE IM
KW IM
KW LI
KW L
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Score 29; DB 1;
Pred. No. 0.23;
                                                                  Mismatches
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                                                                                                                                                                                                       W33787 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R95429 standard; peptide; 12 AA.
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                                 100.0%;
                   Query Match
Best Local Similarity 100...
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Best Local Similarity
Matches 6; Conserv
                                                                                                               1 RIALRY 6
                                                                                                                                                                                                                                                                                                                                Homo sapiens.
WO9744351-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14
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R95429
ID R95
AC R95
DT 12:
DE HL2
KW HLL4
KW T-4
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We immunomodulating dinmer peptide(s) - based on a class I HiA-B alpha-1 domain, used for preventing rejection of transplants or treating autoimmune diseases.

Frample 1; Page 19; 41pp; English.

Peptides W33784-98 and W33778-9 were assayed for their immunomodulating cartivity. A peptide-type compound or variant is claimed which has a cinmunomodulating activity, including the N-terminal acylated and/or c-terminal amidated or esterified forms of up to 60 anino acids, where the peptide-type compound comprises the formula; A-B, where A, B = C the peptide-type compound comprises the formula; A-B, where A, B = C R and 6-T D, (and 8-79) (land 7-76R); and 7 = D, S or N; and 9-R or G; aa80 = I or N; and 1 and 2 = R or L; and 3 = G or R; and a represents amino acid; and 2 = R or L; and 3 = G or R; and a represents amino acid sequences related to a class I HiA-B alphal domain (positions and 10 acids acids equences related to a class I HiA-B alphal domain (positions of 10 acids acids acids acids and a class I HiA-B alphal domain (positions or undesirably attacking cells in a host or in vitro. They can also be used to inhibit the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, response to anti-CD3. The peptide can be used for preventing rejection or remained arthritis and lupus erythematosis. The products can also be used for detection and diagnosis.
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W09744052-A1.
27-NOV-1997.
23-APR-1996; US-651650.
22-MAY-1996; US-651650.
(STRD ) UNIV LELAND STANFORD JUNIOR.
(STRD ) UNIV LELAND STANFORD HORP.
(STRD ) UNIV LELAND STANFORD HORP.
WPI: 90-018220/02.
Novel immunomodulatory peptide-type compound - useful for inhibiting
                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                     The present sequence is an immunomodulatory peptide, which comprises a class I HLA-B alpha-1 domain sequence. It can be used in a pharmaceutical composition together with a subtherapeutic dose of an immunosuppressant, to extend the period of acceptance of a transplant from a major histocompatibility complex (MHC) unmatched donor, i.e. to inhibit transplant rejection. It can also be used in the treatment of autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JUN-1998 (first entry)
Peptide B2702.75-84 tested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CTL activation; transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
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                                                                                                                                                                                                                                                                                                                                             100.0%; Score 29; DB 1; Length 10; 100.0%; Pred. No. 0.23; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                 Peptides using the D-form amino acids are more effective immunomodulators than their diastereomers or enantionmers.
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22-MAY-1997; U08689.
24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Bellow R, Clayberger C, Krensky AM;
WPI; 98-086530/08.
                                                                                                                            transplant rejection
Claim 10; Page 36; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W33784 standard; peptide; 10 AA
                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
WO9744351-A1.
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19-JUN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rejection.
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                                                                                                                                                                                                                                                                                                   Sequence
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PF 22-MAY-1997.

22-MAY-1997 U08689.

PRAY-1997 U08689.

PRAY-1997 U08689.

RAY-1996 US-653294.

RAY-1996 US-653294.

PRAY-1996 US-653294.

PRAY-1996 US-653294.

PRAY-1996 US-653204.

PRAY-1996 US-1
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L-NOV-1996 (first entry)
HLA-B2702 84-79-84 palindrome.
HLA: p74; alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUN-1998 (first entry)
Peptide B2702.75-84D77 tested for immunomodulating activity.
Immunomodulating dimer; immunosupressant drug; CTL activation;
transplantation; autoAmmune disease; Class I HLA-B alpha-1 domain;
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0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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WILL:

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Example 1: Page 19: 41pp; English.
Example 1: Page 19: 41pp; English.
Example 1: Page 19: 41pp; English.
Example 2: Page 19: 41pp; English.
Example 2: Page 2: Page 2: Page 2: Page 2: Page 3: Pa
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Peptide B2702.84-79/79-84 tested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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(STR) ) UNIV LELAND STANFORD JUNIOR.
Bellow R, Clayberger C, Krensky AM;
WPI; 98-086530/08.
                                                                                                                                                                                                                                                                                                                       (STRD ) UNIV LELAND STANFORD JUNIOR
     cytolysis; antigen presenting cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W33798 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                               Krensky AM;
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Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                10-NOV-1993; US-150493
                                                                                                                                                           18-MAY-1995.
10-NOV-1994; U12985
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22-MAY-1997; U08689
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7 RIALRY 12
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                                                                                                                                                                                                                                                                                                                                                                               Clayberger C,
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WO9744351-Al.
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small amino acid; aa82 - R or L; aa83 - G or R; and aa represents amino acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a class I HiA-B alphal domain (positions 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosis. The products can also be
                                                                                                                                                                                                                                                                                                                                                                    used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
          888888888888888
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Gaps ; 0 h 100.0%; Score 29; DB 1; Length 12; Similarity 100.0%; Pred. No. 0.27; 6; Conservative 0; Mismatches 0; Indels Query Match Best Local Similarity Matches 6; Conserv

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ø 1 RIALRY 셤 ö

7 RIALRY 12

Search completed: February 8, 2000, 01:29:35 Job time: 1747 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

February 7, 2000, 11:54:13; Run on:

Search time 117.7 Seconds (without alignments)
2.405 Million cell updates/sec

US-08-653-294-4 29 1 RIALRY 6 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

142080 seqs, 47169319 residues Searched: 142080

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

pir1:* pir2:* pir3:* pir4:* PIR_62:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ф			SUMMAKLES	
Result No.	Score	Query	Length	DB	ID	Description
-	29	100.0	237	7	A71082	hypothetical prote
~	29	100.0	273	~	I38509	ᇨ
m	29	100.0	274	-	HLHU32	clas
4	53	100.0	274	7	154463	
'n	29	100.0	354	~	I59308	class I histocompa
Q	29	100.0	354	~	180168	class I histocompa
_	29	100.0	354	~	180167	н
œ	29	100.0	355	N	I80169	Н
თ	29	100.0	355	~	180171	class I histocompa
2	29	100.0	359	Н	HLHU12	MHC class I histoc
1	29	100.0	362	-	HLHUB8	MHC class I histoc
2	29	100.0	362	~	B30345	MHC class I histoc
	29	100.0	362	~	JH0541	н
4	59	100.0	362	~	JH0539	н
ιŲ	58	100.0	362	~	JH0540	B
ب	53	100.0	362	~	A45834	MHC class I histoc
۲.	29	100.0	362	~	I84486	transmembrane glyc
18	59	100.0	362	~	I62045	gene HLA B-1517 pr
o,	29	100.0	362	7	I84490	ocy
0.	29	100.0	362	~	137521	
21	29	100.0	362	~	A30345	н
2	29	100.0	362	7	159633	MHC HLA-B transmem
33	53	100.0	362	~	S24434	class I histocompa
	29	100.0	362	~	137120	clas
5	29	100.0	363	~	S07113	class I histocompa
	29	100.0	363	N	803537	iist
	29	100.0	364	7	A35997	MHC class I histoc
	29	100.0	364	7	59	н
59	29		365	7	σ ₁	굯
0	29	100.0	365	7	JH0537	class I histocompa

HLA-AW24 protein - MHC class I histoc	neurotransmitter r gene 19.2 protein	probable 84.5K ATP cellulose synthase	Outer membrane pro ATP-dependent heli	glutamyl-tRNA synt coat protein beta	erythronolide synt hypothetical prote		hypothetical prote
I54416 I54493	JC5832 W9BPB7	S57579 T02209	H70347 D64738	G75165 S13520	S23070 S76214	B41629 A41629	140656
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29	28	27	27	26 26	25	22	22
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ALIGNMENTS

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hypothetical protein PH0919 - Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 14-Aug-1998

Chacession: A7108

Rikawarabayasi, Y.: Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Se M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu DNA Res. 5, 55-76, 1998

A;Title: Complete sequence and gene organization of the genome of a hyper-thermophili A;Recence number: A71000; MUID:98344137

A;Accession: A71082

A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Residues: 1-237

A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Residues: 1-237

A;Coss-references: GB:AP000004; NID:93236131; PID:d1030958; PID:g3257332

A;Note: this accession replaces an interim accession for a sequence replaced by GenBa G;Genetics:

A;Gene: PH0919

ö Gaps ô 100.0%; Score 29; DB 2; Length 237; 100.0%; Pred. No. 4.8; tive 0; Mismatches 0; Indels Query Match 100.
Best Local Similarity 100.
Matches 6; Conservative

1 RIALRY 6 õ 18 RIALRY 23

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MHC class I histocompatibility antigen - human (fragment)
C; Species: Homo sapiens (man)
C; Accession: 138509
R; Cereb, N.; Choi, J.W.; Riu, K.Z.; Yang, S.Y.
Tissue Antigens 44, 271-273, 1994
A; Title: HiA-B*5105, a newly identified B51 IEF variant.
A; Reference number: 138509; MUID: 95176331
A; Reference number: 138509
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-273 <RES>
A; Cross-references: EMBL: U06697; NID: 9469544; PIDN: AAA92997.1; PID: 9469545
C; Genetics:
A; Gene: GBB: HIA-B

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A;Cross-references: GDB:120048; OMIM:142830 A;Map position: 6p21.3-6p21.3 C;Superfamily: class I histocompatibility antigen; immunoglobulin homology

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Ouery Match
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R;Mueller, C.A.; Engler-Blum, G.; Gekeler, V.; Steiert, I.; Weiss, E.; Schmidt, H.
Immunogenetics 30, 200-207, 1989
A;Title: Genetic and serological heterogeneity of the supertypic HLA-B locus specificiti
A;Reference number: I54463; MUID:89379286
                                                                                                                                                                                                                                                       MHC class I histocompatibility antigen HLA-A32 alpha chain - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 31-nec-1988 #sequence_revision 31-Dec-1988 #text_change 05-Sep-1997
C;Accession: A26088
R;Wan, A.M.; Entls, P.; Parham, P.; Holmes, N.
J. Immunol. 137, 3671-3674, 1986
A;Title: The primary structure of HLA-A32 suggests a region involved in formation of the A;Reference number: A26088; MUID:87058961
A;Accession: A26088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GDB:119310; OMIM:142800
A;Map position: 6p21.3-6p21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: glycoprotein; heterodimer; transmembrane protein; transplantation antigen
F;196-261/Domain: immunoglobulin homology xIMM>
F;86/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C.Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
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C;Species: Pan paniscus (pygmy chimpanzee, bonobo)
C;Date: 31'May-1996 #sequence_revision 31-May-1996 #text_change 23-Jul-1999
                                                                    Gaps
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C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
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                    Length 273;
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                    100.0%; Score 29; DB 2; 100.0%; Pred. No. 5.6;
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                                                                 0; Mismatches
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154463
MHC HLA-B38 chain - human (fragment)
                                                                 Conservative
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Best Local Similarity
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A; Residues: 1-274 <RES>
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RIALRY 83
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C; Accession: IS9308
S; McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Wat Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A; Title: A uniquely high level of recombination at the HLA-B locus.
A; Reference number: IS9308; MUID: 94286544
A; Reference number: IS9308
A; Reference number: IS9308
A; Reference number: IS9308
A; Molecule type: mRNA
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C;Species: Pan paniscus (pygmy chimpanzee, bonobo)
C;Species: 24 May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999
C;Accession: 180167
R;McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Wat Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A;Title: A uniquely high level of recombination at the HLA-B locus.
A;Accession: 180167
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Cispecies: Pan troglodytes (chimpanzee)
Cispecies: 24-May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999
Cispecies: 24-May-1996 #text_change 23-Jul-1999
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A; Cross-references: EMBL:U05575; NID:g454767; PIDN:AAA50178.1; PID:g454768
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
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A; Cross-references: EMBL:U05579; NID:g454775; PIDN:AAA50182.1; PID:g454776
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
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C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
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A;Molecule type: mRNA
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A;Molecule type: mRNA
A;Residues: 1-354 <RES>
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A;Map position: 6p21.3
A;Map position: 6p21.3
A;Introns: 227,1127,204/1; 296/1; 335/1; 346/1
A;Introns: 227,11127,204/1; 204/1; 335/1; 346/1
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Superfamily: class I histocompatibility antigen Hza lapha chain stanal sequence #status predicted <SIG>
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-359/Product: class I histocompatibility antigen Hza alpha chain #status predicte F;22-354/Domain: alpha-1 <EXIX
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A;Map position: 6p21.3-6p21.3
A;Map position: 6p21.3-5p21.3
A;Introns: 25/1; 115/1; 299/1; 338/1; 349/1
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Superfamily: class I histocompatibility antigen; transmembrane protein; transplant
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-362/Product: class I histocompatibility antigen HIA-Bw58 alpha chain #status pre
F;25-307/Domain: alpha-1 <EXI>
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C;Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 16-Feb-1997
C;Accession: B30345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo saplens (man)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 05-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MHC class I histocompatibility antigen HLA-Bw58 alpha chain precursor
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F:332-362/Domain: intracellular #status predicted <INT>
F:110/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A; Residues: 1.362 CMAY>
A; Rote: the authors translated the codon GCC for residue 349
C; Comment: This protein is a subtype of the HLA-B17 family.
C; Genetics:
                                                                                                                                                                                                                                                                                                                           HLA-Bw58
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F;217-282/Domain: immunoglobulin homology <IMM>
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R;Ways, J.P.; Coppin, H.L.; Parham, P.
J. Biol. Chem. 260, 11924-11933, 1985
A;Title: The complete primary structure of
A;Reference number: A23895; MUID:86008247
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Best Local Similarity
Thes 6; Conserve
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| 100 RIALRY 105
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Proc. Natl. Acad. Sci. U.S.A. 79, 893-897, 1982

A;Title: Exon/intron organization and complete nucleotide sequence of an HLA gene.
A;Reference number: A02189; MUID:82151002
A;Reference number: A02189
A;Molecule type: DNA
A;Residues: 1-359 < AAL>
A;Cross-references: GB:J00191; GB:V00526; NID:g187600; PIDN:AAA36218.1; PID:g386873
C;Comment: The seven exons correspond approximately to the domain structure of this chaic; Genetics:
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(;Species: Pan troglodytes (chimpanzee)

(;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999

(;Accession: 180171

R:McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Watkin Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994

A;Title: A uniquely high level of recombination at the HLA-B locus.

A;Reference number: 159308; MUID:94286544
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                                                                                                                                                               class I histocompatibility antigen - chimpanzee (fragment)
C;Species: Pan troglodytes (chimpanzee)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999
C;Accession: I80169
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C.Date: 05-Apr-1983 #sequence_revision 05-Apr-1983 #text_change 22-Jun-1999
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A;Cross-references: EMBL:U05582; NID:g454781; PIDN:AAA50185.1; PID:g454782
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
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A;Title: A uniquely high level of recombination at the HLA-B locus. A; Reference number: 159308; MUID:94286544
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A;Molecule type: mRNA
A;Residues: 1-355 <RES>
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Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 6; Conservative 0; Mismatches
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Job time: 24324 sec
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'-hns 6; Conserv?
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Matches 6; Conserv
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Superfamily: class I histocompatibility antigen; immunoglobulin homology
Keywords: transmembrane protein
1.24/Domain: signal sequence #status predicted <SIG>
25-362/Product: class I histocompatibility antigen heavy chain, Gogo-B0103 #status pre
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class I histocompatibility antigen Gogo-B0101 heavy chain precursor - lowland gorilla Class I histocompatibility antigen Gogo-B0101 heavy chain precursor - lowland gorilla C; Species: Gorilla gorilla (lowland gorilla)
C; Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C; Accession: JH0539
R; Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
J. Exp. Med. 174, 1491-1509, 1991
A; Rithe: Gorilla class I major histocompatibility complex alleles: comparison to human A; Reference number: JH0534; MUID:92078860
A; Rocession: JH0539
A; Molecule type: DNA
A; Residues: 1-562 CLAW>
A; Cross_references: EMBL:X60255; NID:g22865; PIDN:CAA42807.1; PID:g22866
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C; Species: Gorilla gorilla gorilla (lowland gorilla)
C; Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C; Accession: JH0541
R; Lawlor, D.A.; Warren, E; Taylor, P; Parham, P.
J; Exp. Med. 174, 1491-1509, 1991
J; Title: Gorilla class I major histocompatibility complex alleles: comparison to human A; Reference number: JH0534; MUID:92078860
R; Hayashi, H.; Ennis, P.D.; Ariga, H.; Salter, R.D.; Parham, P.; Kano, K.; Takiguchi, J. Immunol. 142, 306-311, 1989
A; Title: HLA-B51 and HLA-B52 differ by only two amino acids which are in the helical state ference number: A30345; MUID:89080265
A; Reference number: A30345; MUID:89080265
A; Status: preliminary
A; Status: preliminary
A; Residues: 1-362 <HAY>
C; Superfamily: QLass I histocompatibility antigen; immunoglobulin homology
C; Steywords: transmembrane protein
F; 220-285/Domain: immunoglobulin homology <IMM>
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:Molecule type: DNA
:Residues: 1-362 < LLAM
:Cross-references: EMBL.X60254; NID:g22869; PIDN:CAA42806.1; PID:g22870
:Experimental source: EBV-transformed B cell
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:299-362/Domain: intracellular #status predicted <INT>
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class I histocompatibility antigen Gogo-B0102 heavy chain precursor - lowland gorilla C;Species: Gorilla gorilla gorilla (lowland gorilla) C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
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J. Exp. Med. 174, 1491-1509, 1991
A;Title: Gorilla class I major histocompatibility complex alleles: comparison to huma A;Reference number: JH0534; MUID:92078860
A;Accession: JH0540
A; Experimental source: EBV-transformed B cell
C; Genetics:
A; Introns: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
C; Keywords: transmembrane protein
F; 1-24/Domain: signal sequence #status predicted <SIG>
F; 1-25/Domain: alpha-1 <ALI>
F; 25-362/Product: class I histocompatibility antigen heavy chain, Gogo-B0101 #status
F; 25-114/Domain: alpha-2 <ALI>
F; 115-206/Domain: alpha-2 <ALI>
F; 210-298/Domain: alpha-3 <ALI>
F; 220-288/Domain: immunoglobulin homology <IMM>F; 299-362/Domain: intracellular #status predicted <INT>
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Superfamily: class I histocompatibility antigen; immunoglobulin homology

Keywords: transmembrane protein

:1-24/Domain: signal sequence *status predicted <SIG>

25-362/Product: class I histocompatibility antigen heavy chain, Gogo-B0102 *status

:25-114/Domain: alpha-1 <AL1>
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A;Cross-references: EMBL:X60693; NID:q22867; PIDN:CAA43101.1; PID:g22868
A;Experimental source: EBV-transformed B cell
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F;299-362/Domain: intracellular #status predicted <INT>
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Sec. 5. 10

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OM protein - protein search, using sw model

February 8, 2000, 00:59:44; Search time 63.71 Seconds (without alignments) 2.813 Million cell updates/sec Run on:

BLOSUM62 Gapop 10.0 , Gapext 0.5 US-08-653-294-4 29 1 RIALRY 6 Title: Perfect score: Sequence: Scoring table:

82229 seqs, 29864866 residues Searched:

Total number of hits satisfying chosen parameters:

82229

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

SwissProt_38:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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			-1 ALPHA	CHAIN.	
DOMAIN			XTRACELLU	AR ALPHA-1.	
DOMAIN 1			XTRACELLU	.AR ALPHA-2.	
			XTRACELLU	LAR ALPHA-3.	
			DNITCHING	PEPTIDE.	
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2 4 2 2 4 4 5 5 5 5 5 5 5	PPFAM; PF00128 NONC_I; Transn NONC_TER SIGNAL SIGNAL CHAIN CHAIN DOOMAIN DOOMAIN TRANSMEM SIRANSMEM SIRANS	4; PF00129; MHC_ 1: Transmembran 1: Transmembr	4; PF00129; MHC_1; 1. Transmembrane; Glycopr TER	4; PF00129; MHC_1; 1. Transmembrane; Glycoprotein; Sign TER	4; PF00129; MHC_1; 1. 1; Transmembrane; Glycoprotein; Sign TreR

BY SIMILARITY.

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RESULT 2 1801_GORGO ID 1801_G

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                                                                                                                                                                                                                                                                                               LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
"Gorilla class I major histocompatibility complex alleles: comparison to human and chimpanzee class I.";
J. Exp. Med. 174:1491-1509(1991).
-i- FUNTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMONE SYSTEM.
                                                                                                01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0102 ALPHA CHAIN PRECURSOR.
GOTILLA gOTILLA GOTILLA (LOWLand GOTILLA).
ELWATYOLA, METAZOA; CHONDALA; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOANNO STANDARD; PRT; 362 AA.
1803.GGRGO STANDARD; PRT; 362 AA.
P30381;
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
01-APR-1993 (Rel. 25, Last annotation update)
CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0103 ALPHA CHAIN PRECURSOR.
GORIlla gorilla (Lowland gorilla).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
CLASS I HISTOCOMPATIBILITY ANTIGEN,
GOGO-B0102 ALPHA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 362;
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EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
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                                                             362 AA.
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PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
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362 AA;
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"Gorilla class I major histocompatibility complex alleles: comparison
to human and chimpanzee class I.";
to human and chimpanzee class I.";
J. Exp. Med. 174:1491-1509(1991).
-i- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                                                                                                                                                                                               01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0101 ALPHA CHAIN PRECURSOR.
GOTILLA GOTILLA GOTILLA (Lowland gorilla).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
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CLASS I HISTOCOMPATIBILITY ANTIGEN,
GGOG-BOILD ALPHA CHAIN.
EXTRACELULAR ALPHA-1.
EXTRACELULAR ALPHA-2.
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                                                         Length 359;
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                                                         100.0%; Score 29; DB 1; 100.0%; Pred. No. 4;
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  5395FFC9 CRC32;
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                                                                                                  Mismatches
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PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
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11arity 100.0%; Pred. No. 4;
Conservative 0; Mismatches
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  40173 MW;
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                                                                                                    Conservative
                                                                                                                                                                                                                                                                              STANDARD;
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359 AA;
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Best Local Similarity
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Best Local Similarity
Matches 6; Conserv
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P30379;
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SEQUENCE FROM N.A.
PARHAM P., ARNETT K.L., ADAMS E.J.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
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362 AA;
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P30487;
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1B47_HUMAN
     SOLUTION STATES SELECTION STATES SELECTION SEL
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                                                                      MEDLINE: 92078860.
LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
Gorilla class: I major histocompatibility complex alleles: comparison
to human and chimpanzee class I.";
J. Exp. Med. 174:1491-1509(1991).
-:- FONCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
-:- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
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MEDLINE; 86220133.
SEEMANN G.H.A., REIN R.S., BROWN C.S., PLOEGH H.L.;
Gene conversion-like mechanisms may generate polymorphism in human class I genes.;
EMBO J. 5:547-552(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0103 ALPHA CHAIN.
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01-MAR-1989 (Rel. 10, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2702 ALPHA CHAIN
PRECURSOR (B-27K) (B-27K) (B-27K) (B-27K)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
  Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
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PFAM; PF0129; MHC_1: 1.
MHC_1; Transmembrane; Glycoprotein; Signal.
SIGNAL BY SIMITARITY
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Pred. No. 4;
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P10317;
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CARBOHYD
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MEDLINE; 86042671.
VEGA M.A., EZQUERRA A., ROJO S., APARICIO P., BRAGADO R.,
VEGA M.A., EZQUERRA A., ROJO S., APARICIO P., BRAGADO R.,
LOPEZ DE CASTRO J.A.;
Structural analysis of an HLA-B27 functional variant: identification
of residues that contribute to the specificity of recognition by
cytolytic T lymphocytes.";
Proc. Natl. Acad. Sci. U.S.A. 82:7394-7398(1985).
-I- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
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01-FBE-1996 (Rel. 33, Last sequence update)
01-FBE-1996 (Rel. 33, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-49(B-21) B*4901 ALPHA CHAIN
PRECURSOR.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
                                                                                                                                                                                                                                                                  -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
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EXTRACELLULAR ALPHA-2.
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CONNECTING PEPTIDE.
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PFAM; PF00129; MHC_1; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
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Pred. No.
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EMBL; X03664; CAA27301.1; JOINED.
EMBL; 138504; AAA69724.1; -.
PIR; B25092; HLHUDR.
HSSP; P039899; HSA.
MIM; 142830; -.
PROSITE; PS00290; IG_MHC; 1.
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"HIA-B51 and HIA-BW52 differ by only two amino acids which are in the helical region of the alpha 1 domain.";
J. Immunol. 142:306-311(1989).
       ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
"Rapid cloning of HLA-A.B CDNA by using the polymerase chain reaction: frequency and nature of errors produced in amplification.";
Proc. Natl. Acad. Sci. U.S.A. 87:2833-2837(1990).
                                                                                                                                                                                          POHLA H., KUON W., TABACZEWSKI P., DOERNER C., WEISS E.H.; "Allelic variation in HLA-B and HLA-C sequences and the evolution
                                                                                MEDLINE; 89080265.
HAYASHI H., ENNIS P.D., ARIGA H., SALTER R.D., PARHAM P., KANO
TAKIGUCHI M.;
                                                                                                                                                                                                                the HLA-B alleles.";
Immunogenetics 29:297-307(1989).
-i- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS
THE IMMUNE SYSTEM.
                                                                                                                                                                                                                                                               -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
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MIM; 142830; -
PROSITE; PS00290; IG_MHC; 1.
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PIR; A30548; A30548.
HSSP; P30491; 1A1M.
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362 AA;
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Best Local Similarity
                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE; 89233295.
MEDLINE; 90207291
                                                                      SEQUENCE FROM N.A.
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                                                                             HILDEBRAND W.H., MADRIGAL J.A., BELICH M.P., ZEMMOUR J., WARD F.E., WILLIAMS R.C., PARRAM P., "Serologic cross-reactivities poorly reflect allelic relationships in the HLA-B12 and HLA-B21 groups. Dominant epitopes of the alpha 2 helix.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oll-NOV-1990 (Rel. 16, Created)
Oll-NOV-1990 (Rel. 16, Last sequence update)
Oll-REB-1996 (Rel. 33, Last annotation update)
HIRA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-51(B-5) B*5101 ALPHA CHAIN
PRECURSOR.
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                                                                                                                                                      J. Immunol. 149:3563-3568(1992).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                 PARHAM P., LAWLON D.A., LOMEN C.E., ENNIS P.D.; "Diversity and diversification of HLA-A,B,C alleles."; J. Immunol. 142:3937-3950(1989).
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E996F82F CRC32;
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PFAM; PF00047; 19; 1.
PFAM; PF00129; MHC_I; 1.
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115
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362 AA;
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SEQUENCE FROM N.A. MEDLINE; 89235215.
                                                                       REVISION TO 78.
MEDLINE; 93056529.
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| 103 RIALRY 108
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P18464;
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1B49_HUMAN
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EXTRACELLULAR ALPHA-1.
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EXTRACELLULAR ALPHA-3.
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4D846F30 CRC32;
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PFAM; PF00129; MHC_1; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
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100.0%; Pred. No. 4;
Live 0; Mismatches
                                                                                                                1; JOINED.
1; JOINED.
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                                                                                                                                                                                 **HIA-B51 and HIA-BW52 differ by only two amino acids which are in the helical region of the alpha 1 domain.";

J. Immunol. 142:305-311(1989).

-!- FUNCTION. INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.

-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-52(B-5) B*5201 ALPHA CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                      SEQUENCE FROM N.A.
MEDLINE: 89080265.
MATSAHI H., ENNIS P.D., ARIGA H., SALTER R.D., PARHAM P., KANO K.,
TAKIGUCHI M.;
                                                                        Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HLA CLASS I HISTOCOMPATIBILITY P. BW-52(B-5) B*5201 ALPHA CHAIN. EXTRACELLULAR ALPHA-1. EXTRACELLULAR ALPHA-2. EXTRACELLULAR ALPHA-3. CONNECTING PEPTIDE.
                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebra
Eutheria; Primates; Catarrhini; Hominidae; Homo
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EMBL; M22795; AAA59645.1; JOINED.
EMBL; M22796; AAA59645.1; JOINED.
EMBL; M22798; AAA59645.1; JOINED.
PIR; B30345; B30345.
PIR; B30345; B30548.
HSP; P30491; JAJM.
MIM; 142830; -.
PROSITE; PS00491; G_MHC; 1.
PFAM; PF00129; MHC_I; 1.
PFAM; PF00129; MHC_I; 1.
AMC I; Transmembrane; Glycoprotein; Signal.
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25 362 HLA CLASS I HISTO
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EMBL; M22793; AAA59645.1; JOINED.
EMBL; M22794; AAA59645.1; JOINED.
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(Rel. 25,
(Rel. 36,
                                                                                                                                                                                                                                                                                        MICROGLOBULIN).
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362 AA;
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Best Local Similarity
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                                      HLA-B OR HLAB
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ID 1B54_HUMAN

AC P30491;

DT 01-APR-1993 (;

DT 11-APR-1993 (;

DT 15-JUL-1998 (;
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TRANSMEM
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SEQUENCE
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EMBL;
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          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                     01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-51(B-5) B*5104 ALPHA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                  THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 29; DB 1; Length 362; 100.0%; Pred. No. 4; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; 215143; CAA78849-1; -.
HSSP; P30491; 1AJM.
MIM; 142830; -.
PROSITE; P$00047; 1G_MHC; 1.
PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
SIGNAL 25 362 HLA CLASS I HISTO
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Last annotation update)
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SIMILARITY.
SIMILARITY.
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                                                                        362 AA
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(Rel. 25, Last sequ
(Rel. 25, Last anno
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                                                                        STANDARD;
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115
207
209
339
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227
362 AA;
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Best Local Similarity
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| 103 RIALRY 108
                                                                                                                                                                                        HLA-B OR HLAB.
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01-APR-1993 (
01-APR-1993 (
                            1852_HUMAN
ID 1852_HUMAN
AC P30489;
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P30490;
                                                                                                                                                                         PRECURSOR
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DOMAIN

1853_HUMAN ID 1853_HC AC P30490; DT 01-APR-DT 01-APR-DT 01-APR-DT 01-APR-

Matches

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Gaps

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Length 362; Indels

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                                                                                                                                                                                                                                               ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
"Rapid cloning of HaA-A, B CDNA by using the polymerase chain
reaction: frequency and nature of errors produced in amplification.";
Proc. Natl. Acad. Sci. U.S.A. 87:2833-2837(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-57(B-17) B*5701 ALPHA CHAIN. EXTRACELLULAR ALPHA-1. EXTRACELLULAR ALPHA-2. EXTRACELLULAR ALPHA-3. CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 91067476.

MEDLINE; 91067476.

ISAMAT M., GIRDLESTONE J., MILSTEIN C.;

Nuclected sequence of an HLA-BW57 gene.";

Nuclected Acids Res. 18:6702-6702(1990).

-1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE INMUNE SYSTEM.

-1- SUBDMIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                 01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-57(B-17) B*5701 ALPHA
CHAIN PRECURSOR (BW57.1).
                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BY SIMILARITY.
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PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
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100.0%; Pred. No. 4;
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M32318; AAA36231.1; -. EMBL; X55711; CAA3924.1; -. PIR; S12622; S12622. PIR; D35997; D35997. HSSP; P30491; IAIM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS00290; IG_MHC; 1
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE; 90207291.
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                               HLA-B OR HLAB.
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MIM; 142830;
PROSITE; PS0
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P30497;
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TRANSMEM
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DISULFID
SEQUENCE
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1B61_HUMAN
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                                                                                                                                                                                                                                                                                                                                                  MEDILINE; SOLUTION.

MEDILINE; SOLUTION.

MEDILINE, JONES E. W., HARLOS K., MCMICHAEL A.J., STUART D.I.,

BELL J.I., JONES E. Y.,

"Bound water structure and polymorphic amino acids act together to
allow the binding of different peptides to MHC class I HLA-B53.";
                                                                                                                                                                                                                                                                                                                                                                                                                                Immunity 4:215-228(1996).
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-53 B*5301 ALPHA CHAIN
PRECURSOR.
                                                                                                                                                                                                                            "Allospecificities between HLA-Bw53 and HLA-B35 are generated by substitution of the residues associated with HLA-Bw4/Bw6 public
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                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 4;
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                                                                                                                                                                                         HAYASHI H., OOBA T., NAKAYAMA S., SEKIMATA M., KANO K.,
TAKIGUCHI M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BW-53 B*5301 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR ALPHA-3
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                                                                                                                                                                                                                                                                                                                         K-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 25-302.
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                                                                                                                                                                                                                                                                                    Immunogenetics 32:195-199(1990).
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PROSITE; PSO0290; IG_MHC; 1.
PFAM; PF00047; 19; 1.
PFAM; PF00129; MHC_I; 1.
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Best Local Similarity 100.
Matches 6; Conservative
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PDB; IA1M; 08-APR-98.
PDB; IA1O; 08-APR-98.
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227
362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MICROGLOBULIN).
                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                             MEDLINE; 96209672.
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                                                        HLA-B OR HLAB.
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1B60_HUMAN
ID 1B60_HUMAN
AC P18465;
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RANSMEM

MHC I;

DOMAIN DOMAIN DOMAIN CARBOHYD DISULFID DISULFID SEQUENCE

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Gaps

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EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                          INOUE T., OGAWA A.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIAH-HUMAN STANDARD; PRT; 362 AA.
P01893;
21-JUL-1986 (Rel. 01, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
15-DEC-1899 (Rel. 39, Last annotation update)
14LA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN H PRECURSOR
HIAA-AR) (HIA-12.4).
                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
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; 3E5E7534 CRC32;
                                                                                                                                                                                            HLA-Bw58.";
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EMBL; AB008102; BAA22916.1; --
PIR; A23895; HLHUB8.
HSSP; 930491; 1A1M.
MIM; 142830; --
PROSITE; PS00290; IG_MHC; 1.
PRAM; PF00147; 1g; 1.
PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
SIGNAL
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                                                                                                       SECUENCE FROM N.A.
MEDLINE: 86008247.
WAYS J.P., COPPIN H.L., PARHAM P.:
"The complete primary structure of HLJ
J. Blol. Chem. 260:11924-11933(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40337 MW;
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             Homo sapiens (Human).
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362 AA;
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01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
11-APR-1993 (Rel. 25, Last annotation update)
11-APR-1993 (Rel. 25, Last annotation update)
11-APR-1993 (Rel. 25, Last annotation)
11-APR-1993 (Rel. 25, Last sequence update)
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                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MADELINE, 39056508.
LITTLE A.-M., ZEMMOUR J., ENNIS P.D., WARD F.E., PETZL-ERLER M.L.,
LITTLE A.-M., D. TOIT E.D., PARHAM P.,
"Distinctive HLA-A,B antigens of black populations formed by
interallelic conversion.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Immunol. 149:3411-3415(1992).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
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01-MAR-1989 (Rel. 10, Last sequence update)
115-JUL-1998 (Rel. 36, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-58(B-17) B*5801 ALPHA
HLA-B OR HLAB.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PIR; S16774, S16774.
HSSP, P30491; 1A1M.
MIM; 142830. -.
PROSTER; PS00290; IG_MHC; 1.
PFAM; PF00047; 19; 1.
PFAM; PF00129; MHC_I; 1.
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362 AA;
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P10319;
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Search completed: February 8, 2000, 00:59:45 Job time: 3774 sec
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01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-A0501 ALPHA CHAIN PRECURSOR.
GOATILA GOATILA GOATILA (Lowland GOATILA).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Primates; Catarrhini; Hominidae; Gorilla.
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                               MALISSEN M., MALISSEN B., JORDAN B.R.; "Exon/intron organization and complete nucleotide sequence of an HLA
                                                                                                                                                                                                                                                                                                                           HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN H. EXTRACELLULAR ALPHA-1. EXTRACELLULAR ALPHA-2. EXTRACELLULAR ALPHA-3.
                                                                Proc. Natl. Acad. Sci. U.S.A. 79:893-897(1982).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS
-!- THE IMMUNE SYSTEM. COULD BE THE PRODUCT OF A PSEUDOGENE.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
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PIR; A02189; HLHU12.
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MIM; 142800; -.
PROSITE; PS00290; IG_MHC; 1.
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Best Local Similarity 100.
Matches 6; Conservative
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PFAM; PF00129; MHC_I; 1
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227
362 AA;
                                                                                                              MICROGLOBULIN).
         SEQUENCE FROM N.A.
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| 103 RIALRY 108
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P30378;
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1A04_GORGO
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-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-

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R PRAM, PRO0047; 1g; 1.
R PRAM, PRO0129; MHC_I; 1.
RW HC_I; Transmembrane; Glycoprotein; Signal.
RT SIGNAL 25 365 GLASS I HISTOCOMPATIBILITY ANTIGEN,
RT CHAIN 25 365 GOGO-A0501 ALPHA CHAIN.
RT CHAIN 25 114 EXTRACELLULAR ALPHA-1.
RT 200 EXTRACELLULAR ALPHA-2.
298 EXTRACELLULAR ALPHA-3.
298 EXTRACELLULAR ALPHA-3.
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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February 8, 2000, 13:17:28; Search time 209.03 Seconds (without alignments) 1.990 Million cell updates/sec US-08-653-294-4 29 1 RIALRY 6 Title: Perfect score: Sequence: Run on:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

225878 Total number of hits satisfying chosen parameters: 225878 seqs, 69334122 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 08 Listing first 45 summaries SPIREMBL_12 Database :

sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:* sp_vertebrate:*
sp_unclassified:* sp_organelle:*sp_phage:* sp_archea:*
sp_bacteria:* sp_rodent:* sp_plant:* sp_virus:* sp_mhc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Leng	DB	ID	Description	u c
	29	100.0		7	019569	O19569 homo	no sapien
	29	100.0		,	046697	_	gorilla gor
	53	100.0	133	7	019189	O19189 Nomo	no sapien
	29	100.0		7	078209	O78209 homo	no sapien
	59	100.0		7	019770	019770 hошо	_
	59	100.0		7	019774	019774 homo	
	59	100.0	172	7	019775	019775 homo	_
	58	100.0		7	019780	O19780 homo	
_	58	100.0	172	7	095364	Q95364 homo	
10	53	100.0		7	019771	019771 homo	
	58	100.0		1	019772	019772 homo	no sapien
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	29	100.0	175	7	Q2969 4	Q29694 homo	
	58	100.0		7	019607	O19607 homo	
	59	100.0		7	019608	O19608 homo	
မှ	29	100.0		^	019609	O19609 homo	
	29	100.0		7	019610	O19610 homo	
&	29	100.0	180	^	019611	O19611 homo	
	59	100.0	180	7	019612	019612 homo	
	59	100.0	180	7	019613	019613 hошо	

homo sapi homo sapi	1 homo 54 goril 55 homo
7 062917 7 062917 7 062917 7 062920 7 062922 7 062922 7 062922 7 019623 7 029766 7 029766 7 029976 7 029976 7 029976 7 029976	7 02984 7 01935 7 02976
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ALIGNMENTS

Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 100.0%; Score 29; DB 7; Length 89; larity 100.0%; Pred. No. 4.8; Conservative 0; Mismatches 0; Indels SEQUENCE FROM N.A. CAO K., BUNDETT L., ZHANG G., FERNANDEZ-VINA M.; Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases. EMBL, AF017320; AAB70286.2; -01-JAN-1998 (TrEMBLrel. 05, Created) 01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-MAY-1999 (TrEMBLrel. 10, Last annotation update) MHC CLASS I ANTIGEN (FRAGMENT). 1 1 89 89 89 AA, 10606 MW, 99D11089 CRC32; 89 AA. PRT; PRELIMINARY; Query Match Best Local Similarity Matches 6; Conserv NON_TER NON_TER SEQUENCE 019569 RESULT 019569

0; Gaps 01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1999 (TrEMBLrel. 10, Last annotation update)
MHC CLASS I ANTIGEN HIA-H ORTHOLOG (FRAGMENT).
GOILLA gorilla gorilla (Lowland gorilla).
Eukaryota; Metazoa; Chordata; Cranlata; Wammalia; 90 AA. PRT; PRELIMINARY; 1 RIALRY 6 |||||| 78 RIALRY 83 046697 RESULT 2 046697 g SS GENTHARD SS GENTHARD à

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us-08-653-294-4.rspt

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TONGIO M.M.;
"An intronic mutation responsible for a low level of expression of an HLA-874 allele.";
Tissue Antigens 50:340-346(1997).
EMBL: Z72423; CAA96533.1;
PFAM; PF000129; MHC_I; 1.
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CHANDANAYINGYONG D., SIRKONG M., LONGTA K., SRINAK D., RUNGROUNG E.,
BEJCHANDRAS., JUJI T., TOKUNAGA K.;
SUBMILTER (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U90421; AAB50144.1;
EMBL; U90420; AAB50144.1;
PEMBL; PF00129; MHC_I; 1.
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LAFORET M., FROELICH N., PARISSIADIS A., BAUSINGER H., PFEIFFER
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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138 138
138 AA; 15610 MW; B8417FAO CRC32;
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172 172
172 AA; 19909 MW;
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| 103 RIALRY 108
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72 RIALRY 77
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SIGNAL
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   RA RELEASE RELEASE SOLUTION SO
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1-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MHC CLASS I HISTOCOMPATIBILITY ANTIGEN-B (HLA-B-27RSH) (FRAGMENT).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Score 29; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                             GRIMSLEY C., MATHER K.A., OBER C.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: AF022172; AAC99794.1; -.
PFAM: PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases. EMBL; U18659; AAB60357.1; MIN; 142830;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAY-1999 (TrEMBLrel. 10, Last annotation update)
HUMAN LEUKOCYTE ANTIGEN PRECURSOR (FRAGMENT)
Eutheria; Primates; Catarrhini; Hominidae; Gorilla
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133 133
133 AA; 15491 MW; 3A3BC802 CRC32;
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90 90
90 AA; 10689 MW; SESF2495 CRC32;
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Matches 6; Conserv
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TISSUE-LEUKOCYTE;
PETERSDORF E.;
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MEDLINE; 98007772.
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| 79 RIALRY 84
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                                                                                        STRAIN-SHAMBA;
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172 AA;
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172 AA;
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CHANDANAYINGYONG D., SIRIKONG M., LONGTA K., SRINAK D., RUNGROUNG E.,
BUJGHANDRAS S.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U90425; AAB50146.1;
EMBL; U90424; AAB50146.1;
PFAM; PF00129; MHC_L; 1.
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CHANDARAYINGYONG D., SIRIKONG M., LONGTA K., SRINAK D., RUNGROUNG E.,
BEJCHANDRA S., JUJI T., TOKUNAGA K.;
SUDMITTED (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U90419; AABS0143.1;
EMBL; U90418; AABS0143.1; JOINED.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarhini; Hominidae; Homo.
                                                                                                                                                                                         100.0%; Score 29; DB 7; Length 172; 100.0%; Pred. No. 9.7; cive 0; Mismatches 0; Indels
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Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: 0190423; ABB50145.1; -.
EMBL: U90422; AAB50145.1; JOINED.
PFAM: PF00129; MHC_I; 1.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
MI-NOV-1998 (TrEMBLrel. 08, Last annotation update)
HLA-B.
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172 172
172 Aa; 19909 MW; CAAE5641 CRC32;
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6; Conservative
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72 RIALRY 77
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                         7; Length 172;
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                                                                                                                                                                              Indels
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CHANDRAYINGYONG D., SIRIKONG M., LONGTA K., SRINAK D.,
SIRIBOONRIT U., RUNGROUNG E., BEJCHANDRA S.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: 1906612, AAR50151.1; -.
EMBL: 1906611, AAR50151.1; JOINED.
PFAM; PF00129; MHC_I; 1.
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BLASCZYK R.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases:
EMBL, Y964/3; CAA65327.1; -.
PFAM; PF00129; MHC_I; 1.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I HLA-B (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                      Q95364 PRELIMINARY; PRT; 172 AA. Q95364, 01-FEB-1997 (TrEMBLrel. 02, Created) 01-FEB-1997 (TrEMBLrel. 02, Last sequence update) 01-NOV-1998 (TrEMBLrel. 08, Last annotation update) HLA-B*51 PROTEIN (FRAGMENT).
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20026 MW; 4D9A1043 CRC32;
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172 172
172 AA; 19909 MW; CAAE5641 CRC32;
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                                                                                                                      Query Match 100.0%; Score 29; DB 7
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 6; Conservative 0; Mismatches
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eutheria; Primates; Catarrhin1; Hominidae; Homo.
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PETERSDORF E.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
EMBL, 1028759, AAB60367.1; -.
HSSP; P10318; 1ROG.
PFAM; PF00129; MHC_1; 1.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MHC CLASS I HLA-B ANTIGEN (FRAGMENT).
HLA-B.
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019607;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MHC CLASS I HLA-A (FRAGMENT).
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100.0%; Pred. No. 9.7;
tive 0; Mismatches
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Matches 6; Conservative
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Best Local Similarity
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72 RIALRY 77
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                  Query Match 100.0%; Score 29; DB 7; Length 172; Best Local Similarity 100.0%; Pred. No. 9.7; Matches 6; Conservative 0; Mismatches 0; Indels
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CHANDANAYINGYONG D., SIRIKONG M., LONGTA K., SRINAK D.,
SIRIBOONRIT U., RUNGROUNG E., BEJCHANDRA S.;
SUBmitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U906114; AAB50244.1; JOINED.
EMBL; U90613; AAB50244.1; JOINED.
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CHANDANAINGYONG D., SIRIKONG M., LONGTA K., SRINAK D.,
SIRIBOONRII U., RUNGSOUNG E., BEJCHANDRA S.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL. 190615, AAB50245.1;
FRME, 190615, AAB5045.1;
PFAM; PF00129; MRC_I; 1.
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ID 019772
AC 019772
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DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE MHC CLASS I HLA-B (FRAGMENT).
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I HLA-B (FRAGMENT).
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172 AA; 20052 MW; F6214671 CRC32;
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EMBL; AF030921; AAB87057.1; -.
EMBL; AF030921; AAB87057.1; JOINED.
HSSP; P01891; 1TMC.
PFAM; PF00129; MHC_I; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                          Indels
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MHC CLASS I HLA-A (FPAGMENT).
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Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches
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Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                    unidentified.
unidentified
unclassified
(Abases 1 to 18)
Arguello, R., Avakian, H. and Madrigal, A.
METHOD FOR IDENTIFYING AN UNKNOWN ALLELE
PATENT: WO 9720197-78 3 05-JUN-1997;
ANTHONY NOLAN BONE MARROW TRUS (GB)
Other publication AU 7703796 19970619.
Location/Qualifiers
  270
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Hill, A. VivianSinton.
Process for amplifying nucleic acid
Patent: US 5824515-A 13 20-OCT-1998.
Location/Qualifiers
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Sequence 13 from patent US 5824515.
AR049398
AR049398.1 GI:6005437
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Sequence 3 from Patent W09720197.
A63076
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US-08-653-294-4 x AR049398
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US-08-653-294-4 x A63076
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                                                                                                                    seq_documentation_block:
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                                                                              seq_name: gb_pat:A63076
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Database: GenEmbl:*
Database sequences: 821193
Database length: -1518192014
Search time (sec): 11370.480000
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9b_par: 121932

9b_pr: HSHLABHBA

9b_pr: HSHLABHBA

9b_pr: HSHLABBI

9b_pr: HSHLABBI

9b_pr: HSHLABI

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gb_pat:A63076
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SOURCE

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seq_name: gb_pr1:HSHLABHBB
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 250)
Rojas Munoz, A., Mendez, I. and Yunis, I.
Molecular evolution of HIA-B locus in a small population amerindian.
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rojas-Munoz,A.
Direct Submission
Direct Submission
Direct Submission
Submitted (07-OCT-1996) A. Rojas-Munoz, National Institute Of
Health, Immunogenetics, Avenida El Dorado, Carrera 50, Santafe De
Bogota / Zona 6, COLOMBIA
Location/Qualifiers
                                                                                                                                           07-0CT-1996
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                                                                                                                                           PAT
                                                                                                                                                                                                                                                                  1 (bases 1 to 18)
Hill,A.V.S.
Process for amplifying HLA sequences
Patent: US 5525492-A 13 11.-UN-1996;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HLA-B gene; human leukocyte antigen

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      LOCUS
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      DNA

      DEFINITION
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      VERSION
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      GI:1602286

to: 18
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarphin; Hominidae; Homo.
1 (bases I to 250)
1 (bases I to 250)
1 (bases Wunoz, A., Mendez, I. and Yunis, I. Molecular evolution of HIA-B locus in a small population amerindian community: The Nukak-Maku
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Submitted (07-OCT-1996) A. Rojas-Munoz, National Institute Of
Health, Immunogenetics, Avenida El Dorado, Carrera 50, Santafe De
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-OCT-1996
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Location/Qualifiers
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DEFINITION H.sapiens HLA-B gene, exon 2, HB(b) allele.
ACCESSION Y08693
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HLA-B gene; human leukocyte antigen.
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2 (bases 1 to 250)
Rojas-Munoz, A.
                                                                                                                                                                                                                                                                                                                                                             Quality: 29.00
Ratio: 4.833
Percent Similarity: 100.000
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US-08-653-294-4 x HSHLABHBA
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Chandanayo, D., Sirikong, M., Longta, K., Srinak, D., Chandanayo, D., Sirikong, M., Longta, K., Srinak, D., Rungroung, E., Belchandra, S., Juji, T. and Tokunaga, K. Direct Submission Bubmitted (23-FEB-1997) Transfusion Medicine, Faculty of Medicine, Siriral Hospital, Mahidol University, Prannok Road, Bangkok 10700, Thailand
                                                                                                                 HSHLABB1 250 bp DNA PRI 22-MAR-1997 Human cell line THAI DCH010 MHC class I HLA-B gene (allele HLA-B-1513), exon 2. U90420 U90420 GI:1905830
                                                                                                                                                                                                                                                 Homo saplens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Euthoria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 250)
Chandanayingyong, D., Sirikong, M., Longta, K., Srinak, D.,
Rungroung, E., Bejchandra, S., Juji, T. and Tokunaga, K.
Bl5 alleles (B*1513)
Unphilished
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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Human cell line THAI DCH010 MHC class I HLA-B gene (allele
HLA-B+51V), exon 2.
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U90611.1 GI:1905865
                      221 CGGATCGCGCTCCGCTAC 238
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Ratio: 4.833
Percent Similarity: 100.000
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     1 ArgileAlaLeuArgTyr
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US-08-653-294-4 x HSHLABB1
                                                                 seq_name: gb_pr2:HSHLABB1
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                                                                                                  seq_documentation_block:
LOCUS HSHLABD1
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1 (bases 1 to 250)
Rojas-Munoz,A., Mendez,I. and Yunis,I.
Molecular evolution of HLA-B locus in a small population amerindian community: The Nukak-Maku
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Durect Submission
Submitted (07-ocT-1996) A. Rojas-Munoz, National Institute Of
Health, Immunogenetics, Avenida El Dorado, Carrera 50, Santafe De
Bogota / Zona 6, COLOMBIA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                     10-0CT-1996
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Gaps: 0
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HLA-B gene; human leukocyte antigen.
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/note="allel HB(d)"
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/gene="HLA-B"
<14. .>250
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Rojas-Munoz, A.
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     O
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                                                                                 Quality: 29.00
Ratio: 4.833
Percent Similarity: 100.000
 78
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US-08-653-294-4 x HSHLABHBB
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Percent Similarity: 100.000
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US-08-653-294-4 x HSHLABHBD
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22-MAR-1997

us-08-653-294-4.rge

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1. .250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chandanayingyong, D., Sirikong, M., Longta, K., Srinak, D.,
Chandanayingyong, D., Sirikong, M., Longta, K., Srinak, D.,
Siriboonrit, U., Rungroung, E. and Bejchandra, S.
Direct Submission
Submitted (25-FEB-1997) Transfusion Medicine, Faculty of Medicine,
Siriral Hospital, Mahidol University, Prannok Road, Bangkok 10700,
Thailand
                                                                        /map="6p21"
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1 (bases 1 to 250)
Chandanayingyong, D., Sirikong, M., Longta, K., Srinak, D., Siriboonrit, U., Rungroung, E. and Bejchandra, S.
Unpublished
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Human cell line THAI DCH011 MHC class I HLA-B gene (allele HALB*51V), exon 2.
U90615. GI:1906037
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Gaps: 0
Percent Identity: 100.000
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/db_xref="taxon:9606"
/chromosome="6"
 1. .250
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/chromosome="6"
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Ratio: 4.833
Percent Similarity: 100.000
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US-08-653-294-4 x HSHLABF1
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                                                                                                           Chandanayingyong, D., Sirikong, M., Longta, K., Srinak, D., Chandanayingyong, D., Sirikoonit, U., Rungroung, E. and Bejchandra, S. Direct Submission Submitted (25-FFB-1997) Transfusion Medicine, Faculty of Medicine, Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
                                                                                                                                                                                                                                                                                                                                                        /haplotype="(b)HLA-A2,B77,Cw8N,DR12(DR52),DQ7/(c)A11.1,
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Human cell line THAI DCH028 MHC class I HLA-B gene (allele
HLA-B+51V), exon 2.
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1 (bases 1 to 250)
Chandanayingyong, D., Sirikong, M., Longta, K., Srinak, D., Siribooniit, U., Rungroung, E. and Bejchandra, S.
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 250)
Chandanayingyong,D., Sirikong,M., Longta,R., Srinak,D.,
Siriboonrit,U., Rungroung,E. and Bejchandra,S.
B*51V alleles
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 6
Gaps: 0
Percent Identity: 100.000
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82 c 80 g 32 t
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Percent Similarity: 100.000
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US-08-653-294-4 x HSHLABD1
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Unpublished
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LOCUS HSHLABF1
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Ratio:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 250)

2 Chandanayingyong, D., Sirikong, M., Longta, K., Srinak, D., Rungroung, F. and Bejchandra, S.

Bl5 alleles (B*1513)

L Unpublished

2 (Dases 1 to 250)

3 Chandanayingyong, D., Sirikong, M., Longta, K., Srinak, D., Sinitaj Hospital, Mahidol University, Prannok Road, Bangkok 10700, Manistang, Hospital, Mahidol University, Prannok Road, Bangkok 10700,
                                                   HSHLABJI 250 bp DNA PRI 22-MAR-1997
Human cell line THAI DCH028 MHC class I HLA-B gene (allele
HIA-8*1513), exon 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS HSHLABI1 250 bp DNA PRI 22-MAR-1997
DEFINITION HUMAN cell line THAI DCH009 MHC class I HLA-B gene (allele
HLA-B*1513), exon 2.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutherla; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 250)
Chandanayingyong, D., Sirikong, M., Longta, K., Srinak, D.,
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Gaps: 0
Percent Identity: 100.000
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1. .250
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/note="Allele: HLA-B*1513"
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83 c 80 g 32 t
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1. 250
/ Organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="VI"
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                                                                                                                                                                                        U90424.1 GI:1905838
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U90418.1 GI:1905826
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Ratio: 4.833
Percent Similarity: 100.000
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US-08-653-294-4 x HSHLABJ1
seq_name: gb_pr2:HSHLABJ1
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1 (bases 1 to 260; Chandanayingyong, D., Sirikong, M., Longta, K., Srinak, D., Rungroung, E., Belchandra, S., Blasczyk, R. and Grosse-Wilde, H. Bublalleles (B*1513)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSHLABI1 250 bp DNA PRI 22-MAR-19
Human cell line THAI DCH011 MHC class I HLA-B gene (allele
HLA-B*1513), exon 2.
                                                                                    Length: 6
Gaps: 0
Percent Identity: 100.000
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Gaps: 0
Percent Identity: 100.000
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/product-"MHC class I HLA-B"
/product 80 g 32 t
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1. 250
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Ratio: 4.833
Percent Similarity: 100.000
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Ratio: 4.833
Percent Similarity: 100.000
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US-08-653-294-4 x HSHLABG1
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LOCUS
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BASE COUNT ORIGIN

VERSION KEYWORDS SEGMENT SOURCE ORGANISM

TITLE JOURNAL REFERENCE AUTHORS

REFERENCE AUTHORS TITLE JOURNAL

FEATURES

DEFINITION

ACCESSION

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20
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                                          2 (bases 1 to 250)
Chandanayingyong,D., Sirikong,M., Longta,K., Srinak,D.,
Rungroung,E., Bejchandra,S., Juji,T. and Tokunaga,K.
Direct Submission
Submitted (23-FEB-1997) Transfusion Medicine, Faculty of Medicine,
Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
Thailand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 255)
Grimsley,C., Mather,K.A. and Ober,C.
Direct Submission
Submitted (03-SEP-1997) Fred Hutchinson Cancer Research Center,
1100 Fairview Ave. N., M374, Seattle, WA 98109, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF022159 255 bp DNA PRI 05-JAN-1999
Homo sapiens isolate 026 MHC class I antigen HLA-H (HLA-H)
pseudogene, partial sequence.
AF022159.1 GI:2655062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Friencas; Catarrhini; Hominidae; Homo.

1 (bases 1 to 255)
Grimsley,C., Mather, K.A. and Ober,C.
HIA-H: a pseudogene with increased variation due to balancing selection at neighboring loci
MOI. Biol. Evol. 15 (12), 1581-1588 (1998)
Rungroung,E., Bejchandra,S., Juji,T. and Tokunaga,K.
B15 alleles (B*1513)
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps: 0
Percent Identity: 100.000
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/cell_line-"THAI DCH009"
1. 250
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/note-"Allele: HLA-B*1513"
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a 83 c 80 g 32 t
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="VI"
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1. .255
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Ratio: 4.833
Percent Similarity: 100.000
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US-08-653-294-4 x HSHLABT1
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LOCUS AF022159
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Chases 1 to 259)
Grimaley,C., Mather,K.A. and Ober,C.
Grimaley,C., Mather,K.A. and Ober,C.
Direct Submission
Submitted (03-SEP-1997) Fred Hutchinson Cancer Research Center,
1100 Fairview Ave. N., M374, Seattle, WA 98109, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homorosapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 259)
Grimaley,C., Mather,R.A. and Ober,C.
HIA-H: a pseudogene with increased variation due to balancing selection at neighboring loci
Mol. Biol. Evol. 15 (12), 1581-1588 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF022160 259 bp DNA PRI 05-JAN-1
Homo sapiens isolate 034 MHC class I antigen HLA-H (HLA-H)
pseudogene, partial sequence.
AF022160
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Gaps: 0
Percent Identity: 100.000
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/note="African-American individual"
                                                                <1. .>255
/gene="HLA-H"
/note="MHC class I antigen HLA-H"
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/isolate="034"
/db_xref="taxon:9606"
/chromosome="6"
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                                                                                                                                             /pseudo
<1. .>255
/gene="HLA-H"
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/gene="HLA-H"
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Ratio: 4.833
Percent Similarity: 100.000
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US-08-653-294-4 x AF022159
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LOCUS AF022160
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	37 t	
	85 g	
sendo	83 C	
sd/	52 a	
	BASE COUNT	ORIGIN

2 others alignment_scores:
 Quality: 29.00 Length: 6
 Ratio: 4.833 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block: US-08-653-294-4 x AF022160

Align seg 1/1 to: AF022160 from: 1 to: 259

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Staphylococcus aureus contig
Human pancreatic secretory t
Staphylococcus aureus contig
     Downstream sequence of micro
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WPDIS 22-183691/22.

R WPDIS 22-183691/22.

The Ramplification of nucleic acids using buffer soln, and chelating agent - for detecting Hiza class I alleles for determining susceptibility to arthritis etc.

Disclosure; Page 14; 52pp; English.

The sequence is that of a probe which hybridises to one of the bunce of strands) produced during PCR amplification of the Hiza class I alleles. It is specific for a sequence that encodes a Bw4 class I alleles. It is specific for a sequence that encodes a Bw4 class I alleles. It is specific for a sequence that encodes a Bw4 class is alleles. It is specific for a sequence that encodes a Bw4 class is alleles. It is specific for a sequence that encodes a Bw4 class is alleles. It is specific for a sequence that encodes a Bw4 class is alleles. It is specific for a sequence that encodes a Bw4 class is alleles. It is specific for a sequence that encodes a Bw4 class is a sequence that may be indicative of a patients succeptibility to inflammatory arthropathy such as arthritis and arthritis related discenses. Such diseases include reactive arthritis, rheumatoid arthritis, selective arthritis, earthritis, earthrit
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19-FBB-1998 (first entry)
Human leukocyte antigen class I gene URSTO probe 307-324.
Human leukocyte antigen, HLA; probe; tissue transplantation;
Human leukocyte antigen; HLA; probe; tissue transplantation;
MMC gene; major histocompatibility complex; paternity test;
forensic medicine; haematological malignancy; inherited disorder;
adoptive immunotherapy; identification; ss.
                                                                                                                                                                                                                                                    19-NoV-1992 (first entry)
Imman leukocyte antigen probe.
HLA; polymerase chain reaction; inflammatory arthropathy;
susceptibility; arthritis; arthritis related diseases; ss.
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Ratio: 4.833 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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05-NOV-1991; G01935.
05-NOV-1990; GB-024005.
(BRBL-) BRITISH BIO-TECHNOLOGY LTD.
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ID 024902 standard; DNA; 18 BP.
AC 024902;
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ID T94791 standard; DNA; 18 BP.
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                                                                                                                              seq_name: N_Geneseq_36:Q24902
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29-NOV-1996; G02959.
29-NOV-1995; GB-024381
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US-08-653-294-4 x Q24902
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  N_Geneseq_36:033975
N_Geneseq_36:V78694
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N_Geneseq_36:V78034
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Human leukocyte antigen class I
Human leukocyte antigen class I
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IEA-BW53 exon. HIA-BW53 gene,
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Candida neoformans IPC synthas
IN HIA-BW53 exon. HIA-BW53 gene,
Staphylococcus aureus contig S
Human gene signature HUMGSO8571
HIA-BW50 ecllulose Synthase RSW1-1
Staphylococcus aureus contig S
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Staphylococcus aureus contig S
Human secreted protein gene 45
Streptococcus pneumoniae coding
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H Pylori GHPO 1442 gene. New
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Streptococcus pneumoniae contig S
H Pylori GHPO 1442 gene. New
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H Rach organic anion transporter
L Lactis DB1341 pfi gene. Lact
Hepatitis E virus hollow parti
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                                                                                                 About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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Query: US-08-653-294-4
Query length: 6
Database: N_Geneseq_36:*
Database sequences: 311585
Database length: 125096042
Search time (sec): 590.520000
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                                                 Date: Feb 8, 2000 1:27
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N_Genesed_
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human disease
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                                                                    09-MAR-1993 (first entry)
HLA-Bw 52 exon 2 alpha-1 domain.
Human leukocyte antigen; transgenic; germ cells; somatic cells;
expression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 29.00 Length: 6
Ratio: 4.833 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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(NOLA-) NOLAN BONE MARROW IRUST ANTHONY
                        Arguello R, Avakian H, Madrigal A;
WPI; 97-310717/28.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CGGATCGCGCTCCGCTAC 18
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US-08-653-294-4 x T94791
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New DNA for class! I human leucocyte antigens and derived probes and transformed cells, useful for DNA typing, as immunogens etc. Claim 1; Page 11; 23pp; English.
The HLA class I DNA can be used a source of probes for use in DNA typing. Transformed cells, which are useful as immunogens, can be obtained by introducing these DNAs into eucaryotic cells. Sequence 1086 BP; 224 A; 334 C; 356 G; 172 T;
                                                                                                   37
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Ratio: 4.833 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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See also Q29166-72.
59 A; 88 C; 86
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                                                                                                                                                                                                                                                                to: 270
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Sequence encoding HLA-Bw52 antigen.
Probe; HLA class I DNA; immunogen; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-WAR-1991 (first entry)
Sequence encoding HLA-B51 antigen.
Probe; HLA class I DNA; immunogen; ss.
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1. .1086
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11-AUG-1988; JP-200758.
(OLXV) Olympus Optical Co., Ltd.
                                                                                                                                                                                                                                                              Align seg 1/1 to: Q29167 from: 1
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ID Q01834 standard; DNA; 1086 BP.
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ID 001822 standard; DNA; 1086 BP.
AC 001822;
                                                                                                                                                                                                                                                                                                                               234 CGGATCGCGCTCCGCTAC 251
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                                                                                                            Quality: 29.00
Ratio: 4.833
Percent Similarity: 100.000
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11-AUG-1988; JP-200758
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US-08-653-294-4 x Q29167
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US-08-653-294-4 x 001834
                      270 BP;
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WPI; 90-046289/07.
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EP354580-A.
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                                                                                      alignment_scores:
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                      Sequence
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EP-383183-A
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                                                                                                                                                                      Sequence
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Kano K, Takiguchi;
WPI; 90-046289/07.
WPI; 90-046289/07.
WPI; 90-046289/07.
New DNA for class 1 human leucocyte antigens and derived probes and transformed cells, useful for DNA typing, as immunogens etc.
Claim 2; ppl1-12; 23pp; English.
The HLA class I DNA can be used a source of probes for use in DNA typing. Transformed cells, which are useful as immunogens, can be obtained by introducing these DNAs into eucaryotic cells.
Sequence 1086 BP; 223 A; 335 C; 358 G; 170 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Allotype specific monoclonal anti- HLA antibodies prodn. - using hybridomas derived from transgenic animals carrying HLA gene and immunised with HLA antigen of different allotype Disclosure; Fig 1 A-G; 20pp; English.

The human HLA-B51 gene was injected into fertilised mouse eggs and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JAN-1991 (first entry)
HLA-B51 gene for production of monoclonal antibodies.
Alloptype specific monoclonal anti-HLA antibodies; hybridomas;
transgenic animals; HLA-B51 gene; ss.
                                                                                                                                                                                                                                                                                      Quality: 29.00 Length: 6
Ratio: 4.833 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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896. .1012
/*tag= e
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: Q01822 from: 1
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ID Q05693 standard; DNA; 1089 BP.
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/*tag= f
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1043. .1089
/*tag= g
/number=7
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Takiguchi M;
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/number=1
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/*tag= b
/number=2
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22-AUG-1990.
07-FEB-1990; 102424.
08-FEB-1989; JP-029313.
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US-08-653-294-4 x Q01822
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then these introduced into the uterus of a pseudo pregnant mouse. The young were tested to ensure incorporation of the gene into the chromosome, and one of them mated 3 times with a normal male to produce 16 young, seven of which carried the HLA-B51 gene. The transgeneic offspring were immunised with HLA antigen. The spleen lymphocytes were fused with myeloma cells. Hybridomas producing antibodies were selected.
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Allotype specific monoclonal anti- HLA antibodies prodn. - using hybridomas derived from transgenic animals carrying HLA gene and immunised with HLA antigen of different allotype Disclosure; Fig 1 A-G; 20pp; English.

The human HLA-Bw52 gene was introduced into mouse L cells and then these cells used to immunise one of the transgenic mice (See Q05693).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UCJOY, (Mar. 1991) (first entry)
03-JAN-1991 (first entry)
HLA-BW52 gene for production of monoclonal antibodies.
Alloptype specific monoclonal anti-HLA antibodies; hybridomas; transgenic animals; HLA-BW52 gene; ss.
Key
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                                                                                                                                                            173
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344. .619
/*tag= c
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196. .1012
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                                                                                                                                                              335
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                                                                                                                                                            224 A;
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/*tag= f
/number=6
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/*tag= g
/number=7
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07-FEB-1990; 102424.
08-FEB-1989; JP-029313.
(OLYU ) OLYMPUS OPTICAL KK.
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/number=1
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/number=5
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US-08-653-294-4 x Q05693
                                                                                                                                                            1089 BP;
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Quality:
Ratio:
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us-08-653-294-4.rng

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           21-0CT-1998.
14-APR-1998; 302866.
17-0CT-1997; US-062971.
15-APR-1997; US-043591.
22-APR-1997; US-044095.
                                                                                                                                                                                                                                                                                                                                                                         Ratio: 4.833
Percent Similarity: 100.000
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Helder SA, Radding JA;
WPI; 98-533879/46.
P-PSDB; W70520.
                                                                             13-MAY-1997; US-046348
21-JUL-1997; US-053320
                                                                                                      (ELIL ) LILLY & CO ELI
Heider SA, Radding JA;
WPI; 98-533879/46.
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15-APR-1997; US-043591
22-APR-1997; US-044095
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21-JUL-1997; US-053320
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 19-JAN'1999 (first entry)
Candida neoformans IPC synthase mRNA.
Candida: IPC synthase; fungus; inositolphosphoryl ceramide synthase; anti-fungal therapy; sphingolipid biosynthesis; phosphatidylinositol; ss.
The spleen lymphocytes were fused with myeloma cells (P3x63-Ag8.653). Hybridomas producing antibodies were selected. Sequence 1089 BP; 223 A; 336 C; 359 G; 171 T;
                                                                                                                                                                                                                                                                                                                                                Human leukocyte antigen; probe; major histocompatibility complex; MHC; class I; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIA-BW53 gene, DNA probe and transformant cells - used for immunisation, identifying specificity of antiserum etc. Claim 1: Page 1; 11pp; Japanese Claim 1: Page 1; 11pp; Japanese Probes comprising part of the sequence can be used to identify Class I genes. The DNA can be expressed for immunisation of animals and prodn. of monoclonal antibodies specific for the HIA-BW53 antigen. See also J03112485 and J03112486. Sequence 1089 BP; 222 A; 337 C; 356 G; 174 T;
                                                                           Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality: 29.00 Length: 6
Ratio: 4.833 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
                                                                                                                                                                        to: 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: 1089
                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. .1089
/*tag= a
                                                                                                                                                                        from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: Q12114 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
ID V33683 standard; mRNA; 3168 BP
                                                                                                                                                                                                                                                                               seq_documentation_block:
ID Q12114 standard; DNA; 1089 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-SEP-1989; JP-247697.
(OLYU ) OLYMPUS OPTICAL KK.
WPI; 91-182991/25.
                                                                                                                                                                                                                            307 CGGATCGCGCTCCGCTAC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       307 CGGATCGCGCTCCGCTAC 324
                                                                                                                                                                                                                                                                                                                    29-AUG-1991 (first entry)
                                                                                                                                                                                                  1 ArgileAlaLeuArgTyr 6
                                                                                                                                                                                                                                                      seg_name: N_Geneseg_36:012114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: N_Geneseq_36:V33683
                                                                                                        Percent Similarity: 100.000
                                                                              29.00
                                                                                            4.833
                                                                                                                                                                        Align seg 1/1 to: 005701
                                                                                                                                               US-08-653-294-4 x Q05701
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US-08-653-294-4 x Q12114
                                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAY-1991.
22-SEP-1989; 247697
                                                                              Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                     HLA-Bw53 exon.
                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                             J03112487-A
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                                                                                                                                   alignment_block:
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New inositolohosphoryl ceramide synthase genes from fungi - useful for identifying compounds for anti-fungal therapy claim 5; page 49-50; 35pp; English.

The present sequence represents the mRNA of a pure inositolphosphoryl ceramide (IPC) synthase protein from a fungal cell, Candida neoformans. The present invention also describes a method for identifying inhibitory compounds of fungal IPC synthase protein activity. IPC synthase proteins are useful for identifying inhibitors of fungal sphingolipid biosynthesis, as the IPC synthase catalyses a step in the synthesis of biosynthesis of IPC synthase proteins are also useful as probes or primers for identification and isolation of homologous genes or primers sequence 3168 BP; 692 A; 899 C; 812 G; 765 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JAW.1999 (first entry)
Candida neoformans IPC synthase encoding cDNA.
Candida; IPC synthase; fungus; inositolphosphoryl ceramide synthase; anti-fungal therapy; sphingolipid blosynthesis; phosphatidylinositol; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Inositolphosphoryl ceramide synthase genes from fungi - useful for identifying compounds for anti-fungal therapy claim 5; Page 46-49; SJRP; English.

The present sequence encodes a pure inositolphosphoryl ceramide (IPC) synthase protein from a fungal cell, Candida neoformans. The present invention also describes a method for identifying inhibitory compounds of fungal IPC synthase protein activity. IPC synthase proteins are useful for identifying inhibitors of fungal sphingolipid biosynthesis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 6
Gaps: 0
Percent Identity: 100.000
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ID V33682 standard; cDNA; 3168 BP.
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888888

Align seg 1/1

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PEROWILE TABES,
DR P-PSDB; R24033.
DR P-PSDB; R24033.
DR P-PSDB; R24033.
DR P-PSDB; R24033.
DR Soluble extracellular recombinant mannose receptor protein
Soluble extracellular recombinant mannose receptor protein adjances of infections, cancer, etc.
diagnosis of infections, cancer, etc.
Disclosure; page 21-27: 37pp; English.
The mannose receptor protein (MRP).
Disclosure; page 21-27: 37pp; English.
The mannose receptor protein (MRP) or at least one carbohydrate
Tecognition domain of it derived from an extracellular portion, can
specifically bind pro- or eukaryotic pathogens, eg bacteria, fungi
or viruses, with exposed configurations of mannose,
Or viruses, with exposed configurations on the envelope
glycoprotein. The protein lacks the MRP transmembrane and cytoplasmic
regions and is capable of specifically targeting cells expressing the
specified proteins. The MRPS can also target cancer cells which have
any exposed mannose residues resulting from aberrant glycosylation.
The proteins can be used as probes for such cells, or as fusion
molecules for delivery of specific molecules, eg AZT, ricin, pertussis
or cholera toxins, or CD4 to fix complement, or as an in vivo marker
for immune system cells. The hybrid molecules are esp. capable of
causing an effector molecule to be targeted to a cell, eg a virus.
MRP and antibodies raised to it are also useful as therapeutic or
diagnostic agents, eg for Leishmania proamastigotes, Pneumocystis
carinial, candida albicans, Microbacterium tuberculosis, HV or
influenza virus. The antibodies are also useful to purify the MRP.
The protein may be administered as a coating on a liposome, or as a
powder or lotion.

The protein may be administered as a coating on a liposome, or as a
powder or lotion.
                                                                                                                                                                                    DNA encoding soluble mannose receptor peptide.
Soluble mannose receptor peptide; ss DNA; receptor binding;
cancer cells; targeting; probe; drug delivery; cell marker;
fusion molecule; AZT: ricin; pertussis; cholera toxin; liposome;
therapeutic agent; diagnostic agent; opportunistic infections;
immunocompromised patients; HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 6
Gaps: 0
Percent Identity: 100.000
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59. .4429
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-NOV-1991; U08320.
06-NOV-1990; US-609915.
(CHIL-) CHILDRENS MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1598 A;
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ID V74377 standard; DNA; 5838 BP.
                                                                                 seq_documentation_block:
ID Q24977 standard; DNA; 5140
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Ratio: 4.833
Percent Similarity: 100.000
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US-08-653-294-4 x Q24977/rev
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                              seq_name: N_Geneseq_36:Q24977
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                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                              18-NOV-1992
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                                                                                                             19-JAN-1999 (first entry)
Candida neoformans IPC synthase DNA.
Candida; IPC synthase; fungus; inositolphosphoryl ceramide synthase; anti-fungal therapy; sphingolipid biosynthesis; phosphatidylinositol; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New inositolphosphoryl ceramide synthase genes from fungi - useful for identifying compounds for anti-fungal therapy Claim 5: Page 44-45: 53pp. English.

The present sequence encodes a pure inositolphosphoryl ceramide (IPC) synthase protein from a fungal cell, candida neoformans. The present invention also describes a method for identifying inhibitory compounds of fungal IPC synthase protein activity. IPC synthase proteins are useful for identifying inhibitors of fungal sphingoliphol blosynthesis, as the IPC synthase catalyses a step in the synthesis of inositolphosphoryl ceramide from ceramide and phosphatidylinositol. Fragments of IPC synthase proteins are also useful as probes or primers for identification and isolation of homeous genes.

Sequence 3220 BP; 706 A; 910 C; 819 G; 785 T;
as the IPC synthase catalyses a step in the synthesis of inositolphosphoryl ceramide from ceramide and phosphatidylinositol. Fragments of IPC synthase proteins are also useful as probes or primers for identification and isolation of homologous genes. Sequence 3168 BP; 692 A; 899 C; 765 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps: 0
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                            Quality: 29.00 Length: 6
Ratio: 4.833 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                 from: 1
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ID V33681 standard; DNA; 3220 BP.
AC V33681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2608 AGAATAGCICTIAGATAT 2625
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/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ArgileAlaLeuArgTyr 6
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Percent Similarity: 100.000
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22-APR-1997; US-044095.
13-MAY-1997; US-046348.
21-JUL-1997; US-053320.
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Heider SA, Radding JA;
WPI; 98-533879/46.
                                                                                                                                                                                                                                                                                                                                                                                                 to: V33682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-OCT-1997; US-062971
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US-08-653-294-4 x V33682
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US-08-653-294-4 x V33681
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14-APR-1998; 302866.
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                                                                                                                                                                                       alignment_scores:
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Key intron

1373 T;

1175 G;

to: 5140

Staphylococcus aureus contig SEQ ID #66.

16-MAR-1999 (first entry)

SEE

us-08-653-294-4.rng

Human amine receptor cDNA.
Amine receptor 7-transmembrane receptor; neurotransmitter; signal transduction; gene therapy; diagnosis; ss.
Homo sapiens.

BP

seq_documentation_block:
ID T51051 standard; cDNA; 1380
AC T51051;

(first entry)

05-APR-1997

1333 CGCATTGCTTTGCGATAT 1316

seq_name: N_Geneseq_36:T51051

1 ArgileAlaLeuArgTyr 6

Location/Qualifiers 252. .1265

/*tag= a

primer_bind primer_bind

complement (252..269)
/*tag= b
/note= "5' primer binding site"
1245..1265
/*tag= c
/note= "3' primer binding site"

WO9639440-A1

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This sequence represents one of 5191 Staphylococcus aureus DNA sequences of this sequence represents one of 5191 Staphylococcus aureus DNA sequences of this sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable of the invention. The DNA sequences are recorded on a computer readable commonly read-only memory (ROM) or CD-ROM. Homology searches using the Saureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can composition against Saureus infection. The polypeptides can also be used in a kit for the immunodetection of sample. Saureus is implicated in numerous human diseases, including cellulitis, eyelid infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences contained on the contained contained on the contained cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence".
5838
                                                                                                                                                                                                                                                                                                                                                                             "these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
                                                                                                                                                                                                                                             the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
                                                                                                                                Location/Qualiflers
421. 480
/*tag- a
/*note- "these bases represent a line of missing text in
Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JAN-1996; US-009861.
(HUMA-) HUMAN GENOME SCI INC.
Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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/note=
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                                                                                                               Staphylococcus aureus.
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The encoding human amine receptor - used to identify agonists and antagonists, or amine neurotransmitters

Claim 1: Fig 1A-1C; 68pp; English.

Claim 1: Fig 1A-1C; 68pp; English.

C ADNA clone (151051) codes for a human 7-transmembrane receptor of w09110) putatively identified as an amine receptor on the basis of sequence homology to the rat amine receptor. It was disovered in a human genomic library and can be found in human monocytes.

C is a produced the CDNA allows recombinant produ. of human amine receptor in transformed host (e.g. E. coll, COS, insect) host calls. Polynuclectides can be used as probes to detect mutations in the amine receptor gene, and in the gene therapy of conditions associated with under-expression of the receptor.

C sequence 1380 BP; 288 A; 371 C; 324 G; 397 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-0cT-1996 (first entry)

Human gene signature HDMSSO8571.

Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-blased library; diagnosis; detection; cell typing; abnormal cell function; sell typing; bornmal cell function; sell typing; bornmal cell function; sell typing; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 6
Gaps: 0
Percent Identity: 83.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
ID T26331 standard; cDNA to mRNA; 382 BP.
AC T26331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from: 1
                                                                                                                                                                                                                                                                                            12-DEC-1995.
06-JUN-1995; U07221.
06-JUN-1995; WO-U07221.
(HUMA-) HUMAN GENOME SCI INC.
Li Y. Ruben SN;
WPI: 97-043075/04.
P-PSDB; W09110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               696 AGGGTGGCTCTCAGGTAC 713
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4.667
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Ratio:
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WO9514772-A1.
01-JUN-1995.
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Gaps: 6 Gaps: 0 Percent Identity: 100.000

Quality: 29.00 Ratio: 4.833 Percent Similarity: 100.000

alignment_scores:

alignment_block: US-08-653-294-4 x V74377/rev

Align seg 1/1 to reverse of: V74377 from: 1 to: 5838

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Claim 1: Page 2058-2059; 2245pp; Japanese.
A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 783 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared if com various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(7) as the sole primer. Since the 3'-end of mRNA by using poly(7) as the sole primer. Since the 3'-end of mRNA by using poly(7) as the sole primer species, almost in translated sequence is unique to a particular mRNA species, almost is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be cetermined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.

Sequence 382 BP; 118 A; 72 C; 85 G; 102 T;
11-NOV-1994; JO1916.
12-NOV-1993; JP-355504.
(MATSC) MATSUBARA K.
(OKUBA) OKUBO K.
Matsubara K, Okubo K;
WPI; 95-206311/27.
Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                              tissues
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alignment_scores:

Quality: 27.00 Length: 6
Ratio: 4.500 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 83.333

alignment_block: US-08-653-294-4 x T26331

Align seg 1/1 to: T26331 from: 1

to: 382

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AQ330948 nbxb0048020r CUGI R
AI828628 wcl0f08.xl NCI_CGAP
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/lab_host="E. col1 DH5a"
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LOCUS H14029 133 bp DNA EST 03-JUL-1995
DEFINITION EST00056 Chromosome 19p12-p13.1 exon Homo sapiens genomic clone
C5-2 5', mRNA sequence.
ACCESSION H14029
VERSION H14029.1 GI:888038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block: 232 bp mRNA EST 30-JUL-1996 LOCUS C03945 LAMAN heart cDNA (YNAKAMURA) Homo sapiens cDNA clone 3NHC2454, mRNA sequence. ACCESSION C03945 GI:1467196
                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 133)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chromosome 19p12-p13.1 exons
Unpublished (1995)
On Sep 21, 1992 this sequence version replaced gi:279277
Contact: Li OY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: pdzgylepdnl.gene.nottingham.ac.uk
Insert Length: 972 Std Error: 0.00
Seg primer: 502 : 57 ArC TCA GTG GTA TTT GTC AGC 3'
High quality sequence stop: 331.
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Gaps: 0
Percent Identity: 100.000
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122.23
122.05
122.03
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Queen's Medical Centre
Nottingham, NG7 2UH, UK
Tel: 1159249924
Fax: 1159709906
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US-08-653-294-4 x H14029/rev
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                                                                                                seq_name: gb_est3:H14029
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gb_gss11:AQ330948
gb_est35:AI828628
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VERSION
KEYWORDS
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AUTHORS
TITLE
JOURNAL
COMMENT
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Documentation ...
H14029 ESST00056 Chromosome 19p1
C03455 C03945 Human heart cDNA
AL080978 Arabidopsis thaliana g
AAJ51891 z001066.r1 Stratagene
B95928 T1812TF TAMU Arabidopsis
AA263158 PMY0534 KG1-a Lambda
AA263158 PMY0534 KG1-a Lambda
AA2648158 PMY0534 KG1-a Lambda
AA264844 crs1519 lambdaZAPST Rici
D68742 CELK05582F Yuji Kohara u
A1440253 tj01004 xxl NOT_CGAP_Ga
D81221 HUMHBC4626 Human pancrea
AA314058 vt39909.r1 Barstead mc
AA345988 bs19b12.y1 brcsophila
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AA043388 zk53912.r1 Scares mous
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AA043388 zk53912.r1 Scares preg
AA043377 nbxb0006L05r CUGI Rice
AA359907 AV395907 Chlamydomona
AA379094 LD22689.5prime LD Dros
AL087192 Arabidopsis thaliana g
H05321 y180h03.s1 Scares infant
AA62092 HS_5189 B2_A01_T7A RPC
AQ650957 HS_2204_A1_G03_MR CIT
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H05555 y175c04.r1 Soares infant
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-MODEL-frame+_p2n.model -DEV-x1p

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Database: EST:*
Database sequences: 4538634
Database length: 1887831982
Search time (sec): 8553.360000
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                                                 Date: Feb 8, 2000 4:02 AM
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gb_est12:AV298815
gb_est2:AA298815
gb_est5:D68742
gb_est5:D68742
gb_est6:D8221
gb_est6:D82221
gb_est6:AA31131
gb_est13:AA311811
gb_est2:AA312811
gb_est24:AA12811
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gb_est21:AA942135
gb_est31:AI696864
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gb_est10:AA151891
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gb_est20:AA817414
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gb_est21:AA950260
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gb_est8:AA043388
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gb_est3:H05555
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gb_est3:H14029
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us-08-653-294-4.rst

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63 a
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   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 232)
Tanaka, T., Ogiwara, A., Uchiyama, I., Takagi, T., Yazaki, Y. and Nakamura, Y.
Construction of a normalized directionally cloned cDNA library from adult heart and analysis of 3040 clones by partial sequencing Genomics 35 (1), 231-235 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thalland genome survey sequence SP6 end of BAC F2B11 of IGF library from strain Columbia of Arabidopsis thallana, genomic survey sequence.

AL080978.1 GI:5282118
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Submitted (25-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Location/Qualifiers
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Salamoubat, M., Choisne, N., Artiguenave, F., Brottier, P., Wincker, P., Samson, D., Saurin, W., Weissenbach, J. and Quetier, F.
                                                                                                                                                                                                                                                                                                                                                                                       thale cress.
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Uridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JUN-1999
                                                                                                                                                                                                     On Oct 24, 1995 this sequence version replaced gi:1040105.
Contact: Yusuke Nakamura
Institute of Medical Science
University of Tokyo
4-6-1, Shirokanedai, Minato-ku, Tokyo 108, Japan
Tel: 81-3-5449-5572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality: 29.00 Length: 6
Ratio: 4.833 Gaps: 0
Percent Similarity: 100.000 Percent Identity: '100.000
                                                                                                                                                                                                                                                                                                                                       Email: yusuke@ims.u-tokyo.ac.jp.
Location/Qualifiers
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US-08-653-294-4 x C03945
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SOURCE
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Homo sapiens
Butaryota Metzoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 255)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le-M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Trevaskis, E., Underwood, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Febr. 314 286 1810
Fax: 316 2810
Fax: 316
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/clone_lib="Stratagene colon (#937204)"
/lab_host="Solx cells (Kanamycin resistant)"
/note="Organ: colon; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
LOCUS
AA151891
LOCUS
DEFINITION zoolf06.r1 Stratagene colon (#937204) Homo sapiens CDNA clone
IMAGE:566435 5' shimlar to 9D:M15497_cds1 HLA CLASS I
HISTOCOMPATIBILITY ANTIGEN, A-24(A-9) A*2401 (HUMAN);, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 6
Gaps: 0
Percent Identity: 100.000
1. .249
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon" 3702"
/clone_lib="IGF"
/clone="F2B11"
/note="end : SP6"
3 a 55 c 47 g 84 t
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/db_xref="GDB:4590888"
/db_xref="taxon:9606"
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AA151891.1 GI:1720754
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Percent Similarity: 100.000
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thale cress.
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis.

(bases 1 to 256)

Rounsley,S.D., Field,C.E., Bass,S., Linher,R., Linher,R.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Adams,M.D. and
Venter,J.C.

Arabidopsis Genomic Sequencing. Update 3

Unpublished (1997)

Other GSSS: T1812TR
B95928 31-MAR-1998 11812TF TAMU Arabidopsis thaliana genomic clone T1812, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: BeloBACII; Site_1: HindIII; Site_2: HindIII; Produced by Rod Wing"

60 c 67 q 61 t
                                                                    9 others
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: rounsley@tigr.org
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                                                                                                                                                     Gaps: 6 Gaps: 0 Percent Identity: 100.000
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Seq primer: Mi3-21
Class: BAC ends
High quality sequence stop: 256.
Location/Qualifiers
1. 256
/organism="Arabidopsis thaliana"
/strain="Columbia"
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/clone_lib="TAMU"
/sex="hermaphrodite"
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Percent Similarity: 100.000
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Percent Similarity: 100.000
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US-08-653-294-4 x AA151891
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// Caracterian for the sapiens for the sapient                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
LOCUS AA263158 283 bp mRNA EST 02-JUL-1998
DEFINITION PMY0534 KG1-a Lambda Zap Express CDNA library Homo sapiens CDNA 5',
MCCESSION AA263158
VERSION AA263158 GI:1898964
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I (bases 1 to 283)

Claudio,J.O., Liew,C.C., Dempsey,A.A., Cukerman,E., Stewart,A.K., Na,E., Atkins,H.I., Iscove,N.N. and Hawley,R.G.

Identification of sequence-tagged transcripts differentially expressed within the human hematopoietic hierarchy Genomics 50 (1), 44-52 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: r.hawley@utoronto.ca
Similar to M58636 MHC class I HLA-Bw gene. Clone was randomly
picked from KGla primary library.
Seq primer: 5' GAATTAACCTCACTAAAGGG 3'
High quality sequence stop: 283.
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Conclact: Hawley RG
Concology Research Laboratories
The Toronto Hospital
TCS-424, 67 College St., Toronto, Ontario MSG 2M1, Canada
Tel: 416 3403834
Fax: 416 3403453
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Gaps: 0
Percent Identity: 100.000
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                                                                                                                  to reverse of: B95928
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                                                                                                                                                                                                                                        132 CGGATCGCGCTCCGCTAC 149
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alignment_block:
US-08-653-294-4 x B95928/rev
                                                                                                                                                                                             1 ArgileAlaLeuArgTyr 6
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Percent Similarity: 100.000
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US-08-653-294-4 x AA263158
                                                                                                                                                                                                                                                                                                                                               seg_name: gb_est11:AA263158
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COMMENT
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KEYWORDS
SOURCE
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ACCESSION VERSION KEYWORDS REFERENCE AUTHORS

COMMENT

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Rot = 100.0 Second strand cDNA was prepared with the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ArgileAlaLeuArgTyr 6
                                                                                                                                                                                                                                                                                                                              Quality: 29.00
Ratio: 4.833
Percent Similarity: 100.000
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US-08-653-294-4 x AV298815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: gb_est1:T24384
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Ratio:
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                                                                                                                                                                                BASE COUNT
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TITLE
JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                             Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirzane, T., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, Kai, T., Itoh, M., Kojima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ozawa, T., Shigemoto, Y., Shizaki, T., Sogabe, Y., Sugahara, Y., Shigemoto, Y., Shizaki, F., Tateno, M., Tominaga, N., Tsunda, Y., Shigemoto, Y., Watanabe, S., Yamamura, T., Yasunishi, A., Yoshiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Kiken Mouse ESTS (Konno, H., et al.)

In published (1999)

On Mar 16, 1998 this sequence version replaced gi:2961667.

Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center, Genome Science Laboratory

The Institute of Physical and Chemical Research (RIKEN), Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. CDNA went through one round of subtraction to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh.M., Kitsunai, T., Akiyama, J., Shibata, K., Izawai, J., Karainci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. Carninci, P. 3000 (1999) Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anote—"Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Science Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was GAGAGAGAGAGCTCTTTTTTTTTTTTTTYN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: genome-resertc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp/
Sassati,n., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
Hayashizaki,Y.
                                                                                        AV298815 283 bp mRNA EST 10-NOV-1999 AV298815 RIKEN full-length enriched, 8 days embryo Mus musculus cDNA clone 5730461G21 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="5730461G21"
/clone_lib="RIKEN full-length enriched, 8 days embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 283)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
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/lab_host="DH10B"
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                          AV298815.1 GI:6331232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  further details.
seg_name: gb_est42:AV298815
                                                                                                                                                                                                                                                                         house mouse.
Mus musculus
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                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                      SOURCE
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JOURNAL
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FEATURES

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Ricinus communis
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids I; Malpighiales; Euphorbiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                          crs1519 lambda2APST Ricinus communis cDNA clone pcrs1519, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  To (bases 1 to 351)

VandeLoo.F.J. Turner.S. and Somerville.C.

Expressed sequence tags from developing castor seeds

Plant Physiol. 108, 1141-1150 (1995)

Contact: Somerville CR

Carnegie Institution

Carnegie Institution, 290 Panama St, Stanford, CA 94305
                                                                                                                                                         Length: 6
Gaps: 0
Percent Identity: 100.000
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Gaps:
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/clone="pcrs1519"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 4153251521
Email: crs@andrew.stanford.edu
Seq primer: T3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="Baker 296"
                                                                                                                                                                                                                                                                  to: AV298815 from: 1
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CHAIN 4; mRNA sequence.
AI440253
AI440253.1 GI:4281347
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Percent Similarity: 100.000
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Ratio:
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                                                                human.
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              ACCESSION
VERSION
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KEYWORDS
SOURCE
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                                                                                                                                                                                                    COMMENT
                                                                                                                                                                                                Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota, Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis:
1 (bases 1 to 360)
                                                                                                                                                                                                                                                                                                                                                                                     Kohara, Y., Mitsuki, H., Nishigaki, A., Motohashi, T., Sugimoto, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Toward an expression map of the C.elegans genome Unpublished (1994)
On Apr 14, 1993 this sequence version replaced g1:785653. Contact: Yuji Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1...360
/organism="Caenorhabditis elegans"
/strain="EB1489 him=8(e1489)"
/db_xref="taxon:6239"
/clone="yx55b2"
/clone="yx55b2"
/sex="hermaphrodite, male"
/tissue_type="whole animal"
/dev_stage="varied"
3 a 102 83 g 76 t 1 others
 Percent Identity: 100.000
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National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: ykchara@lab.nig.ac.jp
Insert Length: 910 Std Error: 0.00
High quality sequence stop: 326.
Location/Qualifiers
                                                                             from: 1
                                                                           to reverse of: T24384
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                            alignment_block:
US-08-653-294-4 x T24384/rev
                                                                                                          1 ArglleAlaLeuArgTyr 6
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Percent Similarity: 100.000
Percent Similarity: 100.000
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US-08-653-294-4 x D68742
                                                                                                                                                                     seq_name: gb_est5:D68742
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JOURNAL
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ORIGIN
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SOURCE
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Tumor Gene Index
Unpublished (1997)
On Jun 5, 1998 this sequence version replaced gi:3189628.
On Jun 5, 1998 this sequence version replaced gi:3189628.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@inh.gov
Email: Robert_Strausberg@inh.gov
Emmert_Buck, M.D., Ph.D., Michael R.
Emmert_Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /d_xref="taxon:9606"
/clone_lib="kaxon:9606"
/clone_lib="NCI_CGAP_Gas4"
/tissue_type="poorly differentiated adenocarcinoma with
signet ring cell features"
/lab_host="atomach; Vector: pcMV-SPORT6; Site_l: Sall;
/note="Organ: stomach; Vector: pcMV-SPORT6; Site_l: Sall;
/ste_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
/Average insert size l.69 kb. Life Technologies catalog #:
11549-011"
Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria: Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 373)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D82221 375 bp mRNA EST 09-FEB-1996 HUMHBC4626 Human pancreatic islet Homo sapiens cDNA similar to HIA-B, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ww-bio.llnl.gov/bbrp/image/image.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Std Error: 0.00
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/organism-"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert Length: 1410 Std Error:
Seg primer: -400P from Gibco
High quality sequence stop: 97.
Location/Qualifiers
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D82221.1 GI:1183739
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US-08-653-294-4 x AI440253/rev
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SM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Meptera; Endopteryota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophila.

1 (bases 1 to 403)
S. Andrews, J., Boulfard, G. and Oliver, B.
Drosophila melanogaster testis expressed sequence tags
Unpublished (1999)
Contact: Brian Oliver
Contact: Brian Oliver
Laboratory of Cellular and Developmental Biology
NIDDK, National Institutes of Health
6 Center Drive MSC 2715, Bldg 6, Rm Bl-13, Bethesda, MD 20892 USA
Fax: (301) 496 5239
Email: Oliver Behalish of Contact Drive MSC 2715, Bldg 6, Rm Bl-13, Bethesda, MD 20892 USA
Fax: (301) 496 5239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.niddk.nih.gov/intram/people/boliver.htm
Tissue isolation and library construction performed at the National
Institute of Diabetes and Digestive and Kidney Diseases, NIH (see
http://www.niddk.nih.gov/intram/people/boliver.htm). DNA sequencing
and analyses performed by National Institutes of Health Intramural
Sequencing Center (NISC; see http://www.nisc.nih.gov). Chromatogram
data were analyzed and evaluated for high quality using the ted
program (Gleeson T and Hillier L, 1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
LOCUS A1945988 403 bp mRNA EST 17-AUG-1999
DEFINITION bs19b12.yl Drosophila melanogaster adult testis library Drosophila melanogater cDNA clone bs19b12 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 6
Gaps: 0
Percent Identity: 100.000
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1. .403
/organism="Drosophila melanogaster"
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Seq primer: M13RP1 reverse primer (ABI)
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    Location/Qualifiers
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                                                                        /strain-"FVB/N"
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US-08-653-294-4 x AA710058/rev
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Percent Similarity: 100.000
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KEYWORDS
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TITLE
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/dclone_lib="Human pancreatic islet"
/note="vector: Lambda ZAPII; Site_1: Eco RI; Site_2: Xho
I; mRNA was prepared from normal adult human islets. cDNA
was directionally synthesized from the Xho I in the vector
to the EcoRI site. cDNA was size fractionated to remove
sequences clong bp in size.
3 others
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
I (bases 1 to 390)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Materston,R.
The WashU-HMIM Mouse EST Project
                                Human pancreatic islet ESTs
Unpublished (1995)
On Apr 14, 1993 this sequence version replaced g1:785255.
Contact: Jun Takeda
Institute for Molecular and Cellular Regulation, Gunma University
3-39-15 Showa-machi, Maebashi Gunma 371, Japan
Tel: 272-20-8856
Fax: 272-20-8896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA710058 390 bp mRNA EST 24-DEC-1997 vt39g09.rl Barstead mouse proximal colon MPLRB6 Mus musculus cDNA calone IMAGE:1165504 5', mRNA sequence. AA710058 GI:2719976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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On Sep 12, 1996 this sequence version replaced gi:1291974.
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                       Email: jtakeda@sb.gunma-u.ac.jp.
Location/Qualifiers
1. .375
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1 (bases 1 to 375)
Takeda, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 29.00
Ratio: 4.833
Percent Similarity: 100.000
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US-08-653-294-4 x D82221
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AUTHORS
TITLE
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KEYWORDS
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source
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KEYWORDS
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                                                             /strain-"y[*] w[67c1]/Y"
/db_xref="taxon:7227"
/clone-"bs19l2"
/clone_lib-"Drosophila melanogaster adult testis library"
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LOCUS AA817413 415 bp mRNA EST 25-NOV-1998

DEFINITION LD22684.5prime LD Drosophila melanogaster embryo por2 Drosophila

Relanogaster cDNA clone LD22688 5prime, mRNA sequence.

ACCESSION AA817413

VERSION AA817413.
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Drosophila melanogaster

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Meoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 226 row: H column: 4
High quality sequence stop: 402.
Location/Qualifiers
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/db_xref="taxon:7227"
/db_clone="LD22688"
/clone=Lib=LD Drosophila melanogaster embryo pOT2"
/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Harvey, D., Hong, L., Evans-Holm, M., Pendleton, J., Su, C., Brokstein, P., Lewis, S. and Rubin, G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (1997)
On Jan 19, 1998 this sequence version replaced g1:2045600.
Contact: Harvey, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G. M. Rubin-Molecular and Cell Biology
University of California Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to: 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 AGGATCGCACTCAGGTAC 86
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Percent Similarity: 100.000
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US-08-653-294-4 x AI945988
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KEYWORDS
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Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butherla; Rodentla; Sciurognath1; Muridae; Murinae; Mus.
1 (bases 1 to 430)
Marra,M., Hilliar,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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/note="Organ: embryo; Vector: pOT2; Site_1: EcoRI; Site_2:
Xhoi: Sized fractionated cDNAs were directly ligated into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
LOCUS AA067065 430 bp mRNA EST 04-FEB-1997
DEFINITION mm31d10.rl Stratagene mouse skin (#937313) Mus musculus cDNA clone image:523123 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortlum (info@lmage.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Sep 12, 1996 this sequence version replaced g1:1393887.
Contact: Maria M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_l1b="Stratagene mouse skin (#937313)"
/sex="females"
                                                                                                                                                                                                                                                                                                                                                                                         to: 415
                                                                                                                                                                                                                   Length: 6
Gaps: 0
Percent Identity: 100.000
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/db_xref="taxon:10090"
/clone="IMAGE:523123"
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GenCore	(c) 1993
	Copyright

OM protein - protein search, using sw model

February 8, 2000, 01:29:35; Search time 122.56 Seconds (without alignments) 1.160 Million cell updates/sec Run on:

US-08-653-294-5 29

1 RILLRY 6 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

188963 seqs, 23686106 residues Searched:

188963 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

A_Geneseq_36:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Immunomodulatory p	Peptide #3 used in	HLA-B2702 CTL modu	Immunomodulatory p	Immunomodulatory p	Peptide B2702.75-8	Cytomodulating lip	Actinomadura hibis	Murine monoclonal	Human Vpre-B prote	V preB-1 protein.	V preB-2 protein.	xMEF2. New nucleic	dul	#1 used		ij	HLA-B2702 CTL modu		HLA-B2702 CTL modu	1x of	2-84 (L	32705.75-84	HLA-B2702.75-84(D)	_	_	-cell	T-cell modulating	Immunomodulatory p	Immunomodulatory p	Peptide B2702.75-8	Peptide B2705.75-8	Peptide B2702.75-8	8
SUMMARIES	ID	72	W33782	R83096	W47267	W47271	W33789	W82826	W54388	R93159	P80289	P80288	P83001	R50040	W47261	W33780	R41208	R41212	R83062	R83075	R83094	R95413	R95427	R95423	R95425	W07524	W07512	W07513	W07514	W47265	W47269	W33784	W33785	W33787	R95429
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W33782 standard; peptide; 6 AA.
W33782;
19-JUN-1998 (first entry)
Peptide #3 used in immunomodulating dimer peptide.
Immunomodulating dimer; immunosuppressant drug; CTL activation; transplantation; autoimmune disease; Class I HLA-B alpha-1 domain; rejection.
Synthetic.
Flomo sapiens.
W09744351-A1.

RESULT
W33782
ID W3782
AC W3782
DD L19
DE Pe
KW LI
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KW LI
COS S;

Peptide B2702.84-7 Immunomodulating d Glucose transport HLA-B2702 CTL modu Peptide B2702.70-8 Human HLA-B27-(62- Human [Phc 1] and HL Human [Phc 1] and HL Human MHC 1 alpha Human MHC 1 alpha Human MHC 1 alpha
W33798 W33799 W29421 R92912 R932912 R71440 R71443 R71443 R71443
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ALIGNMENTS

RESULT 1 W47262 DT 22-MAY-1998 (first entry) DE Immunomodulatory peptide; 6 AA. W47262; DT 22-MAY-1998 (first entry) DE Immunomodulatory peptide. Nom sapiens. OS Synthetic. Incation/Qualifiers FT Misc_difference 16 FT Misc_ompatibility complex (MHC) CC In a pharmaceutical composition together with a subtherape of an immunosuppressant, to extend the period of acceptance of an immunosuppressant, to extend the period of acceptance 16 FT Misc_difference ce 16 FT Misc_differencencencencencencencencencencencencence	######################################
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Query Match
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Matches 6; Conserv
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10 AA;
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5 RILLRY 10
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Synthetic.
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R83061-R83085, R83096-R83096 and R92907-B92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 75-84 of the alpha-1 domain of the class I MHC HLA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs) of the patient.
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HLA-B2702 CTL modulating peptide (B2702.75-84(L)).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
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05-APR-1994; US-222851.
05-APR-1994; US-222851.
Clayberger C, Krensky AM, Parham P;
WDI; 95-358582/46.
Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
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Best Local Similarity 100.0%; Pred. No. 1.5e+05;
Matches 6; Conservative 0; Mismatches 0;
                               24-MAY-1996, US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR
Beulow R, Clayberger C, Krensky AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R83096 standard; peptide; 10 AA.
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22-MAY-1996; US-651650.
(STRD ) UNIV LELAND STANFORD JUNIOR.
(STRD ) UNIV LELAND STANFORD JUNIOR - USEful for inhibiting transplant rejection
(Claim 10; Page 36; 41pp; English.
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/note- "at least one of the amino acids is the D-isomer
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Immunomodulatory peptide.
Immunomodulator; Class I HLA-B alpha-1 domain; inhibition;
transplant rejection; treatment; autoimmune disease.
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Immunomodulator; Class I HLA-B alpha-1 domain; inhibition;
transplant rejection; treatment; autoimmune disease.
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100.0%; Score 29; DB 1; 100.0%; Pred. No. 0.47;
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                                                              6; Conservative
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Training alpha-1 domain, used for preventing rejection of transplants or treating autochmune diseases.

Example 1: Page 19: Alpp: English.

Peptides W33784-98 and W33778-9 were assayed for their immunomodulating activity, including the N-terminal acylated and/or creminal anidated or estrified forms of up to 60 amino acids, where the peptide-type compound comprises the formula: A-B, where A, B = C creminal anidated or estrified forms of up to 60 amino acids, where the peptide-type compound comprises the formula: A-B, where A, B = C creminal anidated or estrified forms of up to 60 amino acids, where the peptide-type compound comprises the formula: A-B, where A, B = C creminal anidate or estrified forms of usa81 and a represents amino acid; aa82 = R or L; aa83 = G or R; and as represents amino acid; aa82 = R or L; aa83 = G or R; and a represents amino acid; acid: The sequences in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a class I HLA-B alphal domain (positions of T or any peptide type bond within the brackets. They can also be used to inhibit the profiteration of T cells in cresponse to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, chematoid arthritis and lupus erythematosis. The products can also be conserved.
                                                                                                                   Clayberger C, Krensky AM;
WPI; 98-018220/02.
Novel immunomodulatory peptide-type compound - useful for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                      The present sequence is an immunomodulatory peptide, which comprises a Class I HLA-B alpha-1 domain sequence. It can be used in a pharmaceutical composition together with a subtherapeutic dose of an immunosuppressant, to extend the period of acceptance of a transplant from a major histocompatibility complex (MHC) unmatched donor, i.e. to inhibit transplant rejection. It can also be used in the treatment of autoimmune diseases.
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Peptide B-7702.75-84b31 tested for immunomodulating activity.

Immunomodulating dinme: immunosuppressant drug; CTL activation; transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
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23-APR-1997; U06705.
22-MAY-1996; US-651650.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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(STRD ) UNIV LELAND STANFORD JUNIOR.
Beulow R, Clayberger C, Krensky AM;
                                                                                                                                                                                                                                   transplant rejection
Claim 10; Page 36; 41pp; English.
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WO9744351-A1.
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19-JUN-1998
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Tall m 7: Page 37: 48pp; English.

W82804 to W82829 are cytomodulating lipophilic oligopeptides. The algometrian oligopeptides are used to inhibit: (1) activity of lymphocytes
cligopeptides are used to inhibit: (1) activity of lymphocytes.

Competidated are pageorytes); (11) production of inflammatory cytokines, and monounclear phagocytes); (11) production of inflammatory cytokines, and (11) an inflammatory response in mammals (e.g. in cases of septic shock, remumatoid arthritis (RA). Crohm's disease, collitis and allergy). They are also used for modulating activity of haem-containing enzymes and for dispapentes mellitus, RA and systemic lupus erythematosus). In all cases the oligopeptides may be generated from nucleic acids, and treatments are in vitro or in vivo. A specific application is treatment of organs or cells for transplantation, or of the recipient of such transplants.

Apart from therapeutic use, the oligopeptides can be used to study mechanisms of T cell (de)activation and to raise antibodies (used to identify oligopeptides and to raise anti-idiotypic antibodies (used to identify oligopeptides and to raise anti-idiotypic antibodies (used to oligopeptides of the oligopeptides. The oligopeptides are administered by bolus injection or infusion, typically at 0.1-50 (preferably 1.25) mg/Kg.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytomodulating lipophilic oligopeptide (w).

Cytomodulating lipophilic oligopeptide; immune system; inflammation;
Cytomodulating lipophilic oligopeptide; immune system; cell;
Bytotoxic; lymphocytic; inhibition; cytokine; autoimmune disease; T cell;
B cell; mononuclear phagocyte; septic shock; rheumatoid arthritis;
Crohn's disease; colitis; allergy; transplant.
                                                                         Gaps
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Actinomadura hibisca polyketide synthase protein 9.
Multienzyme; infection; fungi; yeast; gram-positive bacteria; virus;
dihydrobenzo(a)naphthacenequinone aglycon; antibiotic; pradimicin.
Actinomadura hibisca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI, 98-594558/50.
When lipophilo peptide(s) that inhibit activation of immune system cells - used for, e.g. production of cytokine(s) and the inflammatory response, and also for modulating haem-containing
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0
100.0%; Score 29; DB 1; Length 10; 100.0%; Pred. No. 0.47;
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83.3%; Pred. No. 1.4;
iive 1; Mismatches 0; Indels
                                                                     0; Indels
                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-OCT-1998.
10-APR-1998; U07231.
23-FEB-1998; US-028083.
11-APR-1997; US-838916.
(SANG-) SANGSTAT MEDICAL CORP.
Buelow R. Calas B. Grassy G;
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                                                                                                                                                                                                                                                                                                                                                                                          W82826 standard; peptide; 10 AA.
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                                                                     Conservative
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Best Local Similarity
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45 RLLIRY 50
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27-NOV-1986; G
14-JUL-1987; G
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                                                                                                           Sequence
                                                                                                                                       Query Match
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P80289
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                                                                         pradimicin
Disclosure; Page 54; 71pp; English.
The Actinomadura hibisca polyketide synthase proteins W54380-W84390 form
The Actinomadura hibisca polyketide synthase proteins W54380-W84390 form
a multienzyme complex. The enzyme is used for the biosynthesis of a
dihydrobenzo(a)naphthacenequinone aglycon preferably a pradimicin which
is an antibiotic useful against systemic fungal infections caused by
Candida albicans, Aspergillus fumigatus and Cryptococcus neoformans. It
is also active against a wide variety of fungi and yeasts, some
Gram-positive bacteria and viruses.
                                                                                                                                                                                                                    Gaps
                                                                   Actinomadura polyketide synthase genes - useful for preparation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Humanisation of non-human immunoglobulin variable regions - for prodn. of humanised antibodies, esp. K20, e.g. as an immunosuppressant
                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                  R93159;
24-OCT-1996 (first entry)
Murine monoclonal antibody K20 kappa chain variable region.
Antibody: light chain; kappa; variable region; K20; integrin;
beta 1 subunit; humanisation; Hu-K20; immunosuppressant;
T cell activation; complementarity determining region; CDR.
                                                                                                                                                                                                                                                                                                                                                                                                                      .note= "complementarity determining region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-
50. 56
/label- CDR2
/note- "complementarity determining region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label- CDR3
/note= "complementarity determining region"
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12-SEP-1994; FR-010858.
(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
(PROT-) PROTEINE PERFORMANCE SA.
                                                                                                                                                                                               Score 25; DB 1
Pred. No. 43;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "framework region"
89. .94
                                                                                                                                                                                                                                                                                                                                                                                                                /note- "framework region"
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                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
        13-SEP-1996; U14791.
13-SEP-1996; WO-U14791.
(BRIM) BRISTOL-MYERS SQUIBB CO. Dairi T, Oxi T; WPI; 98-207391/18.
                                                                                                                                                                                                                                                                                                         R93159 standard; Protein; 108 AA.
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/label- J_kappal
                                                                                                                                                                                               Similarity 66.7%; 4; Conservative

    .23
    /label= FR1

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Best Local Similarity
Matches 4; Conserv
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WPI; 96-162083/17.
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7 RVLVRY 12
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Example 1; Fig 2A; 39pp., French.

The present sequence is that of the variable region of the kappa light chain from murine monoclonal antibody X20. The antibody recognises the beta I subunit (CD29) of integrins and inhibits activation and proliferation of peripheral T cells induced by anti-CD3 antibodies. Monoclonal antibody K20 is a preferred target for humanisation; the humanised version may be useful as an immunosuppressant. In the humanisation process, the complementarity determining regions (CDRS) of a human antibody with framework regions 70-95% homologous to those of K20 were replaced by the K20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; pp; English.

This is encoded by the human pre-B gene which differs from the mouse pre-B-2 gene (of N82441) at several posns. The gene is also selectively expressed in pre-B cell lines. Its pattern of express- lion follows that of Vpre-B1 and lambda-5 in the mouse.

See also N80470-75, N80475 and N82441-42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB, N80476.
Nucleotide sequence selectively expressed in pre-B cells - used
in probes for determining non-T acute lymphoblast leukaemia and
for prepn. of polypeptide(s)
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                                                                                                                                                                                                                                                                                                                                                                  Length 108;
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Pre-B ceils; non-T acute lymphoblast leukaemia; ss.
EP-269127-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Vpre-B protein.
Pre-B cells; non-T acute lymphoblast leukaemia.
El-269127-A.
El-JUN-1988.
                                                                                                                                                                                                                                                                                                                                                                    DB 1;
45;
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                                                                                                                                                                                                                                                                                                                                                                  Score 25; DB :
Pred. No. 45;
2; Mismatches
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27-NOV-1986; GB-028433.
14-UUL-1987; GB-016497.
14-OCT-1987; GB-024100.
(HOFF ) HOFFPANN LA ROCHE AG.
WPIF SR, KUGO A, Melchers GF, Sakaguchi N; WPI; 88-148947/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P80289 standard; protein; 125 AA.
P80289;
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P80288;
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66.7%;
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83.3%;
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Matches 4; Conservative
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GB-028433.
GB-016497.
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Matches 5; Conserv
                                                                                                                                                                                                                                                                                          108 AA;
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MEF2 transcription factors can be used to produce transgenic animals with increased muscle mass, to prevent or counteract muscle atrophy in humans or animals suffering a pathological muscular condition, or codevelop pharmacological agents which regulate the expression of muscle-tissue genes. MEF2 isoforms are given in Q58740-44, R50038-45 and R57772. Nucleic acid encoding a member of the MEF2 protein family pref, comprises a sequence encoding at least eleven sequence SEEELEL (R57773).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel immunomodulatory peptide-type compound - useful for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transplant rejection
Claim 10; Page 36; 41pp; English.
The present sequence is an immunomodulatory peptide, which
The present sequence is an immunomodulatory peptide, which
comprises a Class I HiAP-B alpha-1 domain sequence. It can be used
in a pharmaceutical composition together with a subtherapeutic dose
of an immunosuppressant, to extend the period of acceptance of a
transplant from a major histocompatibility complex (MHC) unmatched
donor, i.e. to inhibit transplant rejection. It can also be used in
the treatment of autoimmune diseases.

    .6
    at least one of the amino acids is the

      myocyte-specific transcipton enhancer factor; muscle; atrophy
                                                                                                                                                                                                                                                                                                  New nucleic acid encoding MEF2-protein family member - i.e. myocyte-specific transcription enhancing factor, useful to increase muscle mass and to counteract muscle atrophy, e.g. muscular dystrophy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunomodulatory peptide.
Immunomodulator; Class I HLA-B alpha-1 domain; inhibition; transplant rejection; treatment; autoimmune disease.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86.2%; Score 25; DB 1; Length 365; 66.7%; Pred. No. 1.6e+02; tive 2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 6;
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23-ARR-1997; U06705.
22-MAY-1996; US-651650.
(STRD ) UNIV LELAND STANFORD JUNIOR.
CLAYDEFGER C, Krensky AM;
WPI; 98-018220/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                     17-MAR-1994.

07-SEP-1993; U08386.

04-SEP-1992; US-939898.

(CHIL-) CHILDRENS MEDICAL CENT.

NAGAL-GINARÚ B;

WPI: 94-101181/12.

N-PSDB; Q58741.
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc_difference
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64 RVLLKY 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RILLRY 6
                               Homo sapiens.
WO9405776-A.
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W47261
AC W447261
DT 22-MAY
DE Immunon
E Immun
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Disclosure; pp. English.
This is encoded by the genomic form of the variable region pre-B-2 sequence. The gene is not rearranged during pre-B cell development. This protein may associate with itself or with heavy chain v domains expressed in pre-B cells. The gene is expressed only in pre-B cells ines. See also N80470-75, N80476-77 and N82442.
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                                                                                                        Nucleotide sequence selectively expressed in pre-B cells - used in probes for determining non-T acute lymphoblast leukaemia and for propen. of polypeptide(s) Disclosure; pp; English.

This is encoded by the genomic form of the variable region pre-B-1 sequence. The gene is not rearranged during pre-B cell development and is 4.6 kb upstream of the lambda-5 gene. This protein can associate with itself or with heavy chain V domains expressed in pre-B cells. Vpre-B-1 and lambda-5 form a complete V domain via non-covalent bonds. The gene is expressed only in pre-B cell lines. See also N89470-74, N80476-77 and N82441-42.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 142;
60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-DEC-1990 (first entry)
V preB-2 protein.
Pre-B cells; non-T acute lymphoblast leukaemia.
EP-269127-A.
01-JUN-1988.
14-OCT-1987; GB-024100.
(HOFF ) HOFFMANN-LA ROCHE AG.
Bauer SR, Kudo A. Melchers GF, Sakaguchi N;
WPI; 88-148947/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HOFF ) HOFFMANN-LA ROCHE AG.
Bauer SR, Kudo A, Melchers GF, Sakaguchi N;
WPI; 88-148947/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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Pred. No. 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Æ
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R50040;
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ilarity 83.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-SEP-1994 (first entry) XMEF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 86.2
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-NOV-1987; 117619.
27-NOV-1986; GB-028433.
14-JUL-1987; GB-016497.
14-OCT-1987; GB-024100.
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Best Local Similarity
Matches 5; Conserv
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66 RFLLRY 71
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P83001;

RESULT 12 P83001

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RESULT 13

R50040

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Gaps

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Sequence

us-08-653-294-5.rag

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Triangle of the sequence represents a specifically claimed peptide which forms part of the immunomodulating dimer peptides of the invention. A peptide-type of the immunomodulating dimer peptides of the invention. A peptide-type compound or variant is claimed which has immunomodulating activity.

Including the N-terminal acylated and/or C-terminal amidated or capture of forms of up to 60 main. A part of the anion of the compound comprises the formula; A-B, where A, B - R mad6-77L) (aa79-84) or campaises the formula; A-B, where A, B - R mad6-77L) (aa79-84) or campaises the formula; aa76 = B or V; aa77 = D, S or N; aa79 = R or G; aa80 - I or N; aa81, aa84 = B hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino acid. The sequences related to a class I HIA-B alphal domain (positions 79-84). They can be used to inhibit cytocoxic T-lymphocytes (CTL) from undesirably attacking cells in a class or proteins of interest to activate CTLs. They can also inhibit the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of transpanse or for treating autoimmune and a surphematorial and an arth-Hitle and lumis autoimmune and an arth-Hitle and lumis carribeant or the proliferation of transpanse.
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                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JUN-1998 (first entry)
Peptide #1 used in immunomodulating dimer peptide.
Immunomodulating dimer: fimunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New immunomodulating dimer peptide(s) - based on a Class I HLA-B
alpha-1 domain, used for preventing rejection of transplants or
treating autoimmune diseases
83.3%; Pred. No. 1.5e+05;
tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 82.8%; Score 24; DB 1; Length 6; Best Local Similarity 83.3%; Pred. No. 1.5e+05; Matches 5; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 NOV-1297;
24 MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beulow R, Clayberger C, Krensky AM; NPI; 98-086530/08.
                                                                                                                                                                                                                                                                                                                                                                                                        W33780 standard; peptide; 6 AA.
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                          1 RILLRY 6
                                                                                                                                                                        Homo sapiens.
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W33780
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Search completed: February 8, 2000, 01:29:36 Job time: 1748 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

February 7, 2000, 11:54:14; Search time 117.7 Seconds (without alignments) 2.405 Million cell updates/sec

US-08-653-294-5 29 I RILLRY 6 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

142080 seqs, 47169319 residues Searched: 142080 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

pirl:* pir2:* pir3:* PIR_62:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ES	Description	hypothetical prote	probable phosphogl		probable coa ligas	prolyl endopeptida	hypothetical prote	ribosomal protein	hypothetical prote	methylmalonate-sem	probable fadD17 pr	hypothetical prote	finger protein sdc	laminin alpha-1 ch	polyketide synthas	ribosomal protein	etical p	VpreB protein - hu	VpreB protein prec	protein p	VPre-B protein - h	C,		hypothetical prote	enhan	myocyte enhancer f	myocyte enhancer f	ption (serum response fac		probable phenylace
SUMMARIES	ID	211	A71467	D72012	G70986	JC4084	B71508	S53849	T15698	B42902	D70806	C72670	A33165	S18253	JC5858	C70161	A72666	S00258	B28344	A28344	I57832	T13342	A42644	671322	JC5883	JC5882	JC5881	JC4221	3948	~~	
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đ	Query	8	100.0	8	8	9.96	93.1	89.7	89.7	89.7	89.7	89.7	89.7	89.7	86.2	86.2	86.2	86.2	86.2	86.2	86.2	86.2	86.2	86.2	86.2	86.2	86.2	86.2	86.2	86.2	86.2
	Score	29	29	59	29	28	27	26	56	56	26	26	26	26	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25
	Result No.		7	m	4	5	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30

rf2 nuclear restor		RNA-directed RNA p		RNA-directed RNA p		vacuolar membrane	probable membrane	RNA-directed DNA p	DNA topoisomerase	DNA topoisomerase	hypothetical BCL2/	class II histocomp	MHC protein - cott
T03983 E71364	T13646	RRVGCN	RRVGCT	RRVGCR	S05456	S25198	S19418	T01610	829969	A39242	152725	538695	168913
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549	735	817	817	817	818	830	832	1412	1612	1626	27	73	16
86.2	86.2	86.2	86.2	86.2	86.2	86.2	86.2	86.2	86.2	86.2	82.8	82.8	82.8
2.5	25	25	25	25	25	22	25	52	25	25	24	24	24
31	33	34	35	36	37	38	39	40	41	42	43	77	45

ALIGNMENTS

RESULT 1 D72110 hypothetical protein - Chlamydia pneumoniae (strain CWL029) C; Species: Chlamydia pneumoniae C; Species: Chlamydia pneumoniae C; Species: Chlamydia pneumoniae C; Species: Chlamydia pneumoniae C; Species: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Apr-1999 C; Species: 10: D72110 R; Ralman, S: Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, Nature Genet. 21, 385-389, 1999 A; Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis. A; Reference number: A72000; MUID:99206606 A; Accession: D72110 A; Status: preliminary A; Accession: D72110 A; Status: preliminary A; Scatus: preliminary A; Scatus: genetiminary A; Cross-references: GB:AE001604; GB:AE001363; NID:94376438; PID:94376450 C; Genetics: A; Gene: CPn0181
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ö Gaps ö Ouery Match 100.0%; Score 29; DB 2; Length 133; Best Local Similarity 100.0%; Pred. No. 4.8; Matches 6; Conservative 0; Mismatches 0; Indels

||||||| 95 RILLRY 100 1 RILLRY 6 ď ö

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probable phosphoglucomutase - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C;Specias: Chlamydia trachomatis
C;Specias: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 29-Sep-1999
C;Accession: A71467
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitche Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia t A;Reference number: A71570; MUD:99000809
A;Reference number: A71570; MUD:99000809
A;Reference number: A71570; MUD:99000809
A;Reference number: A71570; MUD:99000809
A;Cross-references: GB:AE001354; GB:AE001273; NID:g3329280; PIDN:AAC68412.1; PID:g332
A;Gross-references: GB:AE001354; GB:AE001273; NID:g3329280; PIDN:AAC68412.1; PID:g332
A;Genetics:
A;Genetics:
A;Genetics:
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ö Gaps ö Ouery Match 100.0%; Score 29; DB 2; Length 458; Best Local Similarity 100.0%; Pred. No. 17; Matches 6; Conservative 0; Mismatches 0; Indels

413

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hypothetical protein CT484 - Chlamydia trachomatis (serotype D, strain UW3/Cx) C; Species: Chlamydia trachomatis C; Species: Chlamydia trachomatis C; Date: 13.5ep-1998 #sequence_revision 13.5ep-1998 #text_change 21.Nov-1998 C; Accession: B71508 #sequence_revision 13.5ep-1998 #text_change 21.Nov-1998 C; Accession: B71509 E; Eammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitche Science 282, 754-759, 1998 ##seference of an obligate intracellular pathogen of humans: Chlamydia t A; Reference number: A71570; MUID:99000809
                                                                                                   A;Title: A gene from the hyperthermophile Pyrococcus furiosus whose deduced product 1 A;Reference number: JC4084; MJID:95129900 A;Accession: JC4084 A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ribosomal protein S3 - Acanthamoeba castellanii mitochondrion (SGC6)
C; Species: mitochondrion Acanthamoeba castellanii
C; Date: 15-011-1995 #sequence_revision 01-Sep-1995 #text_change 26-Feb-1999
C; Accession: S53849
S; Burger, G; Plante, I.; Lonergan, K.M.; Gray, M.W.
J. Mol. Biol. 245, 522-537, 1995
A; Title: The mitochondrial DNA of the amoeboid protozoon, Acanthamoeba castellanii: A; Reference number: S53825; MuID:95147275
A; Reference number: S53849
A; Status: nucleic acid sequence not shown; translation not shown
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C;Date: 12-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Sep-1997 C;Accession, 7040B.
C;Accession, K.A.; Bartley, D.A.; Robb, F.T.; Schreier, H.J.
Gene 152, 103-106, 1995
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A;Status: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: GB:AE001322; GB:AE001273; NID:g3328916; PID:g3328920
A;Cross-references: GB:AE001322; GB:AE001273; NID:g3328916; PID:g3328920
C;Genetics: Serotype D, strain UW-3/Cx
A;Gene: CT484
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                                                                                                                                                                                                                                                                                                                                                                                                                            Length 616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                    A.Cross-references: GB:U08343; NID:g475591; PID:g475592
C;Keywords: hydrolase; oligopeptidase
F;477,561,592/Active site: Ser, Asp, His #status predicted
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A; Cross-references: GB:U12386; NID:9562028; PID:9562053
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Pred. No. 38;
1; Mismatches
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Pred. No. 40;
1; Mismatches
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83.38;
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Best Local Similarity 83.3
Matches 5; Conservative
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A;Genetic code: SGC6
C;Keywords: mitochondrion
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                              A; Residues: 1-616 <ROB>
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334 RVLLRY 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Molecule type: DNA
A:Residues: 1-458 cARN>
A:Cross-references: GB:AE001677; GB:AE001363; NID:g4377291; PIDN:AAD19103.1; PID:g437729
A:Experimental source: strain CWL029
C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, S37-544, 1998
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                                                                                                                                                                                                                                           C; Species: Chlamydia pneumoniae
C; Species: Chlamydia pneumoniae
C; Accession: D72012
B; Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, Nature Genet. 21, 385-389, 1999
A; Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A; Reference number: A72000; MuID:99206606
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C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 17-Jul-1998
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C;Superfamily: probable phosphorylating protein ureC
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1larity 100.0%; Pred. No. 17;
Conservative 0; Mismatches
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1larity 100.0%; Pred. No. 20;
Conservative 0; Mismatches
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Query Match Best Local Similarity Matches 6; Conserv

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Query Match Best Local Similarity Matches 6; Conserv

419 RILLRY 424

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bypothetical protein APE0785 - Aeropyrum pernix (strain K1)
C; Species: Aeropyrum pernix
C; Species: Aeropyrum pernix
C; Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C; Accession: C72670
R; Kawarabayasi, Y: Hino, Y:; Horikawa, H:; Yamazaki, S:; Haikawa, Y:; Jin-no, K:; Ta awa, H:; Takamiya, M.: Masuda, S:; Funahashi, T.; Tanaka, T:; Kudoh, Y:; Jin-no, K:; Ta awa, H:; Takamiya, M.: Masuda, S:; Funahashi, T.; Tanaka, T:; Kudoh, Y:; Jin-no, K:; Ta awa, H:; Takamiya, M.: Masuda, S:; Funahashi, T.; Tanaka, T:; Kudoh, Y:; Jin-no, K:; Ta awa, H:; Takamiya, M.: Masudece of an aerobic hyper-thermophilic Crenarchaeon, Aero A; Reference number: A72450; MuID:99310339
A; Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero A; Accession: C72670
A; Accession: C72670
A; Status: Preliminary
A; Molecule type: DNA
A; Residues: 1-617 < KAN>
A; Residues: 1-617 < KAN>
A; Residues: 1-617 < KAN>
A; Cross-references: DDBJ:AP000060; NID:95104188; PIDN:BAA79763.1; PID:d1043549; PID:g A; Experimental source: strain K1
C; Genetics:
A; Genetics:
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Cibate: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Sep-1997
CiAccession: S15093; #a3165
R;Nonet, M.L.; Meyer, B.J.
Nature 351, 65-68, 1991
Nature 251, 85-68, 1991
A;Reference number: S15093; MUID:91226537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AL022022; GB:AL123456; NID:g3261554; PID:e1254634; PID:g292444 A;Experimental source: strain H37Rv C;Genetics: A;Genetics: A;Ge
                                                                                                                                                                   C; Accession: D7886
R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon F; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon F; Connor, R.; Davis, R.; Deviin, K.; Feltwell, T.; Gentles, S.; Hamili, N.; Holroyd, Nature 393, 537-544, 1998
A; Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Atther Deciphering the biology of Mycobacterium tuberculosis from the complete geno A; Reference number: A7050; MUID:98295987
A; Reference number: P08806
A; Accession: D70806
A; Reference reliminary; nucleic acid sequence not shown; translation not shown A; Residues: 1-502 <COL>
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                                 probable fadD17 protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 17-Jul-1998
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Pred. No. 1e+02;
2; Mismatches
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llarity 66.7%;
Conservative
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Best Local Similarity
Matches 4; Conservi
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Best Local Similarity
Matches 4; Conserv
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406 RVLMRY 411
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330 RVMLRY 335
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A;Molecule type: DNA
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J. Biol. Chem. 267, 13585-13592, 1992
A; Filie: Characterization of the mmsAB operon of Pseudomonas aeruginosa PAO encoding met A; Reference number: A42902; MUID:92317087
A; Reference number: A42902
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C;Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology
C;Keywords: oxidoreductase
F;43-301/Domain: aldehyde dehydrogenase homology <ALDD>
F;282/Active site: Cys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Species: Caenorhabditis elegans
Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
Accession: T15698
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C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: B42902; S27602
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A;Residues: 1-497 <STE>
A;Cross.references: EMBL:M84911; NID:9151360; PIDN:AAA25891.1; PID:9151362
A;Note: sequence extracted from NCBI backbone (NCBIP:107707)
                                                                                                Gaps
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A; Description: The sequence of C. elegans cosmid C29F5.
A; Reference number: Z18390
A; Accession: T15698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein C29F5.1 - Caenorhabditis elegans
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Pred. No. 77;
1; Mismatches
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Pred. No. 1e+02;
2; Mismatches
Score 26; DB
Pred. No. 60;
2; Mismatches
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Best Local Similarity 83.3
Matches 5; Conservative
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Query Match
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| 200 RILVRY 205
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| 132 RVILRY 137
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68 RVMLRY 73
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Length 103 0; Indels

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A; Molecule type: DNA
A; Residues: 1-103 <DAI>
A; Cross-references: DDBJ:D87924
C; Comment: This enzyme catalyzes repeated condensation cycles of acyl-CoA, affecting
C; Genetics:
                                                                                                                                                        polyketide synthase (EC 2.....) chain 9 - Actinomadura hibisca
C;Species: Actinomadura hibisca
C;Species: Actinomadura hibisca
C;Date: 05-Mar-1998 #sequence_revision 13-Mar-1998 #text_change 17-Mar-1999
C;Accession: UC5858
R;Dairi, T.; Hamano, Y.; Igarashi, Y.; Furumai, T.; Oki, T.
Biosci. Blotechnol. Blochem. 61, 1445-1453, 1997
A;Title: Cloning and nucleotide sequence of the putative polyketide synthase genes
A;Accession: UC5850; MuID:97480928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 25; DB 2
Pred. No. 36;
2; Mismatches
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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C;Keywords: transferase
                                                       885 RIVLRY 890
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7 RVLVRY 12
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A; Residues: 1-3712 <KUS>
A; Cross-references: GB:M96388; NID:g157799; PIDN:AAA28662.1; PID:g157800
R; Garrison, K.; MacKrell, A.J.; Fessler, J.H.
J. Biol. Chem. 266, 22899-22904, 1991
A; Title: Drosophila laminin A chain sequence, interspecies comparison, and domain struct
A; Reference number: S18253; MUID:92078147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;2698-2863/Domain: repeat G1 <RG1>
F;2698-28643/Domain: repeat G2 <RG2>
F;3048-3203/Domain: repeat G3 <RG2>
F;3049-3223/Domain: repeat G3 <RG3>
F;3079-3200/Domain: laminin G repeat homology <LG3>
F;3343-3528/Domain: repeat G4 <RG4>
F;3529-3712_Domain: repeat G5 <RG4>
F;3529-3712_Domain: repeat G5 <RG5>
F;3529-3712_Domain: repeat G5 <RG5>
F;360,1943,2024,215,2267,2301,2323,2482,2524,2538,2569,2699,2720,2890,2938,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Taminin alpha-1 chain precursor - fruit fly (Drosophila melanogaster)
(Species: Drosophila melanogaster
(C) date: 16-Sep-1992 #sequence_revision 24-Jul-1997 #text_change 13-Aug-1999
(C) Accession: 828899; $18253
(R) R: Kusche-Gullberg, M.; Garrison, K.; MacKrell, A.J.; Fessler, L.I.; Fessler, J.H.
(BMED J. 11, 4519-4527, 1992
(A) Title: Laminin A chain: expression during Drosophila development and genomic sequence.
(A) Reference number: $28899; MUID: 93049203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross references: Flybase:FBgn0002526
Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h.
Keywords: basement membrane; cell binding; colled coll; disulfide bond; extracellular, 273-330/Domain: laminin-type EGF-like homology (LEGS)
333-400/Domain: laminin-type EGF-like homology (LEG2)
541-584/Domain: laminin-type EGF-like homology (LEG1)
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Residues: 1762-3712 <GAR>
:Cross-references: EMBL:M75882; NID:g157797; PIDN:AAA28661.1; PID:g157798
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                                                       A;Molecule type: mRNÅ
A;Residues: 1-1203 <NON>
A;Residues: 1-1203 <NON>
A;Cross-references: EMBL:X58520; NID:g6848; PID:g6849
C;Genetics:
A;Gene: sdc-1
C;Keywords: DNA binding; nucleus; transcription regulation; zinc finger
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89.7%; Score 26; DB 2; Length 3712;
Best Local Similarity 83.3%; Pred. No. 7.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                               Score 26; DB 2; Lei
Pred. No. 2.5e+02;
2; Mismatches 0;
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                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 66.7%;
Matches 4; Conservative
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A; Accession: S15093
A; Status: preliminary
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437 RVILRY 442
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A; Residues: 1-132 < KLE>
A; Cross-references: GB:AE001152; GB:AE000783; NID:g2688387; PIDN:AAC66850.1; PID:g268
A; Experimental source: strain B31
C; Superfamily: Escherichia coli ribosomal protein S8
Tibosomal protein S8 (rpsH) - Lyme disease spirochete
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Species: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 13-Aug-1999
C;Sacession: C70161
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Son, D.; Petterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, Nature 390, 580-586, 1997
A;Tulto: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi. A;Reference number: A70100; MUID:98065943
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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8 Z B

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                          OM protein - protein search, using sw model
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February 8, 2000, 00:59:45; Search time 63.71 Seconds (without alignments) 2.813 Million cell updates/sec BLOSUM62 Gapop 10.0 , Gapext 0.5 US-08-653-294-5 29 1 RILLRY 6 Title: Perfect score: Sequence: Run on:

82228 Total number of hits satisfying chosen parameters: 82229 seqs, 29864866 residues Searched:

Scoring table:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

SwissProt_38:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ption	salmon		P28810 pseudomonas		-				P13372 mus musculu					-				_				-	_	Q02880 homo sapien	_	382	544	512	183 escherichi	273	7	738 1	Ø	m
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298 AA.

PRT;

STANDARD;

RESULT 2 RT03_ACACA ID RT03_ACACA

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P51562 pasteurella 028852 archaeoglob P14428 mus musculu P54142 canoorhabdl P30467 homo sapten 005026 neisseria g 059024 neisseria g 983734 trypanosoma P33617 macaca mula P13750 pan troglod
TERB_PASPI YE20_ARCFU HA10_MOUSE SRB7_CAEEL 1B20_HUMAN GALE_NEIGO GALE_NEIME Y83C_METME Y83C_METME PP12_TRYBB HLAF_MACMU
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# ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Early aspects of Caenorhabditis elegans sex determination and dosage compensation are regulated by a 2inc-finger protein.";
Nature 351:65-68(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLOYD C.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: EMBRYONIC TRANSCRIPTION FACTOR REGULATING DOWNSTREAM
-!-FUNCTION: EMBRYONIC TRANSCRIPTION FACTOR REGULATING DOWNSTREAM
GENES INVOLVED SPECIFICALLY IN THE SEX DETERMINATION AND DOSAGE
COMPENSATION PATHWAYS, OR REGULATING OTHER GENES INVOLVED IN THE
COORDINATE CONTROL OF BOTH PROCESSES.
-!- SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Nematoda, Secernentea, Rhabditia, Rhabditida,
Khabditina, Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY
                                                                                                                                                                                                                                                                               HSSP; P56533; 1BPW.
PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; FALSE_NEG.
PFAM. PF00171; Aldedh; 1.
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4D33C45B CRC32;
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01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
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Pred. No. 52;
2; Mismatches
                                                                                                                                                                      or send an email to license@isb-sib.ch).
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496 AA; 53532 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Last a ZINC FINGER PROTEIN SDC-1. SDC-1 OR EGL-16 OR F52E10.1. Caenorhabditis elegans.
                                                                                                                                                                                                                 EMBL; M84911; AAA25891.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
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                                                                                                                                                                                                                                        PIR; B42902; B42902.
PIR; S27602; S27602.
                                                                                                                                                                                                                                                                                                                                                                   Oxidoreductase; NAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 4; Conserv
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SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
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MEDLINE; 91226537.
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SEQUENCE FROM N.A.
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ACT_SITE
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1-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
METHYLMALONATE-SEMIALDEHYDE DEHYDROGENASE [ACYLATING] (EC 1.2.1.27)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STEELE M.I., LORENZ D., HATTER K., PARK A., SOKATCH J.R.; "Characterization of the mmsAB operon of Pseudomonas aeruginosa PAO encoding methylmalonate-semialdehyde dehydrogenase and 3-
                                                                                                                                                                                                                                 -i - CATALYTIC ACTIVITY: 2-METHYL-3-OXOPROPANOATE + COA + NAD(+)
PROPAROYL-COA + CO(2) + NADH.
-i - PATHAX: DISTAL WALINE METABOLIC PATHWAY.
-i - SUBUNIT: HOMODIMER.
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Pred. No. 31;
2; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ribosomal protein; Mitochondrion.
SEOUENCE 298 AA; 36060 MW; 7BA48AD7 CRC32;
                  01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00548; RIBOSOMAL_S3; FALSE_NEG. PFAM; PF00189; Ribosomal_S3_C; 1. PFAM; PF00417; Ribosomal_S3_N; 1.
                                                                                                                                                                      Eukaryota; Acanthamoebidae; Acanthamoeba
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STRAIN-ATCC 15692 / PAO1;
MEDLINE; 92317087.
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J. Biol. Chem. 267:13585-13592(1992).
                                                                                    MITOCHONDRIAL RIBOSOMAL PROTEIN S3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                               Acanthamoeba castellanii (Amoeba)
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Best Local Similarity 66.7%;
Matches 4; Conservative
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| 132 RVILRY 137
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P28810;
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DR PIR; A33165; A33165.

DR PIR; S15093; S15093.

DR WORMPER, F52E10.1; CE03393.

DR PROSITE; P500096; Z1C2H2; 2.

DR PROSITE; P500096; Z1C2H2; 4.

EVAL: PFAM; PF00096; Z1C2H2; 4.

EVAL: PFAM; DOMAIN

SEXUAL differentiation; Transcription regulation; Zinc-finger;

KW Metal-binding; DNA-binding; Developmental protein; Nuclear protein.

FT ZN_FING

TN_FING

TN_FI
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GALLIANO M.-F., ABERDAM D., AGUZZI A., ORTONNE J.-P., MENEGUZZI G.;
"Cloning and complete primary structure of the mouse laminin alpha 3 chain. Distinct expression pattern of the laminin alpha 3A and alpha 3B chain isoforms.";
J. Biol. Chem. 270:21820-21826(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -! - FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Developmental expression of nicein adhesion protein (laminin-5) subunits suggests multiple morphogenic roles."; cell Adhes. Commun. 2:115-129(1994).
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Nassignment of mouse nicein genes to chromosomes 1 and 18.";
"Assignment enone 5:229-233(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Pred. No. 1.3e+02;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                             89.7%;
66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Best Local Similarity
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MEDLINE; 94363405.
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MEDLINE; 94281750.
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LMA3_MOUSE
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EGF-LIKE 4 (C-TERMINAL) EGF-LIKE 5.

LAMININ E

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SEQUENCE OF 1762-3712 FROM N.A.

AGARISON K., MACKRELL A.J., FESSLER J.H.;

AGARISON K., MACKRELL A.J., FESSLER J.H.;

AGARISON K., MACKRELL A.J., FESSLER J.H.;

Tosoophila laminin A chain sequence, interspecies comparison, and domain structure of a major carboxyl portion.";

J. Biol. Chem. 266:22899-22904(1991).

T. FUNCTION: BINIDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ OF CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.

CHICATON: DIVERSE FUNCTION NUTATIONS LEAD TO LATE EMBRYONIC CETHALITY. CERTALIN PARTIAL LOSS-OF-FUNCTION MUTATIONS GIVE RAISE TO ESCAPER ADULTS, WHICH HAVE ROUGH EYES ASSOCIATED WITH CHANGES IN CHANGES IN CELL FATE AND PATTERN, MISSHAPPEN LEGS AND DEFECTS IN WING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - 1- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE DIFFERENT POLYPETIDE CHAINS (ALPHA, BETA, GAMAA), WILCH ARE BOUND TO EACH OTHER BY DISGLIFIDE BONDS INTO A CROSS-SHAPED MOLECULE COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.
- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT MEMBRANES (MAJOR COMPONENT).
- ISSUE SPECIFICITY: URBAL FORMED MESODERM AND LATER PROMINENTLY EXPRESSED IN HEMOCYTES, WHICH ALSO SYNTHESIZE COLLAGEN IV.
- EXPRESSED IN HEMOCYTES, WHICH ALSO SYNTHESIZE COLLAGEN IV.
- DEVELOPMENTAL STAGE: DORING MORPHOGENESIS, MOSTLY IN EMBRYO DEVELOPMENTAL 10-12 HOUNG.
- DOWAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
- DOMAIN: DOMAINS I LAMININ WITH THE DOMAIN VI).
- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV (DOMAIN IV' IS NOT SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                     TISSUE-EMBRYO;
MEDLINE: 94038678.
HENCHCLIFFE C., GARCIA-ALONSO L., TANG J., GOODMAN C.S.;
HENCHCLIFFE C. GARCIA-ALONSO L., TANG J., GOODMAN C.S.;
morphogenesis in Drosophila.";
Development 118:325-337(1993).
                                                                                                                                                                                                             FESSLER J.H.;
"Laminin A chain: expression during Drosophila development and
                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE: 93049203.
KUSCHE-GULLBERG M., GARRISON K., MACKRELL A.J., FESSLER L.I.,
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PROSITE; PS00022; EGF_1; 17.
PROSITE; PS01186; EGF_2; 5.
PROSITE; PS01248; LAMININ_TYPE_EGF; 19.
                                                                                              Ephydroidea; Drosophilidae; Drosophila
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AALGQCLGYGSEQQRVAFLQRPSQNHLQASYMELRPS (IN
LAMININ EGF-LIKE 6.
LAMININ EGF-LIKE 7 (INCOMPLETE).
DOMAIN II AND I (HEPTAT REPEATS).
5 X LAMININ G-LIKE REPEATS (DOMAIN G).
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LAMININ G-LIKE 2.
LAMININ G-LIKE 3.
LAMININ G-LIKE 4.
LAMININ G-LIKE 5.
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INTERCHAIN (PROBABLE).
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01-NOV-1997 (Rel. 35, Last sequence update)
115-JUL-1999 (Rel. 38, Last annotation update)
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LAMININ EGF-LIKE 14.
LAMININ EGF-LIKE 15.
LAMININ EGF-LIKE 16.
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DOMANIN EGF-LIKE 21.
LAMININ EGF-LIKE 22.
LAMININ G-LIKE 23.
LAMININ G-LIKE 3.
LAMININ G-LIKE 4.
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LAMININ G-LIKE 5.
LAMININ G-LIKE 5.
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LAMININ EGF-LIKE 9.
LAMININ EGF-LIKE 9.
LAMININ EGF-LIKE 10.
LAMININ EGF-LIKE 10.
LAMININ EGF-LIKE 11.
A.5 X LAMININ EGF-LIKE REPEATS (DOMAIN 11) 11 11 11 11
                                                                                                                                 LAMININ ALPHA CHAIN.
LAMININ N-TERMINAL (DOMAIN VI).
10.5 X LAMININ EGF-LIKE REPEATS (DOMAIN
PFAM; PF00052; laminin_B; 1.

PFAM; PF00054; laminin_G; 2.

PFAM; PF00054; laminin_G: Extracellular matrix; Colled coil; Laminin EGF-like domain; Cell adhesion; Repeat; Signal.

SIGNAL 1 22 POTENTIAL.

SIGNAL 23 3712 LAMININ ALPA CHAIN.

DOMAIN 25 272 LAMININ N-TERMINAL (DOMAIN VI).

DOMAIN 273 815 10.5 X LAMININ EGF-LIKE REPEATS (DOMAIN
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Mus musculus (Mouse)
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139 AA;
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P13372;
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SEQUENCE
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VPR1_MOUSE
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FRASER C.M., CASJENS S., HDANG W.M., SUTTON G.G., CLAYTON R.A.,
LATHIGRA R., WHITE O., KETCHUM K.A., DODSON R., HICKEY E.K., GWINN M.,
DOUGHERTY B., TOMB J.-F., FLEISCHMANN R.D., RICHARDSON D.,
PETERSON J., KERLAVAGE A.R., QUACKENBUSH J., SALZBERG S., HANSON M.,
VAN VUGT R., PALMER N., ADAMS M.D., GOCAYNE J.D., WELDMAN J.,
UTTERBACK T., WATTHEY L., MCDONALD L., ARTIACH P., BOWMAN C.,
GARLAND S., FUJII C., COTTON M.D., HORST K., ROBERTS K., HATCH B.,
"Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE: 88195069.
BAUER S.R., KUDO A., MELCHERS F.;
"Structure and pre-B lymphocyte restricted expression of the VpreB in humans and conservation of its structure in other mammallan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        species.";
EMBO J. 7:111-116(1988).
-!- FUNCTION: ASSOCIATES WITH THE IG-MU CHAIN TO FORM A MOLECULAR
COMPLEX THAT IS EXPRESSED ON THE SURPACE OF PRE-B-CELLS. THIS
COMPLEX PRESUMABLY REGULATES IG GENE REARRANGEMENTS IN THE BARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                               NATUTE 390:580-586(1997).
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1-OCT-1989 (Rel. 12, Last sequence update)
01-NOV-1991 (Rel. 20, Last annotation update)
11MUNOGLOBULIN IOTA CHAIN PRECURSOR (V(PREB) PROTEIN) (FRAGMENT).
                                                                                                                                                                                                                                                                           RNA (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE S8P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STEPS OF B-CELL DIFFERENTIATION.
TISSUE SPECIFICITY: ONLY EXPRESSED BY PRE-B-CELLS.
SIMILARITY: TO MOUSE V(PREB)1 AND V(PREB)2
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132 AA; 14814 MW; 874CB660 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 25; DB :
Pred. No. 23;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00053; RIBOSOMAL_S8; 1. PFAM; PF00410; Ribosomal_S8; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE001152; AAC66850.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86.2%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ribosomal protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:||:|
61 RVLLKY 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RILLRY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BB0492
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P12018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                              COMPLEMENTARITY - DETERMINING 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 139; 24;
                                                                                                                                                                                                                                                                                          COMPLEMENTARITY - DETERMINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                  IMMUNOGLOBULIN IOTA CHAIN.
FRAMEWORK 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IMMUNGELOBULIN IOTA CHAIN PRECURSOR (V(PREB)1 PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL. IMMUNOGLOBULIN IOTA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                             MW; E1DA1049 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 AA.
                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                       FRAMEWORK 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 25;
Pred. No.
                                                                                                                                                                                                                                                                                                                   FRAMEWORK
                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X05556; CAA29071.1; -.
EMBL; X0557; CAA29072.1; -.
PIR; A2834; A28344.
HSSP; PO1607; IREI.
PSSP, MGI:88936; VPREBI.
PFAM; PF00047; 1g; 1.
Immunoglobulin domain; B-cell; Signal.
                                                                                                                                                          Signal
                                                                                                                                                             B-cell;
                                                            EMBL; M34927; AAA61292.1; -.. PIR; S00258. S00258. MIM; 146770. -. PERM; PRO047; 1; 1. Immunoglobulin domain; B-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                  86.2%;
83.3%;
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STRAIN-C57BL/6 X DBA/2J;
MEDLINE; 88029315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                        ö
                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: ASSOCIATES WITH THE IG-MU CHAIN TO FORM A MOLECULAR COMPLEX THAT IS EXPRESSED ON THE SURFACE OF PRE-B-CELLS. THIS COMPLEX PRESUMABLY REGULATES IG GENE REARRANGEMENTS IN THE EARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KUDO A., MELCHERS F.; "A second gene, VpreB in the lambda 5 locus of the mouse, which appears to be selectively expressed in pre-B lymphocytes."; EMBO J. 6:2267-2272 (1987).
                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
FRAMEWORK 2.
                                      COMPLEMENTARITY-DETERMINING 2. FRAMENORR 3. SEMILARITY. 4 SCS8A1B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPLEMENTARITY-DETERMINING 1. FRAMEWORK 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STEPS OF B-CELL DIFFERENTIATION.
-!- TISSUE SPECIFICITY: ONLY EXPRESSED BY PRE-B-CELLS.
-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPLEMENTARITY - DETERMINING 2.
                                                                                                                          Score 25; DB 1; Length 142;
Pred. No. 25;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                 01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IMMUNOGLOBULIN OMEGA CHAIN PRECURSOR (V(PREB)2 PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
IMMUNOGLOBULIN OMEGA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRAMEWORK 3.

BY SIMILARITY.

6AE40A3B CRC32;
                                                                                                                                                                                                                                                                                       142 AA.
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PIR; B28344; B28344.
HSSP; P01607; IREI.
MGD; MGI:98937; VPREB2.
PFAM; PF00047; 1g; 1.
Immunoglobulin domain; B-cell; Signal.
                                                                                                                                                                                                                                                                                       PRT;
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                                                                                  16125 MW;
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                                                                                                                            86.2%;
                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-C57BL/6 X DBA/2J;
MEDLINE; 88029315.
                                                                                                                                                                                                                                                                                       STANDARD;
 41
56
70
81
115
                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                            Query Match
Best Local Similarity
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66 RFLLRY 71
                                                                                                                                                                                   1 RILLRY 6
                                                                                                                                                        5;
                                                                                                                                                                                                                                                                                    VPR2_MOUSE
P13373;
                                                    DOMAIN
DISULFID
SEQUENCE
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SEQUENCE
DOMAIN
DOMAIN
DOMAIN
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                                         DOMAIN
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Gaps

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Score 25; DB 1; Length 142; Pred. No. 25; 0; Mismatches 1; Indels

86.2%; ilarity 83.3%; Conservative (

Query Match Best Local Similarity Matches 5; Conserv

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAMERDIN J.E.;
submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: TRANSCRIPTION FACTOR WHICH BINDS SPECIFICALLY TO THE
MEPZ ELEMENT PRESENT IN THE REGULATORY REGIONS OF MANY MUSCLE-
SPECIFIC GENES. ACTIVATES TRANSCRIPTION VIA THIS ELEMENT. MAY BE
INVOLVED IN MUSCLE-SPECIFIC AND/OR GROWTH FACTOR-RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SUBUNIT: HETERODIMER.
-1- SUBCELLULAR LOCATION: NUCLEAR.
-1- TISSUE SPECIFICITY: EXPRESSED IN SKELETAL AND CARDIAC MUSCLE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS. MEF2 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      franscription regulation; Nuclear protein; DNA-binding; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLLOCK R., TREISMAN R.; "Human SRF.related proteins: DNA-binding properties and potential regulatory targets."; Genes Dev. 5:2327-2341(1991).
                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
MYOCYTE-SPECIFIC ENHANCER FACTOR 2B (SERUM RESPONSE FACTOR-LIKE
PROFIEIN 2) (XMEF2) (RSRFR2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Human myocyte-specific enhancer factor 2 comprises a group of tissue-restricted MADS box transcription factors."; Genes Dev. 6:1783-1798(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BREITBART R.E., SMOOT L.B., LEE Y., MAHDAVI V.,
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LYS-RICH (BASIC).
                                                                                                                                                                                                                      365 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-HEART, AND SKELETAL MUSCLE;
MEDLINE; 92387551.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00350; MADS_BOX_1; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X68502; CAA48515.1; -.
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HSSP; P11831; 1SRS.
                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00319; SRF-TF;
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86
31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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MEDLINE; 92084105.
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66 RFLLRY 71
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1 RILLRY
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DOMAIN
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us-08-653-294-5.rsp

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SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
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MEDLINE; 97263463
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2 RVLVRY 7
                                                                                                                                                                                                         SEZONOV G.;
Submitted (
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SEQUENCE
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  SO TENT THE PROPERTY OF THE PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
HUNGERER C., WEISS D., THAUER R.K., JAHN D.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
FUNCTION: THE 26S PROTESE IS INVOLVED IN THE REGULATORY
DESCRAPATION OF UBIOUITINATED PROTEINS. THE REGULATORY (OR ATPASE)
COMPLEX CONFERS ANT DEPENDENCY AND SUBSTRATE SPECIFICITY TO THE
26S COMPLEX (BY SIMILARITY).
-: SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
PUTATIVE 26S PROTEASE REGULATORY SUBUNIT HONOLOG MTH1011.
Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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                                                          Length 365;
                                                                                                   Indels
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68;
59008C81 CRC32;
                                                          Score 25; DB 1;
Pred. No. 67;
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90B2F3CB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TRANSFER PROTEIN TRASA.
                                                                                                                                                                                                                                                                                          372 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              415 AA.
                                                                                                   2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 25;
                                                                                                                                                                                                                                                                                            PRT;
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PFAM; PF00004; AAA; 1.
Proteasome; ATP-binding.
38638 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                372 AA; 42689 MW;
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                                                          86.2%;
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                                                                                                     4; Conservative
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                                                                                                                                                                                                                                                                                            STANDARD;
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  365 AA;
                                                          Query Match
Best Local Similarity
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Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methanobacterium
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140 RIIMRY 145
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Q07197; Q07199;
Q1-NOV-1997 (Rel
                                                                                                                                                                    |:||:|
64 RVLLKY 69
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                                                                                                                                          1 RILLRY 6
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SEQUENCE
SEQUENCE
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TRSA_STRAM
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MEDLINE; 93374848.
HAGECE J., PERNODET J.L., SEZONOV G., GERBAUD C., FRIEDMANN A., GUBRINGAU M., P., PERNODET J.L., SEZONOV G., GERBAUD C., FRIEDMANN A., Transfer functions of the conjugative integrating element pSAM2 from Streptomyces ambofactens: characterization of a kil-kor system associated with transfer.;
J. Bacteriol. 175:5529-5538(1993).
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HANLON S. P., HILL T.K., FLAVELL M.A., STRINGFELLOW J.M., COOPER R.A.;
"2-Phenylethylamine catabolism by Escherichia coli K-12: gene
organization and expression.";
Microbiology 143:513-518(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FERRANDEZ A., PRIETO M.A., GARCIA J.L., DIAZ E.;
"Molecular characterization of PadA, a phenylacetaldehyde
dehydrogenase from Escherichia coll.";
FEBS Lett. 406:23-27(1997).
                                                                                                                                                                                                                                                                                                                         Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P80666; P46884; P77637; 032557; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-JUL-1999 (Rel. 36, Last annotation update) PHENYLALCHALDEHYDE DEHYDROGENASE (EC 1.2.1.39) (PAD). FEAB OR PADA OR MAOB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Pred. No. 76;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        468A7AA2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP (POTENTIAL)
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STRAIN-W / ATCC 11105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND SEQUENCE OF 1-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; 219593; CAA79645.1; -.
PFAM; PF01580; FtsK_SpoillE; 1.
Plasmid; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 152 A
415 AA; 45263 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 86.2
Best Local Similarity 66.7
Matches 4; Conservative
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Drosophila melanogaster (Fruit fly). Bukaryota, Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta; Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

SEQUENCE FROM N.A. MEDLINE; 94261646. TISSUE-EMBRYO,

01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-EC-1998 (Rel. 37, Last annotation update)
MYOCYIE-SPECIFIC ENHANCER FACTOR 2.

515 AA

PRT;

STANDARD;

MEF2_DROME

LILLY B., GALEWSKY S., FIRULLI A.B., SCHULZ R.A., OLSON E.N.;
"D-MEF2: a MADS box transcription factor expressed in differentiating mesoderm and muscle cell lineages during Drosophila embryogenesis.";
Proc. Natl. Acad. Sci. U.S.A. 91:5662-5666(1994).

us-08-653-294-5.rsp

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                                                                                                                                                                                                                                AIBA H., BABA T., FUJITA K., HAYASHI K., HONJO A., HORIUCHI T.,
IKEMOTO K., INADA T., ISONO K., ISONO S., ITOH T., KANAI K., KASAI H.,
KASHIMOTO K., KIM S., KIMURA S., KITAGAWA M., KITAKAWA M., WAKINO K.,
MASUDA S., MIKI T., MIZOBUCHI K., MORI H., MOTOMURA K., NAKAMURA Y.,
NASHIMOTO H., NISHIO Y., OSHIMA T., SAITO N., SAMPEI G., SEKI Y.,
TAGAMI H., TAKEMOTO K., WADA C., YAMAMOTO Y., YANO M.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H -> R (IN REF. 3).
DWLDGWCETKSVCVRY -> PLAGRAGC (IN REF. 1).
FFC195E0 CRC32;
MEDLINE; 97426617.
BLATTNER F.R., PLUKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V., RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F., GRECOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J., MAU B., SHAO Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Nucleotide sequence of the gene for monoamine oxidase (maoA) from Escherichia coli.";
J. Ferment. Bloomg. 77:315-319(1994).
-!- FUNCTION: ACTS ALMOST EQUALLY WELL ON PHENYLACETALDEHYDE, 4-HYDROXYPHENYLACETALDEHYDE AND 3,4-DIHYDROXYPHENYLACETALDEHYDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- COFACTOR PREFERS NAD OVER NADP.
-!- PATHWAY: INITIAL STEPS OF 2-PHENYLETHYLAMINE CATABOLISM.
-!- SUBUNIT: HOMODIMER.
-!- SUBLINIT: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAD (ADP PART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- CATALYTIC ACTIVITY: PHENYLACETALDEHYDE + NAD(+) + H(2)O PHENYLACETALE + NADH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-K12 / W3110;
AZAKAMI H., YAMASHITA M., ROH J.-H., SUZUKI H., KUMAGAI H.,
MUROOKA Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 25; DB 1; Length 499;
Pred. No. 93;
1; Mismatches 0; Indels
                                                                                                                    "The complete genome sequence of Escherichia coll K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X99402; CAA67780.1; --
EMBL; X99402; CAA6106.1; --
EMBL; AE000235; AAC74467.1; ALT_INIT.
EMBL; D90776; CAB20903.1; ALT_INIT.
EMBL; D90777; CAB20911.1; ALT_INIT.
EMBL; D36770; -; NOT_ANNOTATED_CDS.
HSSP; P200000; 1A4Z.
ECGENE; EG13179; FEAB.
PROSITE; PS000700; ALDEHYDE_DEHYDR_CYS; 1.
PROSITE; PS000700; ALDEHYDE_DEHYDR_CYS; 1.
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BY SIMILARITY.
H -> R (IN REF
                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY PARTIAL SEQUENCE FROM N.A.
STRAIN-K12 / W3110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86.2%; 8
illarity 83.3%; F
Conservative 1;
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                   STRAIN-K12
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    RANGE SON SERVICE SON SERVICE ```

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S -> R (IN REF. 2).
PAVISRIAMVPRAG -> ASGHQQNSNGSTGS (IN
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POLY-SER.
POLY-GLY.
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Transcription regulation; DNA-binding; Nuclear
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POLY-GLN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FLYBASE: FBGN0011656; Mef2.
PROSITE: PS00350; MADS_BOX_1; 1.
PROSITE: PS50066; MADS_BOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW;
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DB 1; Length 515; 96; Score 25; Pred. No. 86.2%; 66.7%; Query Match Best Local Similarity

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Gaps

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RESULT 15 MEF2\_DROME

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0; Indels

2; Mismatches Matches 4; Conservative Qy Dp

1 RILLRY 6 |:||:| 64 RVLLKY 69

Search completed: February 8, 2000, 00:59:46 Job time: 3775 sec

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Title: Perfect score:

Run on:

Sequence:

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Searched:

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Database

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032459 actinomadur
027161 paramecium
039c18 aeropyrum p
034084 streptococc
047401 escherichia
047401 escherichia
043467 treponema p
055090 mus musculu
055231 mus musculu
055231 mus musculu
0572112 bacillus st
P90340 tomato bush
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-CWL029;
STRAIN-CWL029;
GRIMWOOD J., DAVIS R.W., STEPHENS R.S.;
"Comparative Genomes of Chlamydia pneumoniae and C. trachomatis.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AE001604; AAD18334.1; -.
Hypothetical protein.
SEQUENCE 133 AA; 16132 MW; 8DA54C6A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
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Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
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01-MAY-1999 (TrEMBLrel. 10, L
01-MAY-1999 (TrEMBLrel. 10, L
HYPOTHETICAL 16.1 KD PROTEIN.
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01-NOV-1998 (TYEMBLEEL) 01
01-NOV-1999 (TYEMBLEEL) 1
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Q9201 chlamydia p
P72007 mycobacteri
051714 pyrococcus
01635 caenorhabdi
08491 chlamydia t
Q9201 yersinia pe
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043162 homo sapien
054741 mus musculu
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087689 bacillus me
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O86766 streptomyce
O14637 homo sapien
O77624 bos taurus
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                                                     Compugen Ltd.
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                             GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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Gapop 10.0 , Gapext 0.5
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sp_phage:*
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sp_bacteria:*
sp_fungi:*
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Gaps

Score

Result No.

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is homologous to members of the prolyl oligopeptidase family
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Archaea, Euryarchaeota, Thermococcales, Thermococcaceae, Pyrococcus.
                              Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-DSM 3638;

BEDLINE; 95129900;

ROBINSON K.A., BARTLEY D.A., ROBB F.T., SCHREIER H.J.;

ROBINSON K.A., BARTLEY D.A., ROBB F.T., SCHREIER H.J.;

"A gene from the hyperthermophile Pyrococcus furiosus whose deduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Length 532;
                                                                                                                                                                                                                                                                                    PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; 295890; CAB09316.1; -.
PROSITE; PSO0455; AMP_BINDING; 1.
PRAM; PF00501; AMP-binding; 1.
                                                                                                                STRAIN-H37RV;
OLIVER K., MCLEAN J., HARRIS D.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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Pred. No. 79;
1; Mismatches (
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532 AA; 57413 MW; 7FC653FB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70867 MW; 86AC623A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 29; DB 100.0%; Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   323 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    616 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequ
01-MAY-1999 (TrEMBLrel. 10, Last ann
CO9HS.8 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene 152:103-106(1995).

EMBL; U08343; AAA73423.1; -
PFAM; PFO0326; Peptidase_S9; 1.

PFRMYS: PROU862; PEDLIGOPTASE.

SEQUENCE 616 AA; 70867 MW; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 96.6%;
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Lase 6; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROLYL ENDOPEPTIDASE
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                    SEQUENCE FROM N.A.
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334 RVLLRY 339
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of proteases.'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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Q51714;
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016335
ID 014
AC 010
DT 011
DT 010
DE C0
GN C0
OC EU
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   OC WERE RESERVED BY THE SERVED                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
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                                                                                                                                                                                                                                                                                                                     STRAIN-D/UW-3/CX;
STEPHENS R.S., KALMAN S., LAMMEL C.J., FAN J., MARATHE R., ARAVIND L.,
MITCHELL W.P., OLINGER L., TATUSOV R.L., ZHAO Q., KOONIN E.V.,
                                                                                        Ι.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                   STRAIN-D/UW-3/CX;
STEPHENS R.S., KALMAN S., LAMMEL C.J., FAN J., MARATHE R., ARAVIND
MITCHELL W.P., OLINGER L., TATUSOV R.L., ZHAO Q., KOONIN E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KALMAN S., MITCHELL W., MARATHE R., LAMMEL C., FAN J., OLINGER L., GRIMWOOD J., DAVIS R.W., STEPHENS R.S.;

"Comparative Genomes of Chlamydia pneumoniae and C. trachomatis.";

Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AE001677; AAD19103.1;

PROSITE; PS00710; PGM_PMM; 1.

SEQUENCE 458 AA, 49852 MW; 68C5A8CB CRC32;
                                                                                                                                              DAVIS R.W.;
Genome Sequence of an Obligate Intracellular Pathogen of Humans:
Chlamydia trachomatis.";
Science 0:0-0(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases EMBL; AE001354; AAC68412.1; -. PROSITE; PS00710; PGM_PMM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chlamydia pneumoniae.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NAY-1999 (TrEMBLrel. 12, Last annotation update)
PHOSPHOGLUCOMUTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
HYPOTHETICAL 57.4 KD PROTEIN.
MYCY28.13C.
Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 29; DB 2; 100.0%; Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM; PF00408; PGM_PMM; 1.
SEQUENCE 458 AA; 49391 MW; 8513D3D6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      458 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  532 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 6; Conserv
[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-CWL029;
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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413 RILLRY 418
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| 413 RILLRY 418
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RESULT P72007

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Gaps

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Length 616; Indels Caenorhabditis elegans. Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;

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Gaps

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Indels

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RAKIN A.V., PELLUDAT C., NOELTING C., SCHUBERT S., JACOBI C.,
HEESEMANN J.,
HEESEMANN J.,
You specific characteristics of the high-pathogenicity island
of Yersinia enterocolitica.",
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ132668, CAB46573.1;
EMBL, FRO021I; ABC_TRANSPORTER: 1.
Lipoprotein: ATP-binding; Transport.
SEQUENCE 600 AA: 66413 WW; E074027F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEHRING A.M., DEMOLL E., FETHERSTON J.D., MORI I., MAYHEW G.F.,
BLATTNER F.R., WALSH C.T., PERRY R.D.;
"Iron acquistino in plague: modular logic in enzymatic biogenesis of
yersiniabactin by Yersinia pestis.";
Chem. Biol. 5:573-586(1998).

EMBL; AF091251; AAC69585.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                               YBIP.
Yersinia pestis.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Yersinia.
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Pred. No. 1.3e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.1%; Score 27; DB 2; Length 600;
83.3%; Pred. No. 1.3e+02;
.ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
LIPOPROTEIN INNER MEMBRANE ABC-TRANSPORTER, IRP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66284 MW; D8692F0B CRC32;
                                                                                                                                                                                                                               600 AA.
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                                                                                                                                                                                                                                                                                                Created)
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                                                                                                                                                                                                                                                          09ZG01;
01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-NOV-1999 (TrEMBLrel. 12,
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83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 83.3
Matches 5; Conservative
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                                                                                                                                                                                                                               PRELIMINARY;
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Best Local Similarity F
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388 RLLLRY 393
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388 RLLLRY 393
                                     |:||||
19 RLLLRY 24
1 RILLRY 6
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SEQUENCE 60
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01-NOV-1999
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Q9X915
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Q9ZG01
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                                                                                     RA MELSON R., ANDERSON K., BAYNES C., BERKS M.,
RALLSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA GONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER M., JOHNSTON L.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA LIGHTNING J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA PARSONS J., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIBRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON J.,
RA WATSON A., WEINSTON L., WILKINSON-SPROAT J., WOHLDMAN P.;
R. HEINSTON R., WILKINSON-SPROAT J., WOHLDMAN P.;
R. LIGHTNING J., LAISTER M., WATERSTON R.,
RA WATSON A., WEINSTONE L., WILKINSON-SPROAT J., WOHLDMAN P.;
R. LIGHTNING J., WATERSTON R.,
RA WATSON R., WATERSTON R.,
RA WATSON R., WATERSTON R.,
RA WATSON R
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-D/UW-3/CX;
STRAIN-D/UW-3/CX;
STRAIN-D/UW-3/CX;
MITCHELL W.P., OLINGER L., TATUSOV R.L., ZHAO Q., KOONIN E.V.,
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STEPHENS R.S., KALMAN S., LAMMEL C.J., FAN J., MARATHE R., ARAVIND L.,
MITCHELL W.P., OLINGER L., TATUSOV R.L., ZHAO Q., KOONIN E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome Sequence of an Obligate Intracellular Pathogen of Humans: Chlamydia trachomatis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Pred. No. 75;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-BRISTOL N2;
LD T.T., WATERSTON R.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF016433; AAB65392.1; -.
PFAM; PF01461; 7tm_4; 1.
SEQUENCE 323 AA; 37314 MW; 0AC10232 CRC32;
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Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AR001322; AAC68084.1;
Hypothetical protein.
SEQUENCE 332 AA; 38649 MW; B5C59CE9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TEMBLrel. 08, Last annotation update)
HYPOTHETICAL 38.6 KD PROTEIN.
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 27; DB 5;
Pred. No. 73;
1; Mismatches
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83.3%;
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83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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Best Local Similarity
Matches 5; Conser
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177 RLLLRY 182
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Medicago sativa (Alfalfa).
Eukaryophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
core eudicots; Rosidae; eurosida I; Fabales; Fabaceae; Papillionoideae;
                                                                                                                                                                                                                                                            KOVACS I., AYAYDIN F., OBERSCHALL A., IPACS I., BOTTKA S., PONGOR S., DUDITS D., CSORDAS TOTH E.;
"Immunolocalization of a novel annexin-like protein encoded by a stress and abscistc acid responsive gene in alfalfa.";
Plant J. 15:185-197(1998).
EMBL; Y11348: CAA72183.1;
HSSP; P13214; 1AOW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSET J., COOLESON A.,
CRAATON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HARKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSIAM J., KIRSTEN J., LAISTER M., LAIREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTHMORE B., O'CALLAGHAN M.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SILJSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
MATSON A., WEINSTOCK L., WILKINGON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 26; DB 10; Length 333;
Pred. No. 1.3e+02;
1; Mismatches 0; Indels
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STRAIN-BRISTOL N2;
WATERSTON R.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U23524; AAC46820.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to the EMBL/GenBank/DDBJ databases.
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
CODED FOR BY C. ELEGANS CDNA CM20B2.
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                          333 AA; 37934 MW; 62598772 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.78;
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Best Local Similarity 83.3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
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                                                          ANNEXIN-LIKE PROTEIN
                                                                                                                                                                                                                SEQUENCE FROM N.A.
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MEDLINE; 98388649.
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146 KILLRY 151
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                                                                                                                                                                              Medicago.
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MEDICINE; 97400527.

FERRIGNO O., VIROLLE T., GALLIANO M.F., CHAUVIN N., ORTONNE J.P.,
FERRIGNO C., VIROLLE T., GALLIANO M.F., CHAUVIN N., ORTONNE J.P.,
"Murine laminin alpha3A and alpha3B isoform chains are generated by
usage of two promoters and alternative splicing.";
J. Biol., Cham. 272:20502-20508(1997).

EMBL; Y08850; CAA70073.1;
MGD; MI:99909; Lama3.

MON_TER 42

A2

SEQUENCE 42 AA; 4872 MW; 42FE6150 CRC32;
                                                                                                                                                                                                                                                                                                        TISSUE-BRAIN;
TISSUE-BRAIN;
TISSUE-BRAIN;
TANAKA K., NAGASE T., NAKAJIMA D., SEKI N., OHIRA M., MIYAJIMA
TANAKA A., KOTANI H., NOMURA N., OHARA O.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AB007895; BAA23708.1; --
SEQUENCE 777 AA; 86654 MW; 99B863D5 CRC32;
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia, 
Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.1%; Score 27; DB 4; Length 777;
83.3%; Pred. No. 1.7e+02;
ative 1; Mismatches 0; Indels
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Pred. No. 17;
1; Mismatches 0; Indels
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01-JUN-1998 (TIEMBLREL. 06, Last sequence update)
01-NOV-1999 (TIEMBLREL. 12, Last annotation update)
LAMININ, ALPHA 3 (LAMININ 5 ALPHA3C CHAIN) (FRAGMENT).
                                                                                                                                      Last sequence update)
Last annotation update)
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                                                                              777 AA
                                                                                                                      Created)
                                                                                PRT;
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Best Local Similarity 83.3
Matches 5; Conservative
                                                                              PRELIMINARY;
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                                                                                                                                                                                                                Homo sapiens (Human).
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Best Local Similarity
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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|179 RILIRY 184
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26 RIVLRY
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RESULT 12 Q9ZR53

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89.7%; Score 26; DB 2; Length 540; llarity 83.3%; Pred. No. 2.1e+02; Conservative 1; Mismatches 0; Indels
                                                                        SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE; 98416126.

RAUX E., LANOIS A., WARREN M.J., RAMBACH A., THERMES C.;

"Cobalamin (vitamin B12) biosynthesis: identification and
enarcterization of a Bacillus megaterium cobi operon.";

Biochem. J. 335.159-166(1998).

EMBL; AJ000758; CAA04307.1;

Methyltransferase.

SEQUENCE 540 AA; 59510 MW; BA79DD3D CRC32;
        Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: February 8, 2000, 13:17:31
Job time: 32480 sec
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Best Local Similarity
Matches 5; Conserv
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|182 RILLKY 187
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        OC REPRENT SERVICE SOUTH SERVICE SERVI
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 96181548.
PHILIPP W.J., POULET S., EIGLMEIER K., PASCOPELLA L.,
BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
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Pred. No. 2e+02;
2; Mismatches 0; Indels
                                                                                                                       Length 383
                                                                                                                  Score 26; DB 5; Length 383
Pred. No. 1.5e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=H37RV;
BADCOCK K., CHURCHER C.M.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-H37RV;
COLE S.T., PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
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EMBC: ALO22022; CAA17743.1; -.
HSSP: P08659; LLCI.
PROSTE: PS00455; AMP_BINDING; 1.
PFAM; PF00501; AMP-binding; 1.
EC82938A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53738 MW; D3CF89C5 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
43263 MW;
                                                                                                                  Query Match 89.7%;
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-NOV-1999 (TrEMBLrel. 12, PUTATIVE COA-LIGASE.
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Best Local Similarity 66.7%;
Matches 4; Conservative
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    383 AA;
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SEQUENCE FROM N.A.
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Created)
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087689 PRELIMINARY; 087689; 01-NOV-1998 (TrEMBLrel. 08, C 01-NOV-1998 (TrEMBLrel. 08, L 01-NAY-1999 (TrEMBLrel. 10, L PRECORRIN-3 METHYLASE.

RESULT 15 087689 AC 087689; DT 01-NOV. DT 01-NAV. DF PRECORI GN CBIH60 GN Bacillito OC Bacteri

ò 셤 540 AA

PRT;

Bacillus megaterium. Bacteria; Firmicutes; Bacillus/Clostridium group;

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E13232 PaMMY RNA2 encoding
AB013616 Broad bean wilt vi
AB011007 Patchouli mild mos
                                                                                    HUMSWX2 130 bp DNA STS 12-JUN-1993
HUMBAN Chromosome X STS 8WXD2; single read, sequence tagged site.
L15224
L15224.1 GI:292679
STS: notion-1
                                                                                                                                                                                                                                                                                     Kere, J., Nagaraja, R., Mumm, S.R., Ciccodicola, A., D'Urso, M. and Schlessinger, D. Mapping human chromosomes by walking with sequence-tagged sites from end fragments of yeast artificial chromosome inserts Genomics 14, 241-248 (1992)
                                                                                                                                                                                                                                                                                                                                                                                      Submitted by: David Schlessinger,
Center for Genetics in Medicine,
Washington University School of Medicine, Box 8232 4566 Scott
Avenue, St. Louis, MO 63110, USA
e-mail: davids@wugenmail.wustl.edu
Primer A: CICTIGAGGATTTACIGAG
Primer B: ATTCCAGTGGAATTCTC
STS Size: 125bp.
                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 130)
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Percent Identity: 100.000
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Homo sapiens DNA.
Homo sapiens
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for
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="Xq27"
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Annealing:
Polymerization: 72 degrees C 11
POR Cycles: 35
Thermal Cycler: P-E.
Location/Qualifiers
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40 pmoles/100ul
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/standard_name="sWXD2"
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TrisHCl:
Taq Polymerase: 0
NH4Cl:
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Quality: 29.00
Ratio: 4.833
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PCR Profile:
Denaturation:
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US-08-653-294-5 x HUMSWX2
                                                                                                    seq_documentation_block:
                                                                    seq_name: gb_sts:HUMSWX2
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Primer B:
STS size:
Template:
Primer:
dNTPs:
MGC12:
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primer_bind
BASE COUNT 3
 gb_pat:E13232
gb_v1:AB013616
gb_v1:AB011007
                                                                                                                  LOCUS
DEFINITION
ACCESSION
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KEYWORDS
SOURCE
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MEDLINE
COMMENT
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AF049680 Neotyphodium lolii str
AF049681 Epichloe typhina x Neo
AF064081 Epichloe typhina x neo
AJ008203 Homo sapiens mRNA for
AJ244960 Homo sapiens mRNA for
G14238 human STS SHGC-7374 clon
AJ229903 Kluyveromyces lactis I
AF065445 Homo sapiens clone 45u
AF056445 Homo sapiens clone 45u
G23069 human STS WI-12710, sequ
AJ229696 Kluyveromyces lactis I
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D50468 Arabidopsis thallana mR
AF000270 Borrella burgdorferi
X86442 G.max END040-2 gene. 7/
X70659 C.albicans 25s TRNA. 2/
1219136 S.pombe 255 TRNA gene.
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-MODEL=frame+_p2n.model_DEV=xlp
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-MODEL=frame+_p2n.model_DEV=xlp
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-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -OGAPOP=4.500
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-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cd1
-LIST=45 -DOCALIGG=200 -TRR_SCORE=pct -ALIGN=15 -MODE=LOCAL
-OUTFMT=pfs -NORM=ext -MINLEN=0 -MAXLEN=1000000 -USER=US08653294
-NCPU=6 -ICPU=3 -NO_XLPXY -WAIT -THREADS=1
                                                                 About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
 out_format : pfs
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OM of: US-08-653-294-5 to: GenEmbl:*
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Database length: -1518192014
Search time (sec): 11370.480000
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                                 Date: Feb 8, 2000 4:37 PM
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Query: US-08-653-294-5
Query length: 6
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9b_pr2: pTTRGC

9b_pr2: AFC049681

9b_pr1: AFC049681

9b_pr1: AFC049681

9b_pr1: AFC049681

9b_pr1: HSAJ8203

9b_pr2: G1418

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9b_pr1: AFC050465

9b_pr1: AFC050805

9b_pr1: GG28FN

9b_pr1: GG28FN

9b_pr1: GG28FN

9b_pr1: GG28FN

9b_pr1: GG28FN

9b_pr1: AFCSFNA

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gb_ba1:ECRFBG
gb_ba1:BACASPKIN
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gb_ba2:BBAF000270
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gb_pll:SP25SRNAA
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gb_ph:BPA118PLY
gb_pl1:ATAATP2
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29 CGAATTCTGCTTCGGTAT 12
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Ganley, A.R.D. and Scott, D.B.
Direct Submission
Submitted (23-FEB-1998) Institute of Molecular and Bio Sciences,
Massey University, Private Bag 11222, Palmerston North, New Zealand
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (26-APR-1995) M. Lefranc, Lab d'Immunogenetique
Submitted (26-APR-1995) M. Lefranc, Lab d'Immunogenetique
Moleculaire LIGM, Inst de Genetique Moleculaire, UMR 9942, BP 5051,
1919 Route de Mende, F-34033 Montpellier cedex 1, FRANCE
1. 166
1. 166
/organism="Pen troglodytes"
/db_xref="taxon:9598"
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Noctyphodium lolii strain Lp5 large subunit ribosomal RNA gene, partial sequence.
AF049680 GI:2944414
                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Vertebrata; Mammalla; Eutherla; Primates; Catarrhin; Hominidae; Pan.

1 (bases 1 to 166)
2hang, X.M., Cathala, G., Soua, Z., Lefranc, M.P. and Huck, S.
The human T-cell receptor gamma variable pseudogene V10 is a distinctive marker of human speciation
Immunogenetics 43 (4), 196-203 (1996)
                                                               21-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypocreales;
Neotyphodium
                                                               PTTRGC 166 bp mRNA P.troglodytes mRNA for TcR gamma constant chain.
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Neotyphodium lolii
Eukaryota: Fungi; Ascomycota; Pyrenomycetes;
Clavicipitaceae; anamorphic clavicipitaceae;
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Percent Identity: 100.000
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/note="C-segment"
/product="TcR gamma constant chain"
/product="TcR gamma constant chain"
                                                                                                                                   TCR gamma chain constant region; TRGC gene.
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/gene="TRGC"
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/gene="TRGC"
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                                                                                                                 X86723.1 GI:1568526
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Percent Similarity: 100.000
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LOCUS AF049680
                                               seq_documentation_block:
               seq_name: gb_pr2:PTTRGC
                                                                                                                                                      chimpanzee
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AUTHORS
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AUTHORS
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JOURNAL
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Epichloe typhina x Neotyphodium lolii.
Epichloe typhina x Neotyphodium lolii
Euchloe typhina x Neotyphodium lolii
Euchloe typhina x Seconycota: Pyrenomycetes; Hypocreales;
Clavicipliaceae; Epichloe.
1 (bases 1 to 210)
Canley, A.R.D. and Scott, D.B.
Direct Submission
Direct Submission
Submitted (23-FEB-1998) Institute of Molecular and Bio Sciences,
Massey University, Private Bag 11222, Palmerston North, New Zealand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS AF049679 210 bp DNA
DEFINITION Epichloe typhina x Neotyphodium lolii strain Lp1 large subunit
ribosomal RNA gene, partial sequence.

    210
    Acrganism="Epichloe typhina x Neotyphodium lolii"
/strain="Lp1"
/db_xref="taxon:71426"

                                                                                                            from ntsl-nts2"
1. :204
/organism="Neotyphodium loli!"
/strain="Lp5"
/db_xref="taxon:73839"
/note="asexual form; PCR product from nt
<l. .>204
/note="from 3' region"
/note="from 3' region"
/product="large subunit ribosomal RNA"
5 a 45 c 66 g 47 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="large subunit ribosomal RNA"
48 c 68 g 47 t
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                                                                                                                                                                                                                                                                                                                                             Mercent Identity: 100.000
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Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to reverse of: AF049680 from: 1
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US-08-653-294-5 x AF049680/rev
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US-08-653-294-5 x. AF049679/rev
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1 ArgileLeuLeuArgTyr 6
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Ratio: 4.833
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-08-653-294-5 x HSAJ8203
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AUTHORS
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                                                                                                                                                                                                           ORIGIN
                                                                                                                          Epichloe typhina.
Epichloe typhina.
Epichloe typhina
Eukaryota; Fungi; Ascomycota; Pyrenomycetes; Hypocreales;
Claviciptaceae; Epichloe.
1 (bases 1 to 210)
Ganley, A.R.D. and Scott, D.B.
Garley, A.R.D. and Scott, D.B.
Direct Submission
Submitted (23-FEB-1998) Institute of Molecular and Bio Sciences,
Massey University, Private Bag 11222, Palmerston North, New Zealand
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 300)
Gellrich, S., Rutz, S., Borkowski, A., Golembowski, S.,
Gromnica-Ihne, E., Sterry, W. and Jahn, S.
Analysis of VHDJH gene transcripts in B cells infiltrating salivary
glands and lymph node tissue in patients with Sjoegren's syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (26-APR-1998) Jahn S., Department of Dermatology, Medical Faculty (Charite), Humboldt University Berlin, Schumannstr. 20/21, 10117 Berlin, GERMANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
LOCUS HSA/8203 300 bp mRNA PRI 29-APR-1998
DEFINITION HOMO sapiens mRNA for immunoglobulin heavy chain, VHDJH
rearrangement: VHLI46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 300)
Jahn, S.
               AF049681 210 bp DNA PLN 10-WAR-199
Epichloe typhina strain E8 large subunit ribosomal RNA gene,
                                                                                                                                                                                                                                                                                                                       1. 210
/organism="Epichloe typhina"
/strain="E8"
/db_xref="taxon:5113"
/note="sexual form; PCR product from nts1-nts2"
                                                                                                                                                                                                                                                                                                                                                                                                          /Note="from 3' region"
/note="from 3' region"
/product="large subunit ribosomal RNA"
/AR c 68 g 47 t
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Gaps: 0
Percent Identity: 100.000
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="14"
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IGH; immunoglobulin heavy chain.
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                                                                         ĀF049681
AF049681.1 GI:2944415
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Ratio: 4.833
Percent Similarity: 100.000
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                                                         partial sequence.
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seq_documentation_block:
LOCUS AF049681
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Quality:
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                                   DEFINITION
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ORIGIN
                                                                       ACCESSION
VERSION
KEYWORDS
SOURCE
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AUTHORS
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AUTHORS
TITLE
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Dono,M., Zupo,S., Chlorazzi,N. and Ferrarini,M.
Heterogeneity of tonsilar subepithelial B lymphocytes, the splenic marginal zone equivalents
Unpublished
(bases 1 to 360)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (24-MAY-1999) Dono M., Istituto Nazionale per la Ricerca sul Cancro, Immunología Clinica, L.go Rosanna benzi 10- Genova,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="immunoglobulin mu heavy chain variable region"
/protein_id="CaB44095.1"
/db_xref="GI:4995380"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Product="immunoglobulin mu heavy chain variable region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seg_documentation_block:
LOCUS
LOCUS
DEFINITION Home sapiens mRNA for immunoglobulin mu heavy chain variable
region, partial, clone 1-B73.
ACCESSION AJ244960
VERSION AJ244960.1 GI:4995379
KEYWORDS IGM: 19M heavy chain; immunoglobulin mu heavy chain; variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 360)
                                                                                                                                                          /product-"immunoglobulin heavy chain"
1. .300
                                                                                                                                                                                                                                                                                                                                       Length: 6
Gaps: 0
Percent Identity: 100.000
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1. .360
Corganism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="14"
                                                                                     /tissue_type="lymph node"
<1. .>300
/gene="VHDJH"
/sex="Female"
/cell_type="B lymphocyte"
/dev_stage="adult"
/map="q32.33"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="tonsil"
/cell_type="B-lymphocyte"
/clone="1-B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="IGHV4-34"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="IGHV4-34"
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                                                                                                                                                                                                    /gene="VHDJH"
78 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rearranged,
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NIGMS Human/Rodent Somatic Cell Hybrid Panel #1, Coriell Institue for Medical Research, Camden, NJ 08103.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLAJ9903 436 bp DNA STS 20-NOV-1998
Kluyveromyces lactis DNA fragment for sequence tagged site, clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kluyveromyces lactis.
Kluyveromyces lactis
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 436)
Ozier-Kalogeropoulos, O., Malpertuy, A., Boyer, J., Tekaia, F. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomycetaceae; Kluyveromyces.

1 (bases 1 to 436)
Ozier-Kalogeropoulos, O.
Direct Submission
Direct Submission
Submitted (28-MAY-1998) Ozier-Kalogeropoulos O., Institut
Genetique Moleculaire des Levures25 rue de Dr Roux, 75724
cedex 15 FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Random exploration of the Kluyveromyces lactis genome and comparison with that of Saccharomyces cerevisiae Nucleic Acids Res. 26 (23), 5511-5524 (1998) 99045620
                                                                                                                                          3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: 436
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Gaps: 0
Percent Identity: 100.000
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Gaps: 0
Percent Identity: 100.000
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/strain="CBS2359"
/db_xref="taxon:28985"
/clone="22"
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                          1. 400
/organism="Homo sapiens"
186. 337
186. 206
                                                                                                                                        111
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88 g
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                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to reverse of: G14238
                                                                                                                       complement(317,
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US-08-653-294-5 x KLAJ9903/rev
                                                                                                                                                                                                                                                                                                                                                                                            388 AGAATCCTCTTGAGGTAT 371
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US-08-653-294-5 x G14238/rev
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Ratio: 4.833
Percent Similarity: 100.000
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Ratio: 4.833
Percent Similarity: 100.000
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LOCUS KLAJ9903
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                                                                                                       primer_bind
primer_bind
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                                      FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Gnathostomata; Ostelchthyes; Sarcopterygil; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Catarrhini; Hominidae; Homo.
1 (bases 1 to 400)
 /translation="OVOLQOMGAGLLkPSESISLTCAVYGGSLSGYYMSWIRQPPGKG
LEWIGEINYSGSTINYNSLKSRYTISVDTSKSQFSLKLTSVTAADTAVYWCARGNEAG
YYGMDWWGGGTTVYYS" 75 t
1 13 g 75 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid clones, generated from a lymphoblastoid cell line from a human male. Localized to human chromosome 17 by analysis on the
                                                                                                                                                                                                                                                                                                                                                                                                           22-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seconds
seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Initial incubation: 94 degrees C for 90 seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford Human Genome Center (SHGC)
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259689
Fax: 4157259689
Email: myers@shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               degrees C for 15
degrees C for 23
degrees C for 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94 degrees C for 15
62 degrees C for 23
72 degrees C for 30
30
Perkin Elmer 9600
                                                                                                                                      Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                           SIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STS sequence; primer; sequence tagged site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 ng
each 1 uM
each 200 uM
0.05 units/ul
10 ul
                                                                                                                                                                                                                                                            to: 360
                                                                                                                                                                                                                                                                                                                                                                                                                         human STS SHGC-7374 clone pG-3478.
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Primer B: AGGCCTATGCTCCCTCAATAA
STS size: 152
PCR Profile:
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50 mM
20 mM
8.3
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Total Vol:
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G14238.1 GI:1129977
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Percent Similarity: 100.000
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US-08-653-294-5 x HSA244960
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dNTPs:
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LOCUS G14238
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                                                                                                                                        Quality:
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COMMENT
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Pasteur, Paris

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL REFERENCE AUTHORS TITLE

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2. (bases 1 to 443)
Simmons,A.D. and Lovett,M.L.
Simmons,A.D. and Lovett,M.L.
Submitted (31-MAR-1998) Department of Otorhinolaryngology,
Molecular Biology and Oncology, The McDermott Center, University of
Texas Southwestern Medical Center, 5323 Harry Hines Boulevard,
Dallas, Tx 75235-8591, Use
                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 443)

2 immons, A.D. and Lovett, M.L.

High resolution physical and transcription maps of the Cri-du-chat critical region

Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Whitehead Institute/MIT Center for Genome Research; Physically
AFO56445 443 bp mRNA PRI 16-MAY-1998
Homo sapiens clone TCB1 Cri-du-chat critical region mRNA.
AFO56445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Primates, Catarrhini, Hominidae, Homo.
I (bases 1 to 455)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            623069 455 bp DNA STS 31-MAY-1: human STS W1-12710, sequence tagged site. 623069 623069.1 GI:1343395 STS; STS sequence; primer; sequence tagged site. human STSs derived from sequences in dbEST and the Unigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Whitehead Institute/MIT Center for Genome Research Whitehead Institute for Biomedical Research Cambridge Center, Cambridge MA 02142 USA Tel: 617 252 1900
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Gaps: 0
Percent Identity: 100.000
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143 c 55 g 137 t
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                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               /chromosome="5'
/map="5p15.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="TCB1"
1. .443
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                                                       AF056445.1 GI:3044163
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US-08-653-294-5 x AF056445/rev
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Ratio: 4.833
Percent Similarity: 100.000
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LOCUS G23069
                                                                                                               Homo sapiens
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GGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSLKSRVTISVDTSKNQFSLK
LSSVTAADTAVYYCARDHVVVVAAPEYYYGMDVWGQGTTVTVSSG"
                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 441)
Wang, X. and Stollar.b.D.
Autoreactivity and immunologlobulin VH gene expression in aging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="immunoglobulin heavy chain variable region"
/protein_id="AAC18184.1"
/db_xref="GI:3170759"
                                                                                                                            AF062148 441 bp mRNA PRI 02-JUN-1998
HOmo sapiens clone 45u-23 immunoglobulin heavy chain variable region (IGH) mRNA, partial cds.
AF062148 GI:3170758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="45u-23"
/cell_type="peripheral B lymphocyte"
/tissue_type="blood"
/note="from elderly repertoire 45u"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="14"
/map="14432.33"
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/gene="IGH"
58. .>441
/gene="IGH"
a 126 c
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/gene="IGH"
                        147 CGAATICTGCTTCGGTAT 130
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Percent Similarity: 100.000
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     1 ArgileLeuLeuArgTyr
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                                                                          seq_name: gb_pr3:AF062148
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LOCUS AF062148
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source

FEATURES

gene

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31-MAY-1996

V\_region

BASE COUNT

us-08-653-294-5.rge

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Hampea appendiculata.

SM Hampea appendiculata.

Eukaryoriata; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryoria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; eughyllophytes; Spermatophyta; Majooliophyta; eudicotyjedons; Core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Hampea.

E. 1 (bases 1 to 588)

Seelanan, T., Wendel, J.F. and Schnabel, A. Congruence and consensus in the cotton tribe: Evidence from the nuclear and plastid genomes

Inclear and plastid genomes

In Syst. Bot. (1996) In press

E. 2 (bases 1 to 588)

Seelanan, T., Wendel, J.F. and Schnabel, A. Direct Submission

L. Submitted (25-ARR-1996) T. Seelanan, Botany, Iowa State University, Ames, IA 50011, USA

Ames, IA 50011, USA

    .588
    /organism="Hampea appendiculata"
    /db_xref="taxon:47613"
    /note="Hampea appendiculata (J. Donnell-Smith) Standley"

             Random exploration of the Kluyveromyces lactis genome and comparison with that of Saccharomyces cerevisiae Nucleic Acids Res. 26 (23), 5511-5524 (1998) 99045620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAU56781 588 bp DNA PLN 01-NOV--
Hampea appendiculata 5.8S ribosomal RNA gene and internal
transcribed spacer 1 and 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note-"internal transcribed spacer 1"
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/note="internal transcribed spacer 2"
158 c 145 g 139 t
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Percent Identity: 100.000
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Gaps: 0
Percent Identity: 100.000
                                                                                                    1. .455
/organism="Kluyveromyces lactis"
/strain="CBS2359"
/db_xref="taxon:28985"
/clone="22"
<1. >455
9 a 115 c 96 g 115 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219. .382
/note="5.8S ribosomal RNA"
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                                                                                       Location/Qualifiers
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Percent Similarity: 100.000
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Percent Similarity: 100.000
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US-08-653-294-5 x KLAJ9696
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LOCUS HAU56781
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Dujon, B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
TITLE
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                                                 JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
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                 TITLE
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Paris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kluyveromyces lactis.
Kluyveromyces lactis
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 455)
Ozler-Kalogeropoulos, O., Malpertuy, A., Boyer, J., Tekala, F. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLAJ9696 455 bp DNA STS 20-NOV-199
Kluyveromyces lactis DNA fragment for sequence tagged site,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (28-MAY-1998) Ozier-Kalogeropoulos O., Institut
Genetique Moleculaire des Levures25 rue de Dr Roux, 75724
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. 455.
/organism="Homo sapiens"
/db xref="taxon:9606"
/map="750.8 cR from top of Chrl linkage group"
19. .42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           others
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Derived from dbEST (genbank accession H49567)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 6
Gaps: 0
Percent Identity: 100.000
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                                Primer A: CAGTITITAGIGGACATIGIGAGG
Primer B: AACAGCIGCIGCCCTCAG
STS size: 127
PCR Profile:
                                                                                                                                                                                                                                  Template: 10 ng
Primer: each 5 pM
dNTPs: each 4 nM
Taq Polymerase: 0.025 units/ul
Total Vol: 20 ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomycetaceae; Kluýveromyces.
1 (bases 1 to 455)
Ozier-Kalogeropoulos,O.
Email: thudson@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(128. .145)
106 c 118 g
                                                                                                                                          Annealing: 56 degrees C
Polymerization:
PCR Cycles: 35
Thermal Cycler:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to reverse of: G23069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AJ229696
AJ229696.1 GI:3820146
                                                                                                                                                                                                                                                                                                                                                              MGC12: 1.5 mM
KC1: 50 mM
Tris-HCL: 10 mM
                                                                                                                       Denaturation:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     321 AGAATCTTACTCAGGTAT 304
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Ratio: 4.833
Percent Similarity: 100.000
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US-08-653-294-5 x G23069/rev
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                                                                                                            resoak:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
LOCUS KLAJ9696
                                                                                                                                                                                                                                                                                                                                                                                                                       pH: 9.3
                                                                                                                                                                                                                     Protocol:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104
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primer_bind
BASE COUNT
ORIGIN
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VERSION
KEYWORDS
SOURCE
ORGANISM
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TITLE
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AUTHORS
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10.77

alignment\_block: US-08-653-294-5 x HAU56781/rev

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Genoscope.

Direct Submission

Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage :
Submitted (01-SEP-1999) Genoscope - Centre Sequencage :
CP 5706 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
The CDNA library to be analyzed within the framework of this project was created using a Bortytis chnerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant.
The library was produced in an oriented direction, in the pBSII
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; rungi; Ascomycota; Euascomycetes; Discomycetes; Leotiales; Sclerotiniaceae; Botryotinia.

[ (bases 1 to 636)
Bitton,F., Levis,C., Fortini,D., Pradier,J.M. and Brygoo,Y. Direct Submitsaton
Submitted (01-5EP-1999) Phytopathologie, INRA, route de St Cyr, 78026 versailles, France
2 (bases 1 to 636)
                                                                                                                                                                                BOLYPYD 636 bp mRNA PLN 02-SEP-1999
BOLYPIS cinerea strain T4 cDNA library under conditions of nitrogen deprivation.
AL111345.1 GI:8825964
CDNA library; nitrogen deprivation.
Botryotinia fuckeliana.
Botryotinia fuckeliana
Eukaryora: "...,"
Align seg 1/1 to reverse of: HAU56781 from: 1 to: 588
                                          seq_name: gb_pl2:CNS01995
                                                                                                                                                                                            LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
TITLE
JOURNAL
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TITLE
JOURNAL
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KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMMENT
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/note="Genoscope sequence ID : W69H121" 133 c 172 g 168 t 1 others

162

BASE COUNT ORIGIN

Location/Qualifiers
1. 636
7. organism-"Botryotinia fuckellana"
/strain-"T4"
/db\_xref-"taxon:40559"

source

FEATURES

alignment\_block: US-08-653-294-5 x CNS01995/rev

to: 636 Align seg 1/1 to reverse of: CNS01995 from: 1

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pPIC9/ELF25L cDNA construct
Neisseria meningitidis clas
Neisseria meningitidis clas
Neisseria meningitidis clas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polynucleotide(s) and proteins derived from Staphylococcus aureus -
stored on computer readable medium and used in the production of
anti-S.aureus vaccines
Claim 1; Page 1600-1601; 3271pp; English.
Claim 2; Page 1600-1601; 3271pp; English.
Claim 3; Page 1600-1601; 3271pp; English.
Claim 3; Page 1600-1601; 3271pp; English.
Claim 4; Proferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are be used in a vaccine composition against 5 aureus infection of be used in a vaccine composition against 5 aureus infection of composition against 5 aureus infection of composition and succined skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides of and their fragments) are useful as primers or probes for isolating composition and production of the polypeptides of any of the S.aureus DNA sequences contained on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IncontintyQualifiers

181. .240
/*tag= a
/note= "these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus contig SEQ ID #681.
Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
Staphylococcus aureus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC.
Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 6
Gaps: 0
Percent Identity: 100.000
        8598
8974
9156
9191
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.8e+03
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        81.19
80.84
80.67
80.64
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                                                                                                                                                                                                                                                                                                                  V74992 standard; DNA; 863 BP
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Sequence 863 BP; 252 A;
                                                                                                                                                                                                                                                                                                                                                                                                16-MAR-1999 (first entry)
    27.00
27.00
27.00
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Ratio: 4.833
Percent Similarity: 100.000
                                                                                                                                                                                                seq_name: N_Geneseq_36:V74992
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US-08-653-294-5 x V74992/rev
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07-JAN-1997; 100117.
05-JAN-1996; US-009861
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N_Geneseq_36:V28852
N_Geneseq_36:T77819
N_Geneseq_36:T77817
N_Geneseq_36:T77818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
misc_feature
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                                                                                                                                                                                                                                                                                                                      1688 | Human secreted protein gene 11 1688 | Human secreted protein gene 11 2123 | Borrella burgdorferl polynucle 2223 | Aspartokiaase II gene. DNA end 2223 | Aspartokiaase II gene. DNA end 3907 | Enterococus faecalis genome 4256 | Total contiguous sequence determined 15614 | Enterococus faecalis genome 675 | Total contiguous sequence determined 15614 | Enterococus faecalis genome 67 | Haemophilus influenzae 15 kD ou 2960 | Hastamine HI receptor coding 8 4617 | Rat tripeptidylpeptidase II cD 5072 | CDNA encoding C. elegans UNC-5073 | CDNA encoding C. elegans UNC-5109 | Rat brain homologue of serine 7474 | Plasmid prB13 aused for overedut 1 | Plasmid prB13 aused for overedut 1 | Plasmid prB12 encoding C. elegans UNC-5109 | Plasmid prB12 encoding C. elegans UNC-51000 | Continuation (6 of 17) of 11000 | Continuation (6 of 17) of 1109 | Sequence for a synthetic lacping Synthetic pul gene with pilo 5 Staphylococcus aureus contig 5 | Staphylococcus aureus contig 5 | Clostridium botulinum type D t 2214 | New DNA sequence isolated from 2659 | Plichla pastoris HIS4 gene. Polated from 2011 | New DNA sequence isolated from 2011 | New DNA sequenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ocumentation ...
Staphylococcus aureus contig SE Staphylococcus aureus contig SE Human secreted protein gene il Borrella burgdorferi polynucle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid pWI1802 encoding Trich
Plasmid pHIL-D2 used for expre
Plasmid pHIL-D2 (MFalphaPrePrd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmid pHIL-D2 (MFalphaPrePro
Plasmid pD2pick(MFalphaPrePro:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trichoderma harzianum mutanase
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Protein PR0326 cDNA clone DNA
Mouse 1-alpha-OHase promoter
                                                                                                                                                                                                                                                     Command line parameters:
-MODEL-frame+_p2n.model -DEV-xlp
-MODEL-frame+_p2n.model -DEV-xlp
-MODEL-frame+_p2n.model -DEV-xlp
-MODEL-frame+_p2n.model -DEV-xlp
-MODEL-frame+_p2n.model -DEV-xlp
-MODEL-GPTO_SPOOL/W1080853294/runat_04024000_160701_15807/app_query.fasta.1
-DB-M_Geneseq_36 -OEMT-fastap -SUFFTX=rng -GAPOP=12.000
-GAPOPT-6.000 -MINMATCH=0.100 -LOOPCL=0.000 -XGAPEXT=0.500
-FGAPOP-6.000 -FGAPEXT=0.050 -XGAPOP-10.000 -XGAPEXT=0.500
-FGAPOP-6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62
-TRANS-MUMBANG -G1 -LIST-45 -DOCALIGN=200 -THR_CORE-pct
-ALIGN=15 -MODE-LOCAL -OUTFMT-pfs -NORM-ext -MINLEN-0
-MAXLEN-1000000 -USER-USO8653294 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Documentation
                                                                                                                                                   About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
        out_format : pfs
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sequences: 311585
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Query: US-08-653-294-5
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N_Geneseq_36;Q55183 -
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N_Geneseq_36:T71319
N_Geneseq_36:T71321
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N_Geneseq_36:X52266
N_Geneseq_36:X23315
N_Geneseq_36:V12368
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N_Geneseq_36:V34296
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N_Geneseq_36:V30591
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N_Geneseq_36:T63530
N_Geneseq_36:Q23074
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N_Geneseq_36:X52264
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New isolated Borrelia burgdorferi nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of infections, particularly Lyme disease claim 1: Page 1037-1039; 1128pp; English.

X20248 to X20402 represent polynucleotide sequences isolated from Borrelia burgdorfer! (Bb). Products derived from Bb can be used for the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of blosynthetic products, e.g. enzymes. Borrelia belongs to a family of motile, spiral-shaped bacteria called Spirochetes. Spirochetes are pathogenic in humans and Borrelia causes epidemic and endance relapsing fever, and Lyme borrelisels, more commonly known as
v4-MAY-1999 (first entry)
Borrella burgdorferi polynucleotide sequence #57.
Borrella burgdorferi; spirochete; bacterium; pathogen; Lyme disease; epidemic relapsing fever; endemic relapsing fever; infection; diagnosis; characterisation; detection; ds.
Borrella burgdorferi.
30-npo-10-1
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Dimer; subunit; lysine-sensitive; aspartokinase II; AKII;
Dimer; subunit; lysine-tokinase; thermotolerani; tetramer;
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03-SEP-1997; US-057483,
20-JUN-1997; US-05389,
22-JUL-1997; US-053344,
22-JUL-1997; US-053347,
(HUMA-) HUMAN GENOME SCI INC.
(MEDI-) MEDIMMUNE INC.
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047809;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ArgileLeuLeuArgTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-5 x X20304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2123 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
                                                                                                                                                                                                                         30-DEC-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .35_s1gnal
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                                                                                                                                                                                                                                                                                                                                                                                                                                  White OR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                              results with the distriction of the develop products for the disposals and treatment of e.g. This sequence represents a nucleic acid molecule which encodes a secreted thuman protein. The gene number, and the clone it is derived from, are detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion of the invention relates to 28 novel genes and their fragments (nucleic acid sequences: V44277) for increasing the stability of the fused protein as compared to the human protein only.

The invention relates to 28 novel genes and their fragments (nucleic acid sequences: V44273) stable v43435; amino acid sequences w7519-w7525) which are useful for preventing, treating or amilorating medical conditions are useful for preventing, treating or amilorating medical conditions or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 28 polynucleotides, based on which tissues they are most highly expressed in (see V34286 for described
                                                                                                                        Human secreted protein gene 11 clone HLTBS22.

Human secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflaumation; ischaemic shock; Alzheimer's disease; restenosis; AlDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        427 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC.
Ferrie AM, Fischer CL, Gentz RL, Greene JM, Kyaw H,
Li H, Li Y, Moore PA, Rosen CA, Ruben SM, Soppet DR
Wel YF, Young PE, Zeng Z;
WPI; 98-520811/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps: 6
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 1688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        387 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        430 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to reverse of: V34296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X20304 standard; DNA; 2123 BP. X20304;
                                                          seq_documentation_block:
ID V34296 standard; DNA; 1688 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        443 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             394 AGGATCCTCTTGAGGTAT 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio: 4.833
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ArgileLeuLeuArgTyr 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-08-653-294-5 x V34296/rev
                                                                                                                                                                                                                                                                                                                                                                                                                             12-MAR-1998; U04858.
19-DEC-1997; US-068568.
14-MAR-1997; US-040762.
30-MAY-1997; US-048100.
30-MAY-1997; US-048189.
30-MAY-1997; US-048189.
30-MAY-1997; US-048189.
06-JUN-1997; US-048970.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: N_Geneseq_36:X20304
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P-PSDB; W75206

Homo sapiens

SS.

Quality:

alignment\_scores:

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1 ArgileLeuLeuArgTyr 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: N_Geneseq_36:X13280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterococcus faecalis. WO9850555-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-08-653-294-5 x V03795
   misc_feature
                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                   J09154582-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infection.
   DNA encoding lysine-sensitive aspartokinase II - from methylotrophic, thermotolerant bacillus sp. MGA 3, for producing lysine-vorgrowducing mutants

Tysine-vorgrowducing mutants
Claim 2: Fig 2: 16pp: English.
This sequence encodes a polypeptide which corresponds to the alphabeta dimer subunit of lysine-sensitive aspartokinase II (AKII) of bacillus sp. MGA3. MGA3 is methylotrophic and thermotolerant.
C alphabeta dimer subunit of lysine-sensitive aspartokinase II (AKII) of bacillus sp. MGA3. MGA3 is methylotrophic and thermotolerant.
C The native form of AKII is an alphabeta2 terramer. This DNA sequence was identified by cloning the structural gene from a confidence was identified by cloning the structural gene from a sequence spartokinase isozymes. The open reading frame shown encodes both the alpha and beta subunits in the same reading frame. This gene may be used to produce microorganisms such as new strains of bacteria which overproduce lysine at higher levels or under more stringent environmental conditions.
Sequence 2223 BP; 702 A; 394 C; 498 G; 629 T;
/note- "Indicated in the spec. as having dyad symmetry to the region 490-513" 664.\ .1899
                               /product Lysine-sensitive aspartokinase II
757. 759
/*tag q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PaMMV coat protein coding sequence.

Coat protein; Patchouli mild mosaic virus; PaMMV; ss.

Patchouli mild mosaic virus.

Rey 1591. .3390

/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 29.00 Length: 6
Ratio: 4.833 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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ID V03795 standard; cDNA to mRNA; 3581 BP.
AC V03795;
                                                                                                                /codon= seq:ACC aa:Asn
1237. .1239
/*tag= h
                                                                                                                                                                  /codon= seq:CCT aa:Leu
1936. .1980
                                                                                                                                                                                                    /*tag= i
/rpt_type= INVERTED
1987. .2028
/*tag= j
                                                                                                                                                                                                                                                                      /rpt_type= INVERTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: Q47809 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                       Flickinger MC, Schendel FJ;
WPI; 93-295300/37.
P-PSDB; R48046.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  518 CGTATTTTACTACGTTAT 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ArgileLeuLeuArgTyr 6
                                                                                                                                                                                                                                                                                                                                                 12-MAY-1989; US-351436.
20-MAR-1991; US-673263.
20-MAR-1991; US-673264.
12-APR-1991; US-684135.
(MINU ) UNIV MINNESOTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: N_Geneseq_36:V03795
                                                                                                                                                                                                                                                                                                                  335691.
US-335691.
US-351436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-08-653-294-5 x Q47809
                                                                                    misc_difference
                                                                                                                                     misc_difference
                                                                                                                                                                                                                                                                                                    07-SEP-1993.
10-APR-1989;
                                                                                                                                                                                                                                                                                                                                     10-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                      US5243039-A
                                                                                                                                                                                      repeat_unit
                                                                                                                                                                                                                                     repeat_unit
                                 cds
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claim 1; Page 1461-1463; 2084pp; English.

A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. X12938 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for of Enterococcus faecalis in samples. They can also be used for progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the
                                                                                                                                                                                                                                             F 05-DEC-1995; J16431.

No5-DEC-1995; J7-316431.

KAGOS ) KAO CORP.

R PF2DSDS #441021, W41022.

R P-ESDS #441020, W41021, W41022.

Example 5; Page 4-7; 10pp; Japanese.

T recombinant expression of viral protein

S Example 5; Page 4-7; 10pp; Japanese.

T recombinant expression of viral protein

S Example 5; Page 4-7; 10pp; Japanese.

T recombinant expression of viral protein of packouli mild mosale virus (Pakkov), and is a DNA sequence of the patchouli mild mosale virus (Pakkov), and is a DNA sequence of the invention. The coat protein of Pakkov), and is a DNA sequence of the invention. The coat protein of Pakkov, which cannot be synthesised on maturally from a plant genome, can be produced by the plant cell transformed by the DNA.

Sequence 3581 BP; 1020 A; 654 C; 852 G; 1055 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-NOV-1998.
04-MAY-1998 U08985.
14-NOY-1997; US-066009.
06-MAY-1997; US-044031.
16-MAY-1997; US-044655.
(HUMA-) HUMAN GENORE SCI INC.
MPI: 99-045171/04.
New isolated Enterococcus faecalis polynucleotides and polypeptides used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-MAR-1999 (first entry)
Enterococcus faecalis genome contig SEQ ID NO:343.
Enterococcus faecalis; contig; detection; Enterococcal infection; vaccine; attenuation; computer readable medium; ds.
/*tag= c
/note= "encodes 26K coat protein (see W41021)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps: 6 Gaps: 0 Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to: 3581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: V03795 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
ID X13280 standard; DNA; 3907 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        590 CGAATATTACTCCGGTAC 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality: 29.00
Ratio: 4.833
Percent Similarity: 100.000
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V83003;
23-FPB-1999 (first entry)
Contiguous sequence determined for P. carinil from immunosuppressed rats. PCR amplification; sequencing; assay; inhibitor; nuclear rRNA gene; catalytic Group I self-splicing intron reaction; drug screening; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Screening assays for drugs against Pneumocystis carinii - based on inhibition of 26s rRNA gene intron self-splicing Example 1; Fig 2; 51pp; English.

Example 1; Fig 2; 51pp; English.

The present sequence represents the contiguous sequence determined for Pneumocystis carinii from immunosuppressed Sprague-Dawley rats, using the in vitro method of the invention. The method assays for an inhibitor of the catalytic Group I self-splicing intron reaction in the nuclear rRNA genes of P. carinii. The method is useful for screening potential drugs for treating P. carinii infections before more costly animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D-MAR.1999 (first entry)
Enterococcus faecalis genome contig SEQ ID NO:45.
Enterococcus faecalis genome contig SEQ ID NO:45.
Enterococcus faecalis contig; detection; Enterococcus faecalis.
MO9850555-A2.
12-NOV-1998.
                                                                                                                                                         /*tag= a
/note= "3'-terminal portion of intron 1"
                                                                                                                                                                                                                                                                         /*tag= c
/note= "internal transcribed spacer 1"
                                                                                                                                                                                                                                                                                                                                                                                            /*tag= e
/note= "internal transcribed spacer 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 6
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1124 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 4256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-1998.
19-JUN-1995; 491690.
27-MAX-1993; US-088248.
30-JUL-1992; US-922987.
19-JUN-1995; US-491690.
(UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to reverse of: V83003 from: 1
                                                                                                                                                                                                             /*tag= b
/note= "exon 2 of 16SrRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             766 C;
                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                      .8S rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "26S rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:

D_X12982 standard; DNA; 15614 BP.

AC X12982;
DT 19-MAR-1999 (first entry)
DE Enterococcus faecalis genome cont
KW Enterococcus faecalis; contig; de
KW vaccine; attenuation; computer re
OS Enterococcus faecalis.
PN W0985055-A2.
PD 12-NOV-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1190 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3792 CGAATTCTGCTTCGGTAT 3775
                                                                                                                                                                                                                                                                                                                                                                                                                                .4256
                                                                                                                                                                                                                                                                                                                                  /*tag= d
/note= "5.
375. .556
                                                                                                                                                                                                                                                                                                                .374
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                                                                                                                                                                                                                                                     54. .216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-653-294-5 x V83003/rev
                                                                                                                                                                                             23. .53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: N_Geneseq_36:x12982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio: 4.833
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           testing is conducted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lelbowitz MJ, Llu Y;
WPI; 99-069716/06.
                                                                                                  Pneumocystis carini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US5849484-A
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                                                                                                                                      intron
                                                                                                                                                                                                 exon
                                                                                                                                                                                                                                                                                                                    exon
                                                                                                                                                                                                                                                                                                                                                                                                                                    exon
    polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from sample with PCR primers specific for the 26S rRNA gene of from sample with PCR primers specific for the 26S rRNA gene of from mamocystis cartinits cartinits cartinits.

The present sequence represents the total contiguous sequence of pneumocystis cartinit in immunosuppressed Sprague-Dawley rats. The specification describes a method for the diagnosis of Pneumocystis cartinit which comprises detecting the presence of a nucleic acid sequence containing the 26S rRNA gene specific for P. cartinit in a sample. The 26S rRNA gene in a sample is amplified, and the primer extension products detected by hybridisation with a labbled colligonucleotide. The methods can be used for the diagnosis of P. cartinit infection and for the detection of various species of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-SEP-1998 (first entry)
Total contiguous sequence of P. carinii in immunosuppressed rats.
Detection: diagnosis; 26S rRNA gene; P. carinii specific; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1176 T;
                                                            1424 T;
                                                                                                                                  Gaps: 6
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 4256
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                                                          ë
                                                          717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to reverse of: V36211 from: 1
                                                          698 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      766 C;
                                                                                                                                                                                                                                                                             to: 3907
                                                                                                                                                                                                                                                                           Align seg 1/1 to: X13280 from: 1
                                                        1056 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1190 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
ID V36211 standard; DNA; 4256 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
ID V83003 standard; DNA; 4256 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             species identification; ss.
Pneumocystis carinii.
US5776680-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3792 CGAATTCTGCTTCGGTAT 3775
                                                                                                                                                                                                                                                                                                                                                      968 AGAATATTATTGAGGTAT 985
                                                                                                                                                         Ratio: 4.833
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                          seq_name: N_Geneseq_36:V36211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio: 4.833
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-5 x V36211/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ArglleLeuLeuArgTyr 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: N_Geneseq_36:V83003
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                                                                                                                                      29.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1995; 505509.
30-JUL-1992; US-922987.
31-AUG-1994; US-298087.
(UNNE-) UNIV NEW JERSEY
                                                                                                                                                                                                                                                                                                                  1 ArgileLeuLeuArgTyr
                                                                                                                                                                                                                 alignment_block:
US-08-653-294-5 x X13280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leibowitz MJ, Liu Y;
WPI; 98-398016/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4256 BP;
                                                        3907 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
Ratio:
                                                                                                                                        Quality:
                                                                                                                    alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    carinii.
                                                            Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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1176 T;

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alignment_scores:
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                                                                                                                                                                                                                                            Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1
88888888
                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 419-427; 2084pp; English.

A computer readable medium has been developed which has recorded on it
A computer readable medium has been developed which has recorded on it
X12938 to X13919 represent these nucleotide sequences which are primary
nucleotide sequences, also known as contigs. The computer-based system
can identify fragments of the Enterococcus faecalis genome with
commercial importance. The products can be used to detect the presence
of Enterococcus faecalis in samples. They can also be used for
diagnosing Enterococcal infection in an animal and monitoring
modulate the growth or pathogenicity of Enterococcus faecalis, or
another related organism, in vivo or in vitro. In particular the
can be used in vaccines to prevent or attenuate an Enterococcal
                                                  (HUMA-) HUMAN GENOME SCI INC.

Barash SC, Dillon PJ, Kunsch CA;

WPI; 99-045171/04.

New isolated Enterococcus faecalis polynucleotides and polypeptides

- used to develop products for the detection of Enterococcus and for

use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example; Page 3; 10pp; German.
The sequence is that of a PCR primer used to obtain a 360bp fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .18
/*tag= a
hote="complementary to SERP gene bases 3022-3045"
19. .45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SERP gene PCR primer p3."
Polymerase chain reaction; hybrid antigen; Plasmodium falciparum; malaria; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                    4326 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Plasmodium falciparum hybrid proteins for use in vaccines comprise at least two T-cell epitopes of SERP and a partial sequence of HRPII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= b
/note= "complementary to bases 226-252 of the
partial sequence 31-1 Ird of MSA I"
                                                                                                                                                                                                                                                                                                                                                    3169 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to: 15614
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                    2567 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JUN-1992.
24-DEC-1990; 041836.
24-DEC-1990; DE-041836.
(BEHW ) BEHRINGWERKE AG.
Enders B, Hundt E, Knapp B, Kupper H;
WPI; 92-218121/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to reverse of: x12982
                                                                                                                                                                                                                                                                                                                                                    5535 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
ID Q26060 standard; DNA; 51 BP.
AC Q26060;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6777 CGAATATTATTGCGATAC 6760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                     Quality: 29.00
Ratio: 4.833
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-08-653-294-5 x X12982/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ArglleLeuLeuArgTyr 6
         14-NOV-1997; US-066009.
06-MAY-1997; US-044031.
16-MAY-1997; US-046655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: N_Geneseq_36:Q26060
                                                                                                                                                                                                                                                                                                                                                   15614 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DE4041836-A
                                                                                                                                                                                                                                                                                                                                      infection.
                                                                                                                                infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                     Sequence
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Probes to the color of the content membrane protein - for produ. of recombinant polypeptide useful in vaccines, etc.

Claim 1; Column 9-10; Ilpp; English.

This sequence represents the coding sequence for a 15 kD outer membrane protein (OMP) of Haemophilus influenzae. The 15 kD OMP is conserved among type b and non-typable H.influenzae. Epitopes of the protein encoded by this sequence can be used as a standard or reagent in diagnostic tests. The protein can also be used in vaccines against type b and non-typable H.influenzae. Monoclonal antibodies directed against the encoded protein can be used as diagnostic reagents, and as the ancoded protein can be used as diagnostic reagents, and as thereapeutic agents for passive immunisation.

Sequence 607 BP; 206 A; 97 C; 108 G; 196 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-500-1996 (first entry)
Haemophilus influenzae 15 kD outer membrane protein coding sequence.
Outer membrane protein; immunoreactive; OMP; type b H.influenzae;
non-typable H.influenzae; murine monoclonal antibody; vaccine; therapy;
passive immunisation; ss.
which codes for amino acids 140-254 of the Plasmodium falciparum antigen MSA I. The obtd. fragment is used in the construction of hybrid antigen SERP/MSAI/HRPIT which can be used in anti-malarial vaccines which have a significantly stronger protective effect than those using individual proteins. The vaccines are also easier to purify and are less likely to be rendered ineffective by a mutation of the pathogen. See Q26061.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/product= 15 kD outer membrane protein
                                                                                                                                                                                                                                                                                                                                                 Length: 6
Gaps: 0
Percent Identity: 83.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 6
Gaps: 0
Percent Identity: 83,333
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07-SEP-1993; 061314.
07-SEP-1993; 02-061314.
(CNDG ) CANADA MIN HEALTH.
(UNIW ) UNIV WASHINGTON.
Brodden BK, Grass S, Hamel J, Munson RS;
P-PSDB; R95448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to reverse of: Q26060 from: 1
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171. .542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
ID T26893 standard; DNA; 607 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-08-653-294-5 x Q26060/rev
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US-08-653-294-5 x T26893/rev
                                                                                                                                                                                                                                                                                                                                                    Quality: 28.00
Ratio: 4.667
Percent Similarity: 100.000
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Ratio: 4.667
Percent Similarity: 100.000
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1 ArgileLeuLeuArgTyr 6
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                             INSERM INST NAT
                         (INRM ) INSERM INST NAT
Bambal RB, Bishop PB,
Leblond B, Moore ANJ,
            09-MAY-1995; FR-005489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-08-653-294-5 x T72653
                                                                          Lihua Z, Rose C;
WPI; 96-518693/51.
                                                                                                          P-PSDB; W21571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9638555-A2.
05-DEC-1996.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores
15-SEP-1993 (first entry)
Histamine H1 receptor coding sequence.
Bovine: histamine; H1; receptor; expression vector; pBH1; pEF-BOS-H1;
E. coli; allergy; ss.
Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                New bovine histamine HI receptor - used for treating allergy Claim 2; Fig 1-5; 11pp; Japanese.
Claim 2; Fig 1-5; 11pp; Japanese.
This sequence encodes bovine histamine HI receptor. This sequence can be used in the construction of the expression vectors, pBHI or pEF-BOS-HI. These vectors may be use to transform E. coli, such that they produce the HI receptor protein. The histamine HI receptor may be used for the treatment of allergy.

Sequence 2960 BP; 745 A; 743 C; 758 G; 714 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label- Alternative_splice_site
//note- "A second clone was isolated which differed
upstream of this site and was identical
downstream of it (see T72654)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-AUG-1997 (first entry)
Rat tripeptidylpeptidase II cDNA clone.
Tripeptidylpeptidase II; TPP II; rodent; rat; cerebral cortex;
neuropeptide; cholecystokinin; CCK; inactivation; degradation;
anorexials schizophrenia; Parkinson's disease; depression;
irritable bowel syndrome; bulimia; pathological obesity;
alternative splicing; ss.
Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to reverse of: Q42561 from: 1 to: 2960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps: 0
Percent Identity: 83.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag- a
product Tripeptidylpeptidase_II
357. 358
/*tag- b
                                                                                                                                                                                                                                                                                         17-OCT-1991; 269275.
17-OCT-1991; JP-269275.
(OSB-) ZH OSAKA BIOSCIENCE KENKYUSHO.
WPI: 93-171831/21.
P-PSDB; R36979.
                                                                                                                                                                                                               Location/Qualiflers
108. .1583
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
ID T72653 standard; cDNA; 4617 BP.
                                                                                                          Q42561 standard; DNA; 2960 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  538 CGGGTCTTGTTACGATAC 521
           64 AGGGTGCTACTTAGATAC 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouality: 28.00
Ratio: 4.667
Percent Similarity: 100.000
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US-08-653-294-5 x Q42561/rev
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                                                          seq_name: N_Geneseq_36:Q42561
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                                                                                          seq_documentation_block:
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14-NOV-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                               J05103674-A
                                                                                                                                                                                                                                                                            27-APR-1993
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                                                                                                                                                                                                                  Key
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Disclosure; Pages 161-165; 212pp; French.

Disclosure; Pages 161-165; 212pp; French.

An enzyme with specificity for cholecystokinin (CCK) substrates

(specifically the non-sulphated CCKB and the CCKS peptides) was

c purified from rat cerebral cortex membranes using high performance

1 quid chromatography. Based on amino acid sequence data from the

purified enzyme, PCR primars were designed to amplify oligonucleotide

purified enzyme, PCR primars were designed to amplify oligonucleotide

purified enzyme, PCR primars were designed to amplify oligonucleotide

probes A and B of lengths 350 and 380 nucleotides, respectively.

Using these probes, two distinct clones were identified in a rat

brain cDNA library. The first clone had the present sequence and

is the rodent homologue of human tripeptidylepetidase II. The

second clone (see T72653) differed in the 5' region, probably as a

result of alternative splicing, and appears to be a serine

ectopeptidase. The rat enzymes are preferred for use in a new

method of screening for medicaments for treating disorders linked

to the inactivation or degradation) of endogenous neuropeptides. In the

method, a candidate molecule is contacted with a membrane tripeptidyl-
                                                                                                                                                                                                                                              Screening medicaments for treating disorders linked to inactivation of endogenous neuro:peptide(s) - by contacting candidate molecule with membrane tri:peptidyl-peptidase (homologue) and measuring enzyme activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptidase or homologue, and enzyme activity is measured.

Blosorders linked to inactivation or degradation of endogenous neuropeptides, include food intake disorders, cognitive and motor disorders such as anorexia, schizophrenia, Parkinson's disease and depression, as well as gastrointestinal transit disorders such as irritable bowel syndrome, bulimia and pathological obesity.

Sequence 4617 BP; 9014 905 6; 999 6; 1284 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-5EP-1997 (first entry)
CDNA encoding C. elegans UNC-53 protein variant 7A.
UNC-53; neuronal reqeneration; revascularisation; wound healing; neurodegenerative disease; Alzheimer's disease; Huntingdon's; peripheral neuropathies; metastasis inhibition; cancer; ss. Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= b
/note= region of seven A bases; the 8A UNC-53
variant has eight bases at this position
resulting in a different product"
                                            Ganellin CR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity: 100.000 Percent Identity: 83.333
                                        Chan S, Gar
, Vargas F;
SANTE & RECH MEDICALE.
Bourgeat P, Chan S, (
Schwartz JC, Vargas F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>:</u>
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64. .4815
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ID T71315 standard; cDNA; 5072 BP.
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4594. .4600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2100 CGTGTTCTTCTGAGGTAT 2117
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processing macros of the process of the requirements of the control of the contro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-SEP-1997 (first entry) cDNA encoding C. elegans UNC-53 protein variant 8A. CDNA encoding C. elegans UNC-53 protein variant 8A. UNC-53; neuronal regeneration; revascularisation; wound healing; neurodegenerative disease; Alzheimer's disease; Huntingdon's; peripheral neuropathies; metastasis inhibition; cancer; ss. Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1203 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualiflers
64. 4650
4. 4650
4. 4640

/*tag= b
//tag= b
//orde= region of eight A bases; the 7A UNC-53
position resulting in a different product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1019 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to reverse of: T71315 from: 1 to: 5072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality: 28.00 Length: 6
Ratio: 4.667 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 83.333
                                                                                                                                     Vandekerckhove J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vandekerckhove J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1325 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T71314 standard; cDNA; 5073 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1525 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (STRI) STRINGHAM E.
(VAND)) VANDEKERCKHOVE J.
Bogaert I. Stringham E, V.
WPI: 97-034369/03.
P-PSDB: W20056.
                                                                                                                          Bogaert T, Stringham E, WPI; 97-034369/03.
P-PSDB; W20057.
                                                                                                      (VAND/) VANDEKERCKHOVE J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-08-653-294-5 x T71315/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: N_Geneseq_36:T71314
31-MAY-1996; E02311.
31-MAY-1995; GB-010944.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-DEC-1996.
31-MAY-1996; E02311.
31-MAY-1995; GB-010944.
(BOGA/) BOGAERT T.
                                                                                STRINGHAM E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5072 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
                                                  BOGA/) BOGAERT T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9638555-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
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Claim 1; Page 101-103; 278pp; English.

CDNA sequences encoding UNC-53 protein 8A and 7A variants of C. elegans are new. The UNC-53 proteins and nucleic acids are useful as medicaments to promote neuronal regeneration, revascularisation or wound healing, or for treatment of chronic neurodegenerative diseases (e.g. Alzheimer's or Huntingdon's disease) or acute tranmatic injuries. Transgenic cells and organisms transfected with UNC-53 cDNA can be used to determine whether a substance is an inhibitor or enhancer of the regulation of cell shape or motility or the direction of cell migration by screening for a phenotypic change in the cell. Inhibitors can be used to alleviate the spread of disease inducing cells or metastasis. Probes derived from the CDNA sequences can be used to identify proteins which are active in the signal transduction pathway that can be used as
                                                                                                                                                                                                                                                                                                                                                                                               1203 T;
                                                                                                                                                                                                                                                                                                                                                                                               1019 G;
                                                                                                                                                                                                                                                                                                                                                                                               1325 C;
                                                                                                                                                                                                                                                                                                                                                                                            1526 A;
                                                                                                                                                                                                                                                                                                                                                                                            5073 BP;
                                                                                                                                                                                                                                                                                                                                                                         mentioned above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                    Seguence
          %CCCCCCCCCCCCCCCC
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Length: 6 Gaps: 0 Percent Identity: 83.333 Ratio: 4.667 Percent Similarity: 100.000 28.00 Quality: Ratio:

1 ArgileLeuLeuArgTyr 6

to: 5073

to reverse of: T71314

Align seg 1/1

alignment\_block: US-08-653-294-5 x T71314/rev

1230 CGAGTCTTGTTGAGATAT 1213

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

February 8, 2000, 01:29:36 ; Search time 122.56 Seconds (without alignments) 1.160 Million cell updates/sec Run on:

US-08-653-294-6 29 1 YRLLIR 6

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

188963 segs, 23686106 residues Searched:

188963 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 08 Listing first 45 summaries

A\_Geneseq\_36:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### STIMMARIES

|           | Description    | , , | Peptide #4 used in | Immunomodulatory p | Immunomodulatory p | A partial gidAl pr | rlation enzy | Corn threonine dea | Soba   |        |        | Nonsense-mediated | £      | Drosophila-12 cadh | Protocadherin clon | Rat spleen pro-hor |        |     | rotein | odulato |        | Peptide fragment ( | Immunomodulatory p | Immunomodulatory p | HLA-B2702 84-79-84 | Peptide B2702.84-7 | lati   | HLA-B2702 CTL modu | CIL    | CIL    | 84-7   | HLA-B2702 84-75T/7 | Immunomodulating d | odulating | Peptide B2702.84-7 |
|-----------|----------------|-----|--------------------|--------------------|--------------------|--------------------|--------------|--------------------|--------|--------|--------|-------------------|--------|--------------------|--------------------|--------------------|--------|-----|--------|---------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------|--------|--------|--------------------|--------------------|-----------|--------------------|
| SUMMARIES | ΩI             | LO. | 78                 | 26                 | W47272             | -                  | 42           | W97739             | W62842 | W89445 | R93081 | W01897            | W01896 | R58902             | R87142             | W27113             | Y06848 | -*  | W89443 | W47263  | W33781 | R61548             | W47266             | W47270             | R95429             | W33798             | W33799 | R92909             | R92911 | R92907 | R95428 |                    | ~                  | 337       | 5                  |
|           | DB             | -   | -                  | -                  | -                  |                    |              | -                  | -      | -      | Н      | ~                 | ч      | -                  | H                  | -                  | н      | н   | н      | -       | -      |                    | Н                  | -                  | Н                  | -                  | -      | -                  | -      | -      | -      | -                  | ~                  |           | ⊣.                 |
| •         | Length         | 9   | ø                  | 10                 | 10                 | œ                  | 389          | σ                  | ~      | ~      | 2      | 9                 | æ      | 43                 | 43                 | æ                  | 174    | ~   | က      | 9       | 9      | 10                 | 10                 | 10                 | 12                 | 12                 | 12     | 20                 | 20     | 20     | 20     | 20                 | 20                 | 20        | 20                 |
|           | Query<br>Match | 0.0 | 0.                 | 0.                 | 0.                 | 3.1                |              |                    |        | 3.1    |        |                   | 3.1    | 7.                 | 7.                 | .7                 | .2     | . 5 | .5     | 8.      | 8.     | 8.                 | 8.                 | 8.                 | 8.                 | æ.                 | 8.     | 8.                 | 8.     | 8.     | 8.     | 8.                 | 8.                 | 8.        | 8.                 |
| ď         | ROUS.          | 100 | 100                | ĕ                  | ä                  | 6                  | 9,           | 9                  | 9      | ö      | ö      | 6                 | ö      | æ                  | æ                  | 80                 | ĕ      | æ   | æ      | œ       | œ      | œ                  | 80                 | òò                 | 80                 | œ                  | œ      | 80                 | æ      | 80     | œ      | 80                 | œ                  | 85        | 8                  |
|           | Score          | 29  | 29                 | 59                 | 29                 | 27                 | 27           | 27                 | 27     | 27     | 27     | 27                | 27     | 26                 | 26                 | 56                 | 25     | 25  | 25     | 24      | 24     | 24                 | 24                 | 24                 | 24                 | 24                 | 24     | 24                 | 24     | 24     | 24     | 24                 | 24                 | 24        | 24                 |
|           | Result<br>No.  | н   | 7                  | m                  | 4                  | S                  | 9            | 7                  | æ      | O      | 10     | 11                | 12     | 13                 | 14                 | 12                 | 16     | 17  | 18     | 19      | 20     | 21                 | 22                 | 23                 | 24                 | 25                 | 56     | 27                 | 28     | 53     | 30     | 31                 | 32                 | 88        | 34                 |

| Antigen 3 from clu<br>HPV18 E6/E7 protei | HPV-18 E6 protein.<br>EpiQ protein. Nove<br>Antigen 1 from clu | Protein encoded by HPV 18 E6 protein Prot.D1/3-E6-H1s/H | Rat FRAG1 protein.<br>Prot.D1/3-E6-E7-H1<br>Erythrobacter long |
|------------------------------------------|----------------------------------------------------------------|---------------------------------------------------------|----------------------------------------------------------------|
| W89901<br>R63866                         | R79656<br>R39353<br>W89889                                     | W89840<br>R27728<br>Y02641                              | W41592<br>Y02642<br>R95698                                     |
|                                          |                                                                |                                                         | ппп                                                            |
| 158                                      | 158<br>205<br>225                                              | 225<br>271<br>278                                       | 383<br>4383<br>44                                              |
| 82.8<br>82.8                             | 82.8<br>82.8<br>82.8                                           | 82.8<br>82.8                                            | 888                                                            |
| 2 <b>4</b><br>2 <b>4</b>                 | 5 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5                        | 2 4 4<br>2 4 4                                          | 5 4 4<br>5 4 4                                                 |
| 35                                       | 37<br>38<br>39                                                 | 0 4 4<br>0 1 2                                          | 4 4 4<br>5 4 4 5                                               |

# ALIGNMENTS

RESULT

| AND THE PROPERTY OF THE PROPER | W47264 standard; peptide; 6 AA. W47264 W47264; W6726101; treatment; autoimmune disease. W6726261; W6726261; W672626261; W67262626261; W6726262626260; W7787671997; W77879 J W17 LELAND STANFORD JUNIOR. Clayberger C. Krensky AM; W71: 98-018220/02. Novel immunomodulatory peptide-type compound - useful for inhibiting transplant rejection Clayma 10; Page 36; 41pp; English.                                                                        |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 88888888888                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | The present sequence is an immunomodulatory peptide, which comprises a class I HiA-B alpha-1 domain sequence. It can be used in a pharmaceutical composition together with a subtherapeutic dose of an immunosuppressant, to extend the period of acceptance of a transplant from a major histocompatibility complex (MHC) unmatched donor, i.e. to inhibit transplant rejection. It can also be used in the treatment of autoimmune diseases. Peptides using the D-form amino acids are more effective immunomodulators than their diastereomers or enantlomers. Sequence 6 AA; |

ö Indels ; 0; Mismatches 6; Conservative Matches

ö

Gaps

1 YRLLIR 6 ||||||| 1 YRLLIR 6 δ 셤

RESULT W33783

W33783 standard; peptide; 6 AA.
W33783;
19-JUN.1998 (first entry)
19-JUN.1998 (first entry)
Peptide #4 used in immunomdulating dimer peptide.
Immunomodulating dimer, immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
rejection.
Synthetic.
Homo sapiens.
W09744351-A1. 

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RESULT
W89446
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                                                                           Per Bebluow, N. Clasyperger C, Nensky Ann;

WPI: 98-086530/08

New immunomodulating dimer peptide(s) - based on a Class I HLA-B

PT alpha-1 domain, used for preventing rejection of transplants or

treating autoimmune diseases

S Claim 15; Page 35; 41pp; English.

C This sequence represents a specifically claimed peptide which forms part

of the immunomodulating dimer peptides of the invention. A peptide-type

c compound or variant is claimed which has immunomodulating activity,

or the immunomodulating dimer peptides of the invention. A peptide-type

c compound or variant is claimed which has immunomodulating activity,

or variant is claimed which has immunomodulating activity,

c comprises the formula; A-B, where A, B = (R aa76-77L) (aa79-84) or

c caterified forms of up to 60 amino acids, where the peptide-type compound

c comprises the formula; A-B, where A, B = (R aa76-77L) (aa79-84) or

c case17-768; aa76 = E or V; aa77 = D, S or N; aa79 = R C

c case3 = G or N; and aa represents amino acid; aa82 = R

c or L; aa83 = G or R; and aa represents amino acid; as82 = R

c or L; aa83 = G or R; and aa represents amino acid; as82 = R

c or L; aa83 = G or N; and aa represents amino acid; as82 = C

c or Lisas I HLA-B alphal domain (positions 79-84). They can be used to

nihibit cytotoxic T-lymphocytes (CTL) from undesirably attacking calls in

c a host or in vitro. They can also be used in combination with antiqenic

c peptides or proteins of interest to activate CTLS. They can also inhibit

c the proliferation of T cells in response to anti-CD3. They can be used be

controlled to the peptides or proteins of interest to activate of the peptides or automin to a treating autolimmune

c challed the automin of treating of treating and autolimmune

controlled the control of treating and autominity of treating autolimmune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosis. The products can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel immunomodulatory peptide-type compound - useful for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 10. Page 36. 41pp, English.

The present sequence is an immunomodulatory peptide, which comprises a Class I HiA-B alpha-1 domain sequence. It can be used in a pharmaceutical composition together with a subtherapeutic dose of an immunosuppressant, to extend the period of acceptance of a transplant from a major histocompatibility complex (MHC) unmatched donor, i.e. to inhibit transplant rejection. It can also be used in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualiflers
1. 10
/note= "at least one of the amino acids is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-MXY-1998 (first entry)
Immunomodulatory peptide.
Immunomodulator: Class I HLA-B alpha-1 domain; inhibition;
transplant rejection; treatment; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              using the D-form amino acids are more effective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 29; DB 1; 100.0%; Pred. No. 1.5e+05; 1ve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune diseases
                                24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Beulow R, Clayberger C, Krensky AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W47268 standard; peptide; 10 AA. W47268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clayberger C, Krensky AM;
WPI; 98-018220/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-APR-1997; U06705.
23-APR-1996; US-651650.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transplant rejection
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Peptides using the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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A partial gidAl protein sequence. GidAl: bacterial infection; mentiogitis; Helicobacter pylori infection; cancer; ulcer; gastritis; antibacterial; in-dwelling device; wound treatment; bacterial adhesion; matrix protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-NOV-1997.
23-ARR-1997, U06705.
22-MAY-1996, US-651650.
22-MAY-1996, US-651650.
CIRY D VINY LELAND STANFORD JUNIOR.
CLAYDEGE C, Krensky AM;
WPI: 98-018220/02.
NOVEL immunomodulatory peptide-type compound - useful for inhibiting
                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transplant rejection

Claim 10; page 36; 41pp; English.

The present sequence is an immunomodulatory peptide, which

comprises a Class I HiA-B alpha-1 domain sequence. It can be used
in a pharmaceutical composition together with a subtherapeutic dose
of an immunosuppressant, to extend the period of acceptance of a

transplant from a major histocompatibility complex (MHC) unmatched
donor, i.e. to inhibit transplant rejection. It can also be used in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note- "unspecified amino acid encoded by ATN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72-7M7-1998 (first entry)
Immunomodulatory peptide.
Immunomodulator; Class I HLA-B alpha-1 domain; inhibition;
transplant rejection; treatment; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 29; DB 1; Length 10; 100.0%; Pred. No. 0.52; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                    100.0%; Score 29; DB 1; Length 10; 100.0%; Pred. No. 0.52;
immunomodulators than their diasterecmers or enantiomers. Sequence 10\ \mathrm{AA};
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the treatment of autoimmune diseases.
Peptides using the D-form amino acids are more effective immunomodulators than their diastereomers or enantiomers.
                                                                                                                                                                                            Indels
                                                                                                                                                                                         ö
                                                                                                                                                                                         0; Mismatches
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Key Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                        W47272 standard; peptide; 10 AA.
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                                                                                                                                                                Best_Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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1 YRLLIR 6
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| YRLLIR 6
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07-JAN-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9744052-A1
                                                                                                                                      Query Match
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This is the amino acid sequence of a near full-length corn threonine deaminase, as deduced from a coun close (see x07180), threonine deaminase, as deduced from a coun endosperm CDNA clone (see x07180), designated cenl.pk0064 f4, obtained from a corn endosperm CDNA.

Ibrary. The amino acid sequence shows similarity to the Burkholderia capacia enzyme. The invention relates to new isolated nucleic acid fragments (see x07186 98) encoding plant enzymes (see x07186) encoding plant enzymes (see x0776 98) encoding plant enzymes (see x07777-44) that catalyse steps in the biosynthesis of lysine, threonine, methionine, cysteine and isolated from aspartate, the enzyme being selected from dihydropicolinate reductase, diaminopimelate epimerase, threonine synthese, threonine deaminase or S-adenosymethionine synthetase. The invention also relates to the construction of a chimeric gene encoding all or a portion of the biosynthetic pathway enzyme, in sense or antisense orientation, where expression of the enzyme in a transformed host cell. Overexpression or reduction of expression of genes encoding the amino acids in human food and animal feed. Transformed host cells can acids in human food and animal feed. Transformed host cells can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to identify compounds that inhibit one of the enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New plant amino acid biosynthetic enzymes, DNA and chimeric genes encode: dihydropicolinate reductase; diaminopimelate epimerase; threonine synthase; threonine deaminase; S-adenosylmethionine
                                                                                                                   Corn threonine deaminase. Threonine acid; lysine; threonine; Threonine deaminase; corn; matze; amino acid; lysine; threonine; methionine; cysteine; isoleucine; transgenic plant; crop improvement; food; feedstuff.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-0cT-1998 (first entry)
Helicobacter pylor1 DapE protein.
N-succinyl-diaminopimelic acid desuccinylase; DapE; vaccine;
Immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 27; DB 1; Length 392;
Pred. No. 63;
                                                                                                                                                                                                                                                   10-DEC-1998.
10-DEC-1998.
116-DEC-1998.
116-DUN-1997; US-049443.
12-JUN-1997; US-048771.
(DUPO ) DU PONT DE NEMOURS & CO E I.
Abell LM, Allen SM, Falco SC, Hitz WD, Kinney AJ, Rafalski JA, Thorpe CJ; WPI, 99-0702483/06.
N-PSDB; X07180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                             W97739 standard; Protein; 392 AA.
W97739;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W62842 standard; Protein; 621 AA.
W62842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Helicobacter pylori strain 60190.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.1%;
83.3%;
                                                                                           21-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9827819-A1.
02-UUL-1998.
23-DEC-1997; U24147.
23-DEC-1996; US-03824.
(UYVA-) UNIV VANDERBILT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  383 YRLLLR 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ဖ
                                                                                                                                                                                                                 Zea mays.
WO9855601-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                also be used
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                                                                                                            The present sequence and prevent bacterial infections e.g. S. aureus and diagnose, treat and prevent bacterial infections e.g. S. aureus and diagnose, treat and prevent bacterial infections e.g. S. aureus and diagnose, treat cancers, ulcers and gastritis
Claim 1: Page 6: 43pp: English.
C. The present sequence represents a partial gidAl protein of Staphylococcus aureus. GidAl proteins, nucleic acids and agonists are used to treat conditions requiring increased activity or expression of gidAl, while conditions (particularly bacterial infections) requiring inhibition of gidAl are treated by administering an antagonist, inhibition of gidAl are treated by administering an antagonist.
C. inhibition of gidAl are infection, particularly meningitis and also Helicobacter pylori infections e.g. related cancers, ulcers and cast in-dwelling devices to prevent infection or generally as wound treatments to prevent adhesion of bacteria to matrix proteins.
C. gequence 387 AA;
                                                                                                                                                                                                            Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence was deduced from DNA sequence obtd. from plasmid p53A, a subclone of a DNA library prepd. from genomic DNA of S.thermotolerans. The 3-acylation enzyme is involved in the synthesis of macrolide antibiotics. Microorganisms, ep. Streptomyces, transformed with the gene can be used for the commercial prodn. of macrolide antibiotics, e.g. 3-acylated tylosin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene encoding 3-acylation enzyme for macrolide antibiotics - used to transform Streptomyces sp. to have acylation activity, for use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arisawa A, Kawamura N, Kojima I, Tone H, Okamoto R;
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(SMIK ) SMITHKLINE BEECHAM CORP.
(SMIK ) SMITHKLINE BEECHAM PLC.
Burnham M, Kallender H, Lenox AL, Palmer LM;
WPI; 99-062660/06.
N-PSDB; V82078.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 27; DB :
Pred. No. 62;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 27; DB :
Pred. No. 62;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3-acylation enzyme.
Macrolide antibiotics; acylation; Streptc
Spriamycin; leucomycin; nidamycin; acyA.
Streptomyces thermotolerans ATCC 11416.
EP-459525-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R15428 standard; Protein; 389 AA.
R15428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 7; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.1%;
83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-JUN-1991; 109033.
01-JUN-1990; JP-141625.
22-FEB-1991; JP-048753.
(SAOC ) MERCIAN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity
--hea 5; Conserv?
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Best Local Similarity
Matches 5; Conserv
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N-PSDB; Q14978.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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RESULT

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Gaps

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Indels

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(first entry)

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from Bacillus thuringiensis ser. jegathesan 367 (Bfjeg367); it is a crystal torin to find. Wt. 80 kD which is active against dipteran insects, esp. mosquitces. The full-length, recombinant DEG80 toxin, had mean LC50 values (in ng/ml) after 48 hours of 18.8, 42.7 and 10.1 against larvae of Aedes agapyti. Anopheles stephensi and Culex pipiens, respectively. Wild-type Btjeg367 crystals gave values of 47.4, 54.5 and 9.6. The JEG80 protein is far more toxic (6-40 times more toxic against the mosquito species tested) than the Bt CryIVD toxin, despite their close sequence similarity.
                                                                                                                                                                                 Bacillus thuringiensis insecticidal protein JEG80.
Insecticidal crystal toxin; jeg80; anti-diptera; mosquito; larvae;
Aedes aegypti; Anopheles stephensi; Culex pipiens; Btjeg 367.
Bacillus thuringiensis ser. jegathesan 367.
                                                                                                                                                                                                                                                                                                                                                                                                                             New B.thuringlensis ser. jegathesan insecticidal proteins - and related DNA, with high activity against dipteran larvae, e.g. A.aegypti, A.stephensi or C.pipiens Claim 17; Fig 5; 55pp; French.
                                                                                                                            R93081 standard; Protein; 724
                                                                                                                                                                                                                                                                                                         24-AUG-1995; F01116.
25-AUG-1994; FR-010299.
(INSP ) INST PASTEUR.
Delecluse A, Thiery I;
                                                                                                                                                                                                                                                                                                                                                                      Delecluse A, Thie
WPI; 96-151374/15.
    1111:1
432 YRLLLR 437
                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; T17044
                                                                                                                                                                -OCT-1996
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                                                                                                                                             R93081
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Claim 1: Page 4-5: 43pp: English.

The present sequence represents a gidal protein of Staphylococcus aureus. Gidal proteins, nucleic acids and agonists are used to treat conditions requiring increased activity or expression of gidal, while conditions (particularly bacterial infections) requiring inhibitory nucleic acid or competitive polypeptide. The products are used to treat S. pneumoniae infection, particularly meningits and side these antibacterial infections e.g. related cancers, ulcers and gastritis. These antibacterial agents may also be used to treat in-dwelling devices to prevent infection or generally as wound treatments to prevent adhesion of bacteria to matrix proteins.
                                                                                               Example: Page 45-47; 77pp; English

Example: Page 45-47; 77pp; English

This N-succinyl-L-diaminopimelic acid desuccinylase is encoded by
This N-succinyl-L-diaminopimelic acid desuccinylase is encoded by
This N-succinyl-L-diaminopimelic acid desuccinylase is encoded by
the newly isolated dapE gene (see V42319 and V4232) of
Helicobacter pylori strain 60190. It shows 37.9% identity and
(1.0% similarity with the DapE protein of E. coli. Conditionally
lethal dapE- mutant H. pylori strains are provided; a claimed dapE-
mutant is deposited as ATCC 55897. Such mutants can be used in a
claimed method of immunising a subject against H. pylori infection.
The dapE- mutants can also be used as hosts of nucleic acids
encoding foreign proteins. Such mutants can be used in claimed
methods of immunising against bacterial, viral, fungal or parasite
infections. Sperm antigens may also be expressed for use in birth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-1999 (first entry)
A gidAl protein sequence.
GidAl; bacterial infection; meningitis; Helicobacter pylori infection; cancer; ulcer; gastritis; antibacterial; in-dwelling device; wound treatment; bacterial adhesion; matrix protein.
Blaser MJ, Karita M;
WPI: 98-377287/32.
N-PSDB; V42319 and V42322.
Helicobacter pylori dapE gene and related protein - used to create a mutant used in immunisation against infection by e.g. HIV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 27; DB 1; Length 621;
Pred. No. 1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SMIK ) SMITHKLINE BEECHAM CORP.
(SMIK ) SMITHKLINE BEECHAM PLC.
Burnham M. Kallender H, Lenox AL, Palmer LM;
WPI; 99-062660/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W89445 standard; Protein; 625 AA W89445;
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83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.1%;
ilarity 83.3%;
Conservative
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01-JUL-1997; US-052758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus.
EP-889129-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                            621 AA;
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Gaps
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Claim 10; Page 54-56; 73pp; English.

The NWD2 gene (T31993) is named after its role in the Nonsense-Mediated mRNA Decay pathway. The protein, Nmd2p, binds to Upflp.

A C-terminal fragment of the protein (T31994) also binds to Upflp and, when overexpressed in the host cell, the fragment inhibits the function of Upflp, thereby inhibiting the nonsense-mediated
                                    ö
 Length 724;
                                    Indels
                                                                                                                                                                                                                                                Nonsense-mediated mRNA decay 2 C-terminal.
Nonsense-mediated mRNA decay; NMD2; Upflp; inhibition.
93.1%; Score 27; DB 1; Le
83.3%; Pred. No. 1.2e+02;
tive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                      25-JUL-1996.
27-DEC-1995: U16930.
20-JAN-1995: US-375300.
(UYMS-) UNIV MASSACHUSETIS MEDICAL CENT.
He F, Jacobson AS;
                                                                                                                                                                                               W01897 standard; Protein; 764 AA.
                                                                                                                                                                                                                                   (first entry)
                                    5; Conservative
                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae
 Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA decay pathway
                                                                                                                                                                                                                                                                                                                                                                                              He F, Jacobson AS
WPI; 96-354469/35.
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548 YRLIIR 553
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                                                                     1 YRLLIR 6
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Gaps

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0; Indels

1; Mismatches

Conservative

1 YRLLIR 6

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Query Match
Best Local Similarity
Matches 5; Conserv
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|11 YRLVIR 16
                                                                                                                                                                                                                                                                                 1 YRLLIR 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Suzuki S;
                                                                                                                                                                                                        Sequence
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Polynucleotide sequences encoding new proto:cadherins - useful for modulating natural binding and regulating activities.
Example: Page 63; 114pp; English.
Two regions of conserved AA sequence, one from the middle of the third cadherin extracellular subdomain (EC-3) and the other from the C-terminus of the fourth extracellular subdomain (EC-4) were identified. The corresp. degenerate oligos (Q68949, Q68950) were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                     Gaps
                                                                                                                                                                                                                                                                                                   Note that the protein of develop methods for inhibiting the decay pathway for producing netrologous or endogenous proteins
Claim 8: Page 49-52; 73pp; English.

The NWD2 gene (T31993) is named after its role in the Nonsense-Mediated mRNA Decay pathway. The protein, NMd2p, binds to Upflp, when overexpressed in the host cell, the fragment inhibits the function of Upflp, thereby inhibiting the nonsense-mediated mRNA decay pathway.

Sequence 1089 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 27; DB 1; Length 1089;
Pred. No. 1.8e+02;
1; Mismatches 0; Indels
                              Length 764;
                              Score 27; DB 1; Length 764
Pred. No. 1.2e+02;
1; Mismatches 0; Indels
                                                                                                                                                                     24-NOV-1996 (first entry)
Nonsense-mediated mRNA decay 2 protein.
Nonsense-mediated mRNA decay; NMD2; Upflp; inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-APR-1995 (first entry)
Drosophila-12 cadherin-related molecule.
Cadherin; cell adhesion molecule.
                                                                                                                                                                                                                            25-JUL-1996.
27-DEC-1995; U16930.
20-JAN-1995; US-375300.
(UYMA-) UNIV MASSACHUSETTS MEDICAL CENT.
He F, Jacobson AS;
WPI; 96-354469/35.
                                                                                                                                                    W01896 standard; Protein; 1089 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R58902 standard; Protein; 43 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                93.1%;
83.3%;
                              93.1%;
83.3%;
                                                    5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Conservative
                                                                                                                                                                                                        Saccharomyces cerevisiae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (DOHE-) DOHENY EYE INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUL-1994.
23-DEC-1993; U12588.
29-DEC-1992; US-998003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 5; Conserv
                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94-293849/36.
 764 AA
                                                                                               255 YRILIR 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          580 YRILIR 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; Q68993
                                                                         1 YRLLIR 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YRLLIR 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila.
WO9414960-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Suzuki S;
 Sequence
                                                                                                                              RESULT 12
W01896
                                                    Matches
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NPIN 96 068873/07.

NPSDB; T03617.

NPSDB; T03617.

NPSDB; T03617.

PP Polynucleotide(s) encoding human protocadherins pc3 and pc4 and rat pc1, nucleotide(s) encoding human protocadherins pc5 - involved in cell-cell adhesion and regulation activities

Example 2; Page 67-68; 146pp; English.

R87142-R87144 represent partial fragments of the drosophila protocadherin consequence. The CDNAs encoding these sequences were isolated after consequences. The primers were constructed from portions of the in T03575 and T03576. The primers were constructed from portions of the canno acid sequences of the third and fourth extracellular domains of published cadherin sequences. The cytoplasmic domain of cadherin catherins and other cytoskeleton through catenins and other cytoskeleton associated proteins. The cytoplasmic domain is not present in all cadherins, but in those which possess it, it is essential for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-AUG-1996 (first entry)
Protocadherin clone DROSOPHILA-12.
Protocadherin; pc3; pc4; pc5; human; rat; cadherin; cell adhesion; mouse; catenin; therapy; clone; frog; fruit fly.
designed for use as PCR primers. PCR was carried out on a rat brain cDNA prepn. Two major bands of about 450 bps and 130 bps were found. The 450 bp band corresponded to the expected length between the two primer sites, but the 130 bp band could not be predicted from any of the previously identified cadherin sequences. The 450 bp and 130 cf the previously identified cadherin sequences. The 450 bp and 130 clones were extracted and sequenced. Nineteen novel partial cDNA clones were isolated. The DNA and deduced AA sequences of the clones (including sequences corresp. to the PCR primers) are given in 068951-068969 and R58860-R58978. Various cDNA fragments structurally similar to the rat cDNAs were isolated from human, mouse and Xenopus brain cDNA prepns. and from Drosophila and c. elegans whole body cDNA prepns. by PCR using the above primers. The DNA and deduced AA sequences of the resulting PCR fragments (including sequences corresp. to the PCR primers) are given in 068971, Q68972-Q68994 and R58882-R58905 and R49143. Comparison cf the deduced AA sequences indicates a similarity, in particular, there are three sets of clones that appear to be cross-species commons. The DNA mouses: RAT-218, MOUSE-322 and HUMAN-43; RAT-314, MOUSE-321 and HUMAN-11; and MOUSE-322 and HUMAN-43; RAT-314, MOUSE-321 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89.7%; Score 26; DB 1; Length 43; 83.3%; Pred. No. 11; 0; Indels ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "encoded by CGA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "encoded by ATG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "encoded by ACA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "encoded by ATG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "encoded by CGC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R87142 standard; Peptide; 43 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-JAN-1996.
26-JUN-1995; UO8071.
27-JUN-1994; US-268161.
(DOHE-) DOHENY EYE INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster
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cadherins adhesive function. The cadherins which do not possess a cytoplasmic domain appear to function via a different method from those with a cytoplasmic domain. These protein sequences are involved in cell-cell adhesion. These sequences may have regulatory functions in the cell, as well as the cell-cell adhesive properties. Antibodies produced against these sequences are useful for modulating the binding activity of these protocadherins, and can be used therapeutically.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a purified rat pro-hormone convertase, designated PC7. PC7 is a member of the subtilisin-kexin protein family, it is widely distributed (especially in lymphoid tissue) and is a possible maturation enzyme for gp160 in target CD4+ cells. Since PC7 has been found in many brains of patients with Alzheimer's disease and
                                                                                                                                                                                                                                                                                                                                                                        Rat spleen pro-hormone convertase 7.
PC7: HIV gpl60; human immunodeficiency virus; Alzhelmer's disease;
Down's syndrome; AIDS; inhibitor; antibody; subtilisin-kexin protein;
lymphoid tissue; CD4+ cell; rat; human.
Rattus rattus.
                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human and rat pro-hormone convertase, PC7, can cleave HIV gp160 may allow early diagnosis of Alzheimer's disease and Down's syndrome, also PC7 inhibitors are used to prevent development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Putative transmembrane anchoring domain"
                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137. .140
/note= "Putative zymogen activation site"
                                                                                                                                                          Length 43;
                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "Putative glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note- "Putative glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note- "Putative glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note- "Putative glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "Putative phosphorylation"
                                                                                                                                                          DB 1;
11;
                                                                                                                                                                                        Mismatches
                                                                                                                                                          Score 26;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                label- Oxyanion_hole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-OCT-1995; US-545562.
02-AUG-1995; US-510347.
18-AUG-1995; US-517015.
(FECL-) INST RECH CLINIQUES MONTREAL.
Chretien M, Day R, Seidah NG:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 29-31; 52pp; English.
                                                                                                                                                                                                                                                                                                                             W27113 standard; Protein; 783 AA.
                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . . . 36
label = Signal
                                                                                                                                                          89.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label- PC7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "F
                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 783
                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-AUG-1996; CA0520
                                                                                                                                                          Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 97-145693/13.
N-PSDB: T85113.
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                                                                                                                                                                                                                                        |||:||
11 YRLVIR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     active_site
active_site
modified_site
                                                                                                                                                                                                                     1 YRLLIR 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               active_site
modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09705256-A2
                                                                                                                                                                                                                                                                                                                                                           20-NOV-1997
                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
                                                                                                                                                                                                                                                                                                                                             W27113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               region
                                                                                                                                                                                                                                                                                                  RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AIDS
                                                                                                                                                                                                                                                                                                                                                              셤
    888888888
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CC also contemplated that over-expression of PC7 may protect against the disease. Antibodies against PC7 are used to detect/quantify PC7 in cells and tissues, and oligonucleotides able to hybridise to a PC7 coding sequence, are used similarly at the nucleic acid (especially CC mRNA) lavel. Oligonucleotides can also be used to amplify PC7-encoding convert precursors to mature proteins, especially HIV gp160 to CC mRNA) lavel. Oligonucleotides or vectors expressing them, are used to prevent expression of PC7 in cells susceptible to HIV CC infection; they prevent expression of PC7 in cells susceptible to HIV CC infection to AIDS.

Query Match

R89.7%; Score 26; DB 1; Length 783;

Best Local Similarity 83.3%; Pred. No. 2.2e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps

Qy 1 YRLIN 6

1 YRLIN 6

Search completed: February 8, 2000, 01:29:36
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

February 7, 2000, 11:54:16; Search time 117.7 Seconds (without alignments) 2.405 Million cell updates/sec Run on:

US-08-653-294-6 29 1 YRLLIR 6 Title: Perfect score:

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

142080 segs, 47169319 residues

Searched:

142080 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\* PIR\_62:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

| SUMMAKLES | Description                  | 75 probable |      | hypotheti | hypothetical | hypothetical |      | macrolide 3-0 |      | E64546 glucose inhibited |      | 164078 gida protein - Hae |      | A48723 replication licens | 4    |      | hypothetical pr | hypothetical | endonuclease | A71869 integrase/recombin | hypothetical | hypothetical | hypothetical |      | 6 subtilisin- |      | proteasome ch |      | T08009 probable ribosomal |   |
|-----------|------------------------------|-------------|------|-----------|--------------|--------------|------|---------------|------|--------------------------|------|---------------------------|------|---------------------------|------|------|-----------------|--------------|--------------|---------------------------|--------------|--------------|--------------|------|---------------|------|---------------|------|---------------------------|---|
|           | DB ID                        | :           | 2 S6 |           |              |              |      |               |      |                          |      |                           |      |                           | 2 T1 |      |                 |              |              |                           |              |              |              |      |               |      |               |      |                           | • |
|           | g<br>Query<br>Match Length D | :           | 1489 |           |              |              |      |               |      |                          |      |                           |      |                           |      | 680  |                 |              |              |                           |              |              |              | m    |               |      |               | _    | 271                       |   |
| d         | Query<br>Match               | . 9         | 96.6 | m         | 93.1         | 93.1         | 93.1 | 93.1          | 93.1 | 93.1                     | 93.1 | 93.1                      | 93.1 | 93.1                      | 93.1 | 93.1 | 89.7            | 89.7         | 89.7         | 89.7                      | 89.7         | 89.7         | 89.7         | 89.7 | 89.7          | 86.2 | 86.2          | 86.2 | 86.2                      |   |
|           | Score                        | 28          | 28   | 27        | 27           | 27           | 27   | 27            | 27   | 27                       | 27   | 27                        | 27   | 27                        | 27   | 27   | 26              | 56           | 26           | 26                        | 56           | 26           | 56           | 56   | 26            | 25   | 25            | 25   | 25                        |   |
|           | Result<br>No.                | 1           | 7    | m         | 4            | 5            | Ø    | 7             | 89   | σ                        | 10   | 11                        | . 12 | 13                        | 14   | 15   | 16              | 17           | 18           | 19                        | 20           | 21           | 22           | 23   | 24            | 25   | 26            | 27   | 28                        | • |

| hypothetical prote | perinuclear bindin | hypothetical prote | glucose inhibited | qidA protein - Pse | hypothetical prote | probable DNA-direc | hypothetical 9.1K | hypothetical prote | hypothetical prote | hypothetical prote | DIL protein - vari | hypothetical prote | E6 protein - human | E6 protein - human |  |
|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--|
| D72684             | A56486             | H71303             | BVECQA            | BWPSAP             | S76371             | T07448             | S47689            | D70886             | IEECE9             | E71728             | A36837             | D71689             | W6WL18             | W6WL39             |  |
| n                  | ~                  | N                  | н                 | Н                  | 0                  | ~                  | ~                 | ~                  | Н                  | ~                  | ~                  | -                  | Н                  | н                  |  |
| 380                | 416                | 605                | 629               | 630                | 635                | 1075               | 81                | 87                 | 96                 | 149                | 153                | 156                | 158                | 158                |  |
| 7                  | ۲.                 | ď                  | ņ                 | ~                  | 7                  | ?                  | æ                 | æ                  | æ                  | œ.                 | œ                  | æ                  | œ                  | ω.                 |  |
| 86                 | 86                 | 86                 | 86                | 98                 | 86                 | 86                 | 82                | 82.8               | 82                 | 82                 | 82                 | 82                 | 82                 | 82                 |  |
| 25                 | 25                 | 25                 | 25                | 25                 | 25                 | 25                 | 24                | 24                 | 24                 | 24                 | 24                 | 24                 | 24                 | 24                 |  |
| 31                 | 32                 | 33                 | 34                | 32                 | 36                 | 37                 | 38                | 33                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |  |

### ALIGNMENTS

A; Gene: APE2443

Gaps ö 96.6%; Score 28; DB 2; Length 325; 83.3%; Pred. No. 21; ive 1; Mismatches 0; Indels Conservative Query Match Best Local Similarity Matches 5; Conserv

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||||:| 209 YRLLVR 214 1 YRLLIR 6 à 셤

Solution by Alternate names: protein G1880

N.Alternate names: protein G1880
C.Species: Saccharomyces cerevisiae
C.Accession: S60416; S53049; S60421; S64166; S64164
R.James, C.M.; Indge, K.J.; Oliver, S.G.
A.Description: DNA Sequence analysis of a 35kb segment from Saccharomyces cerevisiae
A.Residues: 1-1489 c.JMA
A.Residues: 1-1489 c.JMA
A.Residues: 1-1489 c.JMA
A.Residues: C.M.; Indge, K.J.; Oliver, S.G.
Submitted to the EMBL Data Library, March 1995
A.Description: DNA sequence analysis of a 35kb segment from S.cerevisiae chromosome V
A.Reference number: S33045
A.Decession: S53049
A.Rocicule type: DNA
A.Residues: B16-1489 c.JAW>
A.Residues: B16-1489 c.JAW>
A.Residues: B16-1489 c.JAW>
A.Residues: B16-1489 c.JAW>
A.Residues: EMBL: EMBL: B48618; NID:9728690; PID:9728695

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hypothetical protein YFR008w - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 02-Sep-1995 #sequence_revision 19-Oct-1995 #text_change 05-Dec-1997
C;Accession: S56263
R;Murakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sas submitted to the EMBL. Data Library, May 1995
A;Description: Analysis of the nucleotide sequence of chromosome VI from Saccaromyces A;Reference number: S56186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-221 <MUR>
A;Cross-references: EMBL:D50617; NID:g836685; PID:d1009888; PID:g836763; MIPS:YFR008w
                                                                                                                                                                                                                                                                             A.Cross-references: GB:AJ248287; GB:AL096836; NID:95458657; PIDN:CAB50333.1; PID:e151
A.Experimental source: strain Orsay
Genetics: A.Genetics: A.Gene
sucmitted to the EMBL Data Library, July 1999
A; Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome
A; Reference number: A75001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 06-Feb-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: EMBL: 249635; NID: 91015871; PID: 91015872; MIPS: YJR135c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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25;
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Llarity 83.3%; Pred. No. 27;
Conservative 1; Mismatches
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Pred. No. 18;
1; Mismatches
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Pred. No. 25;
1; Mismatches
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A;Cross-references: SGD:S0003896; MIPS:YJR135c
A;Map position: 10R
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R.Ross, M.; Koetter, P.; Entian, K.D.
submitted to the Protein Sequence Database,
A.Reference number: S56848
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83.3%;
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Matches 5; Conserv
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Best Local Similarity
Matches 5; Conserv
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-157 < KAW>
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211 YRLLLR 216
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                          R;James, C.M.; Indge, K.J.; Oliver, S.G.
Yeast 11, 1413-1419, 1995
A;Title: DNA sequence analysis of a 35 kb segment from Saccharomyces cerevisiae chromosof A;Title: DNA sequence analysis of a 35 kb segment from Saccharomyces cerevisiae chromosof A;Reference number: $60417; MUID:96158061
A;Accession: $60421
A;Status: nucleic acid sequence not shown
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A;Description: Saccharomyces cerevisiae chromosome V cosmids 9871, 8199, 9867, 9495 and A;Reference number: S50428
A;Accession: S50445
A;Molecule type: DNA
A;Residues: 1-101 <DIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL: Z72672; NID:g1322733; PID:e243594; PID:g1322734; MIPS:YGL150c A;Experimental source: strain S288C
R;Volckaert, G.; Voet, M.; Verhasselt, P.; Defoor, E. submitted to the protein Sequence Database, May 1996
A;Reference number: S64153
A;Accession: S64164
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C;Species: Saccharomyces cerevisiae
C;Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 26-Aug-1999
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C;Species: Pyrococcus abyssi
C;Bate: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: H75054
R;anonymous, Genoscope
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A; Residues: 728-767, 808-862; 865-969; 1001-1021; 1296-1347; 1360-1468 <JAF>
A; Cross-references: EMBL: 248618
R; James, C.M.; Indge, K.J.; Oliver, S.G.
submitted to the Protein Sequence Database, May 1996
A; Reference number: S64165
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C;Superfamily: Saccharomyces hypothetical protein YEL014c
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93;
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Pred. No. 93;
1; Mismatches
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A;Experimental source: strain $288C
Genetics:
A;Map position: 7L
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Best Local Similarity 83.3%;
Matches 5; Conservative
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A; Molecule type: DNA
A; Residues: 1-1489 <JAA>>
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R;Dietrich, F.S.
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92 YRMLIR 97
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C) Accession: 140440; S6625; 669631; J01216; S18076

R) CAccession: 140440; S6625; 669631; J01216; S18076

R) Concession: 140440; S6625; 669631; J01216; S18076

R) Concession: 140440; MIDD:92204018

A) Reference number: 140435; MIDD:92204018

A) Reference number: 140435; MIDD:92204018

A) Reference number: Strain CRK2000

A) RCTOSS TESTERCENCES BEALL: REAL ORGANOW

A) Residues: 1-628 CRES

A) ACCOSS TESTERCENCES BEALL: REAL ORGANOW

A) Residues: 1-638 CRES

A) ACCOSS TESTERCENCES

A) Residues: Systematic C sequencing of the 180 kilobase region of the Bacillus subtilis ch

A) Residues: Systematic C sequencing of the 180 kilobase region of the Bacillus subtilis ch

A) Residues: Systematic C sequencing of the 180 kilobase region of the Bacillus subtilis ch

A) Residues: Systematic C sequencing of the 180 kilobase region of the Bacillus subtilis ch

A) Residues: Systematic C sequencing of the 180 kilobase region of the Bacillus subtilis ch

A) Residues: Sostematic C sequencing of the 180 kilobase region of the Bacillus Subtilis ch

A) Residues: Sostematic C sequencing of the 180 kilobase region of the Bacillus Subtilis ch

A) Residues: Declaration

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A) Adultors: Declaration

A) Adultors: Declaration

A) Adultors: Poulgar, D, Fritz, C.; Fulta, M.; Fulta, M.; Fulta, M.; Mauda, S.; Hallo, M.; Ber

C,; Broom, S,; Broulliet, S,; Bruschin, C. V.; Caldeell, S.; Rosnow, V.; Carter, M.; Ruschin, C. V.; Sealle, M.; Rivitta, M.; Rosnow, M.; Kurita, K.; Fabre, M.; Randon, M.; Anthors: Labolus, A.; Sealle, S.; Schroeter. R.; Scoffone, F.; Sealle, M.; Sealle, S.; Schroeter. R.; Scoffone, F.; Sealle, M.; Rathors: Scollesch, S.; Schroeter. R.; Scoffone, F.; Vasunoco, K.; Yata, K.; Yat
C; Accession: E64546

R; Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R
Peterson, S.; Loffus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; MoKe
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey,
Nature 388, 539-547, 1997

A; Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
A; Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A; Reference number: A64520; MUID:97384467

A; Reference number: A64520; MUID:97384467

A; Residues: 1-621 cmx
A; Residues: 1-621 cmx
A; Residues: 1-621 cmx
A; Residues: GB:AE000541; GB:AE000511; NID:92313299; PIDN:AAD07281.1; PID:9231
C; Superfamily: gidA protein
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Pred. No. 70;
1; Mismatches
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83.3%;
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Best Local Similarity
Matches 5; Conserv
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Residues: 1-628 <KUN>
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432 YRLLLR 437
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C;Species: Helicobacter pylori
A;Variety: strain 599
C;Species: Helicobacter pylori
A;Variety: strain 599
C;Saccession: D71961
B;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A;Reference number: A71800; MUD:99120557
A;Recession: D71961
A;Status: preliminary
A;Molecule type: DNA
A;Status: preliminary
A;Molecule type: DNA
A;Status: alsolusis: 1-621 ARN>
A;Cross-references: GB:AE001458; GB:AE001439; NID:g4154713; PIDN:AAD05783.1; PID:g415472
A;Experimental source: strain J99
C;Genetics:
A;Gene: gidA
C;Superfamily: gidA protein
                                                                                                                                                                                                                                                                                                                                                                  Cipate: Streptomyces sp.
Cipate: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 18-Jun-1999
Riatiate: Structure 1995 #sequence analysis of the carbomycin biosynthetic genes including the A; Fitle: Nucleotide sequence analysis of the carbomycin biosynthetic genes including the A; Reference number: JC4001 MUID:95290751
A; Molecule type: DNA
A; Molecule type
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glucose inhibited division protein - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Species: O9-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 26-Aug-1999
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Pred. No. 70;
1; Mismatches
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C;Superfamily: 4''-0-acyltransferase
C;Keywords: acyltransferase
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83.38;
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83.3%;
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Best Local Similarity 83.3
Matches 5; Conservative
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C:Species: Helicobacter nvl
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Best Local Similarity
Matches 5; Conserv
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205 YRLLLR 210
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replication licensing factor MCM5 - fission yeast (Schizosaccharomyces pombe)
N;Alternate names: cell division control protein CDC46; cell division control protein C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 13-Aug-1999
C;Accession: A48723
R;Miyase, S:,Okishio, N:; Samejima, I:; Hiraoka, Y:; Toda, T:; Saitoh, I:; Yanagida, Mol. Biol. Cell 4, 1003-1015, 1993
A;Title: Fission yeast genes ndal(+) and nda4(+), mutations of which lead to S-phase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A) Description: part of the replication licensing system that permits DNA replication C; Superfamily: replication licensing factor MCM5; MCM homology C; Reywords: cell cycle control; DNA replication initiation; nucleus
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A; Description: Cloning, sequencing and characterization of a beta-mannanase gene of A; Reference number: 217115
A; Reference number: 217115
A; Accession: T10748
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Complex: The predominant form is a heterohexamer of MCM2, MCM3, MCM4, MCM5, MCM6, C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: not compared with conceptual translation
A;Status: not compared with conceptual translation
A;Status: not compared with conceptual translation
A;Residues: 1-720 CMIY>
A;Cross-references: GB:S68467; NID:g545210; PIDN:AAC60568.1; PID:g545211
C;Comment: The complex of six MCM proteins is one of several proteins that must be phosphorylated and dissociate from the chromatin.
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  Gaps
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  Indels
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A;Cross-references: EMBL:X90947; NID:e1249550; PID:e1249551
A;Experimental source: strain ATCC 43812
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Pred. No. 1.1e+02;
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A;Accession: A48723
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A,Gene: manA
C,Keywords: glycosidase; hydrolase
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83.3%;
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Best Local Similarity 83...
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R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
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A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rifieischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, P. Godsyne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weldman, J.D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
Alvathors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630
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A; Residues: 1-629 <TICR>
A; Cross-references: GB:U32739; GB:L42023; NID:g1573559; PIDN:AAC22240.1; PID:g1573570; C; Genetics: A; Gene: gida
C; Superfamily: gida protein
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A;Experimental source: strain MSB8
C;Genetics:
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N:Alternate names: glucose-inhibited division protein
C;Species: Haemophilus influenzae
C;bate: 18-Aug.1995 #sequence_revision 18-Aug-1995 #text_change 26-Aug-1999
C;Accession: I64078
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C;Date: 11-Jun_1999 #sequence_revision 11-Jun-1999 #text_change 23-Jul-1999
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A;Status: nucleic acid sequence not shown; translation not shown
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71;
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71;
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Pred. No. 71;
1; Mismatches
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1; Mismatches
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Pred. No.
                                                                                                                                                          93.1%;
83.3%;
A; Experimental source: strain 168
C; Genetics:
A; Gene: gidA
C; Superfamily: gidA protein
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83.3%;
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83.3%;
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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C,Superfamily: gidA protein
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                1111:1
435 YRLLLR 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |||||:|
| 435 XRLLLR 440
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                                                                                                                                                                                                                                                               1 YRLLIR 6
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A:Molecule type: DNA
A:Residues: "MYQO',3-1089 <FAV>
A:Cross-rescences: EMBL:U10556; NID:9500825; PID:9500836; MIPS:YHR077c
A:Lee, S.I.; Umen, J.G.; Varnus, H.E.
Aroc. Natl. Acad. Sci. U.S.A. 92, 6587-6591, 1995
A:Title: A genetic screen identifies cellular factors involved in retroviral -1 frameshials Reference number: S64648; MUID:95327692
NWD2 protein - yeast (Saccharomyces cerevisiae)

N;Alternate names: IFS1 protein; protein YHR077c

C;Species: Saccharomyces cerevisiae

C;Date: 28-Oct-1994 #sequence_revision 10-Feb-1995 #text_change 06-Feb-1998

C;Accession: S48244; S46815; S64648; S64738

R;He, F; Jacobson, A

submitted to the EMBL Data Library, September 1994

A;Description: Identification of a novel component of the nonsense-mediated mRNA decay |

A;Reference number: S48244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Pred. No. 1.2e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                     A.Molecule type: DNA
A.Residues: 1-1089 <HEF>
A.Residues: 1-1089 <HEF>
A.Cross references: EMBL:014974; NID:9555938; PID:9555939
R.Favello, T.
Submitted to the EMBL Data Library, June 1994
A.Description: The sequence of S. cerevislae cosmid 9205.
A.Reference number: $46794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Molecules: 1-1089 < LEE>
A:Cross-references: EMBL:U28158
A:Varmus, H.E.
submitted to the EMBL Data Library, May 1995
A:Reference number: S64738
A:Accession: S64738
A:Accession: S64738
A:Molecule type: DNA
A:Residues: 'MYQQ',3-1089 < VAR>
A:Cross-references: EMBL:U28158; NID:9967212; PID:9967213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: SGD:NMD2; IFS1
A;Cross-references: SGD:S0001119; MIPS:YHR077c
A;Map position: 8R
A;Introns: 2/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 93.1%;
Best Local Similarity 83.3%;
Matches 5; Conservative
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Search completed: February 7, 2000, 11:54:18 Job time: 24328 sec

1 YRLLIR 6 ||:||| 580 YRILIR 585

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1. 1. 1. 1. 1.

# GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

February 8, 2000, 00:59:46; Search time 63.71 Seconds (without alignments) 2.813 Million cell updates/sec

US-08-653-294-6 29 1 YRLLIR 6

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

82229 seqs, 29864866 residues Searched:

82228 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

SwissProt\_38:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           |            | Description | sac  | P39999 saccharomyc |            | P47167 saccharomyc |            |            |            |            |            |      | P49425 rhodothermu |            |            |           | O76190 bombyx mori | carassiu   |            |            |            |           |            |            |           | P26321 saccharomyc |           |     |            |            |            |            |            | P37618 escherichia | arap       | 095276 sus scrofa |
|-----------|------------|-------------|------|--------------------|------------|--------------------|------------|------------|------------|------------|------------|------|--------------------|------------|------------|-----------|--------------------|------------|------------|------------|------------|-----------|------------|------------|-----------|--------------------|-----------|-----|------------|------------|------------|------------|------------|--------------------|------------|-------------------|
|           |            |             |      |                    |            |                    |            |            |            |            |            |      |                    |            |            |           |                    |            |            |            |            |           |            |            |           |                    |           |     |            |            |            |            |            |                    |            |                   |
| SUMMARIES |            | ΙD          | - 1  | YEB4_YEAST         | YFH8_YEAST | YJ9D_YEAST         | TF2B_SULSH | GIDA_HELPY | GIDA_COXBU | GIDA_BACSU | GIDA_HAEIN |      | MANA_RHOMR         | NMD2_YEAST | YF1M_CAEEL | RL5_CAEEL | RL5_BOMMO          | PRC3_CARAU | PRC3_XENLA | PRC3_DROME | LPXA_CHRVI | RL5_DUNSA | RL5A_SCHPO | RL5B_SCHPO | RL5_HELAN | RL5_YEAST          | RL5_NEUCR |     | GIDA_ECOLI | GIDA_PSEPU | GIDA_SYNY3 | RPOB_PINTH | LML2_CAEEL | YHHP_ECOLI         | SR14_ARATH | RL5_PIG           |
|           |            | DB          | Н    | Н                  | Н          | Н                  | Н          | -          | ٦          | Н          | Н          | -1   | -1                 | ~          | Н          | П         | Н                  | -          | Н          | Н          | ٦          | н         | -          | -          |           | -                  | Н         | Н   |            |            | -1         | Н          | -          | 7                  | н.         | П                 |
|           |            | Length      | 1489 | 101                | 221        | 239                | 309        | 621        | 627        | 628        | 629        | 720  | 1021               | 1089       | 1459       | 293       | 299                | 233        | 233        | 234        | 259        | 271       | 294        | 294        | 297       | 297                | 301       | 535 | 629        | 630        | 635        | 1075       | 3672       | 81                 | 121        | 124               |
|           | %<br>Ouerv |             | 9.96 | 93.1               | 93.1       | 93.1               | 93.1       | 93.1       | 93.1       | ω.         | æ.         | 93.1 | m.                 | m          | 3          | σ         | O                  | 9          | 9          | 9          | 9          | 9         | 9          | ø          | Ø         | o                  | ø         | മ   | S          | o          | Ø          | o          | o          | 87.8               | N I        | 82.8              |
|           |            | Score       | 28   | 27                 | 27         | 27                 | 27         | 27         | 27         | 27         | 27         | 27   | 27                 | 27         | 27         | 56        | 56                 | 25         | 25         | 25         | 25         | 25        | 25         | 25         | 25        | 25                 | 25        | 25  | 25         | 25         | 25         | 25         | 25         | 24                 | 24         | 24                |
|           | Result     | NO.         | н    | 7                  | m          | . 4                | 2          | 9          | 7          | ω          | 6          | 10   | 11                 | 12         | 13         | 14        | 15                 | 16         | 17         | 18         | 19         | 20        | 21         | 22         | 23        | 24                 | 25        | 26  | 27         | 28         | 29         | 30         | 31         | 32                 | 33         | 34                |

| 092dj8 rickettsla<br>P06463 human papil<br>P24835 human papil<br>P21735 human papil<br>P21100 vaccinia vi<br>065729 cicer ariet<br>P42791 arabidopsis<br>P44189 haemophilus<br>P30198 staphylococ<br>Q10474 schizosacch |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
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|                                                                                                                                                                                                                         |
| Y330_RICPR<br>VE6_HPV18<br>VE6_HPV39<br>VE6_HPV45<br>VE6_HPV68<br>VC16_VACCC<br>VC16_VACCC<br>RL18_CICAR<br>RL18_ARAIH<br>YE18_HARIN<br>YE18_HARIN<br>YET8_SCHPO                                                        |
| ненненненне                                                                                                                                                                                                             |
| 1158<br>1158<br>1158<br>1158<br>1158<br>1158<br>1158<br>1158                                                                                                                                                            |
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# ALIGNMENTS

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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                  211 YRLLLR 216
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205 YRLLLR 210
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ID TF2B_SULSH
AC P50387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical
SEQUENCE 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996
01-OCT-1996
                                                                                                                                                                                                                                                                                         1 YRLLIR
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                                                                                                                                                                                                                                                                                                                                                                             YJ9D_XEAST
P47167;
                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                        STRAIN-S288C / AB972;
DIETRICH F.S., MULLIGAN J.T., HENNESSEY K.M., ALLEN E., ARAUJO R., AVIETRICH F.S., MULLIGAN J.T., CHENTER J., CHEN E., CHENRY J.M., AVIETRE E., BERNO A., BRENNO A., GUZMAN E., HARTZELL G., HUNICKE-SMITH S., HYMAN R., KAYSER A., KOMP C., LASHKARI D., LEW H., LIN D., MOSEDALE D., NAKAHARA K., NAWATH A., NORGREN R., OSEPNER P., OH C., PETEL F.X., ROBERTS D., SEHL P., SCHRAMM S., SHOGREN I., SMITH V., SUDMILLED (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-S288C / AB972;
MEDLINE: 95400292.
MURAKAMI Y., NAITOU M., HAGIWARA H., SHIBATA T., OZAWA M.,
SASANUMA S.-I., SASANUMA M., TSUCHIYA Y., SOEDA E., YOKOYAMA K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
HYPOTHETICAL 25.9 KD PROTEIN IN MPRI-GCN20 INTERGENIC REGION
                                                                                                                                                               01-FEB-1995 (Rel. 31, Created)
1-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL 12.2 KD PROTEIN IN PMP2-VAC8 INTERGENIC REGION.
DB 1; Length 1489;
49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 27; DB 1; Length 101;
Pred. No. 5.3;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 protein.
101 AA; 12209 MW; BE5A484B CRC32;
                                                                                                                                        101 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           221 AA
                        1; Mismatches
 Score 28;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                         PRT;
                                                                                                                                                                                                                                                       Saccharomycetaceae; Saccharomyces.
 96.6%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.1%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U18530; AAB64491.1; -.
                          5; Conservative
                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 5; Conserv
           Best_Local Similarity
Matches 5; Conser
                                                                                                                                                              01-FEB-1995 (Rel.
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                 ||||:|
1420 YRLLVR 1425
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92 YRMLIR 97
                                                 1 YRLLIR 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical
SEQUENCE 1(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YFH8_YEAST
P43592;
                                                                                                                                        YEB4_YEAST
P39999;
  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
                                                                                                               RESULT 2
YEB4_YEAST
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01-FEB-1996 (Rel. 33, Last sequence update)
01-007-1996 (Rel. 34, Last sequence update)
HYPOTHETICAL 27.6 KD PROTEIN IN NMD5-HOM6 INTERGENIC REGION.
HYPOTHETICAL 27.6 KD PROTEIN IN NMD5-HOM6 INTERGENIC REGION.
Saccharomyces cereviae (Baker's yeast).
Eukaryota; Fungl; Ascomycota; Hemiascomycetes; Saccharomycetales;
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0
YAMAZAKI M., TASHIRO H., EKI T.; "Analysis of the nucleotide sequence of chromosome VI from Saccharomyces cerevisiae."; Nat. Genet. 10:261-268(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 27; DB 1; Length 221; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 27; DB 1; Length 239; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROSE M., KOETTER P., ENTIAN K.D.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                       POLY-GLN.
3D34764A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l protein.
239 AA; 27567 MW; OBF23C6E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 AA.
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(Rel. 34, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   221 AA; 25915 MW;
                                                                                                                                                                                                                                                                                                                                                                              EMBL; D50617; BAA09247.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.1%;
83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein
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Best Local Similarity
Matches 5; Conserv
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493
505
621 AA;
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432 YRLLLR 437
                                                                                                                                                                                                                                                                                                                                                                                                                           1 YRLLIR 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GIDA_COXBU
P94613;
                                                                                                                                                                                                                                                                                                                                 VARIANT
VARIANT
SEQUENCE
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VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAILVE-26695 ATCC 700392;

MEDLINE; 97394467.

TOMB J.-F., WHITE O., KERLAVAGE A.R., CLAYTON R.A., SUTTON G.G.,

TOMB J.-F., WHITE O., KETCHUM K.A., KLENK H.-P., GILL S., DOUGHERTY

TOME J.-F., PETERSON S.,

DEJSON K., QUACKENBUSH J., ZHOU L., KIRKNESS E.F., PETERSON S.,

LOFTUS B., RICHARDSON D., DODSON R., KHALAK H.G., GLODEK A.,

MCKENNEY K., PITZGERALD L.M., LEE N., ABAMS M.D., HICKEY E.K.,

BERG D.E., GOCAINE J.D., UTTERBACK T.R., PETERSON J.D., KELLEY J.M.,

COTTON M.D., WEIDMAN J.M., FUJII C., BOWMAN C., WALTHEY L., WALLIN E.,

HAYES W.S., BORODOVSKI M., KARP P.D., SMITH H.O., FRASER C.M.,
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                          Helicobacter pylori (Campylobacter pylori),
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
Helicobacter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                Length 309;
                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
01-NOV-1997 (Rel. 35, Last annotation update)
TRANSCRIPTION INITIATION FACTOR IIB HOMOLOG (TFIIB).
                               Sulfolobus shibatae.
Archaea; Crenarchaeota; Sulfolobales; Sulfolobus
                                                                                                                                                                                                                                                                                                                                                                Score 27; DB 1;
Pred. No. 17;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                   309 AA; 34756 MW; 0921E52C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GIDA_HELPY
P56138 (032632)
P10-00V-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
GIDA OR HPIBITED DIVISION PROTEIN A.
                                                                                                                                                                                                                                                                       HSSP; P29095; 1AIS.
PSOGITE; PSO0702; TFIIB; 2.
PFMM; PF00382; transcript_fac2; 2.
Transcription regulation; Repeat.
                                                                                                                                                                                                                                                                                                                                                                93.1%;
illarity 83.3%;
Conservative 1
                                                                                                                                                                                                                                                            EMBL; U20899; AAA81380.1; -.
HSSP; P29095; 1AIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 388:539-547(1997)
                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                    1111:1
201 YRLLLR 206
                                                                                                                                                                                                                                                                                                                                                                                                         1 YRLLIR 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VENTER J.
                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pylori.
                                                                                                                                                                                                                                                                                                                         REPEAT
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                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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KARITA M., ETTERBEEK M.L., FORSYTH M.H., TUMMURU M.K.R., BLASER M.J.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.1%; Score 27; DB 1; Length 621;
83.3%; Pred. No. 35;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V -> I (IN STRAIN 60190).
L -> F (IN STRAIN 60190).
T -> A (IN STRAIN 60190).
S -> N (IN STRAIN 60190).
T -> A (IN STRAIN 60190).
T -> A (IN STRAIN 60190).
A -> D (IN STRAIN 60190).
I -> V (IN STRAIN 60190).
YI -> CV (IN STRAIN 60190).
EV -> KL (IN STRAIN 60190).
EV -> KL (IN STRAIN 60190).
D -> N (IN STRAIN 60190).
D -> N (IN STRAIN 60190).
D -> N (IN STRAIN 60190).
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STRAIN-NINE MILE PHASE I;
STRAIN-NINE MILE PHASE I;
SUDMITTED (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: NOT KNOWN.
-!- SIMILARITY: BELONGS TO THE GIDA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Coxiella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-UL-1998 (Rel. 36, Last annotation update)
GLUCOSE INHIBITED DIVISION PROTEIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               627 AA
                                                                -i - FUNCTION: NOT KNOWN.
-i - SIMILARITY: BELONGS TO THE GIDA FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE000541; AAD07281.1; -. EMBL; AF008565; AAB63296.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS01280; GIDA_1; PROSITE; PS01281; GIDA_2; PFAM; PF01134; GIDA, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69683
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Best Local Similarity 83.3
Matches 5; Conservative
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GIDA OR HI0582
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P41389;
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                                                                                                                                                                                                                                                                                                                 VENTER J.C.;
                                                                                                                                                           Haemoph1lus
                                                 GIDA_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                          RESULT 9
GIDA_HAEIN
                                                 쉽
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                     OGASAWARA N., YOSHIKAWA H.; "Genes and their organization in the replication origin region of the
                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 96051385.
OGASAWARA N., NAKAI S., YOSHIKAWA H.;
OSASAWARA N., NAKAI S., YOSHIKAWA H.;
Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chromosome containing the replication origin.";
DNA Res. 1:1-14(1994).
                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 93.1%; Score 27; DB 1; Length 628; Best Local Similarity 83.3%; Pred. No. 35; Matches 5; Conservative 1; Mismatches 0; Indels
                                                                                   Length 627;
                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                    Score 27; DB 1;
Pred. No. 35;
EMBL; Y10436; CAA71459.1; -.
PROSITE: PS01280; GIDA_1: 1.
PROSITE: PS01281; GIDA_2: 1.
PEAM: PF01134; GIDA: 1.
SEQUENCE 627 AA; 69951 MW; B9AF4071 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFAM; PF01134; GIDA; 1.
SEQUENCE 628 AA; 69752 MW; F9B082BB CRC32;
                                                                                                                                                                                                                                          01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last Sequence update)
01-NOY-1995 (Rel. 32, Last annotation update)
GLUCOSE INHIBITED DIVISION PROTEIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: NOT KNOWN.-!- SIMILARITY: BELONGS TO THE GIDA FAMILY.
                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            bacterial chromosome.";
Mol. Microbiol. 6:629-634(1992)
                                                                                    93.1%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X62539; CAA44404.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D26185; BAA05231.1; -. EMBL; 299124; CAB16138.1; -. PIR; JQ1216; BWBSGA. SUBTILIST; BG10059; GIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS01280; GIDA_1; 1. PROSITE; PS01281; GIDA_2; 1.
                                                                                   Query Match
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                   Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                               STRAIN-168 / CRK2(
MEDLINE; 92204018
                                                                                                                                                  436 YRLLLR 441
                                                                                                                                    1 YRLLIR 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 YRLLIR 6
                                                                                                                                                                                                                    GIDA_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-168;
                                                                                                                                                                                             RESULT 8
GIDA_BACSU
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||||:| 435 YRLLLR 440

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                                                                                                                                                                                                                                                                                                                                                                                                   FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F., KERLEAVAGE B.K., BULT C.J., TOMB J.-F., DOGGHERTY B.A., MERRICK J.M., MCKENNEY R., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M., WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D., UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C., FINE L.D., FRIFCHMAN J.L., FUHRWANN J.L., GEOGRAGEN N.S.M., GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                     Haemophilus influenzae.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Whole-genome random sequencing and assembly of Haemophilus influenzae \mathrm{Rd}\,. ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.1%; Score 27; DB 1; Length 629; 83.3%; Pred. No. 35; 1:ve 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Archiascomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70103 MW; 6FD83D06 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
CLL DIVISION CONTROL PROTEIN NDA4.
NDA4 OR SPAC3F10.01.
                                                      01-NoV-1995 (Rel. 32, Created)
01-NoV-1995 (Rel. 32, Last sequence update)
10-NOV-1995 (Rel. 32, Last annotation update)
GLUCOSE INHIBITED DIVISION PROTEIN A.
629 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SIMILARITY: BELONGS TO THE GIDA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U32739; AAC22240.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS01280; GIDA_1; 1. PROSITE; PS01281; GIDA_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 83.3
Matches 5; Conservative
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM; PF01134; GIDA;
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                      STRAIN-RD / KW20;
MEDLINE; 95350630.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         435 YRLLLR 440
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NDA4_SCHPO
AC P4138_S)
AC P4138_S)
DT 01-0CT
DE CELL D
GN NDA4 0
OS SCHIZO
OC SCHIZO
CC SCHIZO
RN SEQUEN
RN SEQUEN
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95189082.
                                                                                                                                                                     1 YRLLIR 6
                                                                                                                                                                                                                                         NMD2_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE;
                                                                                                                                                                                                                   RESULT 12
NMD2_YEAST
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                                                                                                                                                                              쉱
                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                  "Fission yeast genes nda1+ and nda4+, mutations of which lead to S-phase block, chromatin alteration and Ca2+ suppression, are members of the CDC46/MCM2 family "
Mol. Biol. Cell 4:1003-1015(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
           MIYAKE S., OKISHIO N., SAMEJIMA I., HIRAOKA Y., TODA T., SAITOH I.,
YANAGIDA M.;
                                                                                                                 MURPHY L., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.; Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
- FUNCTION: ROLE IN DNA REPLICATION AND ESSENTIAL FOR VIABILITY
-!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE MCM FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GALACTOGLUCOMANNANS.
-!- SIMILARITY: BELONGS TO FAMILY 26 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-ATCC 43812;
POLITZ O., KRAH M., BORRIESS R.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: RANDOM HYDROLYSIS OF 1,4-BETA-D-LINKAGES IN MANNANS, GALACTOMANNANS, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 720; 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Cytophagales; Rhodothermus group; Rhodothermus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                              Transcription regulation; DNA-binding; Nuclear protein; DNA replication; Cell cycle; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                              ATP (POTENTIAL).
A -> R (IN REF. 1
29D61458 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1996 (Rel. 33, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
MANNAN ENDO-1,4-BETA-MANNOSIDASE (EC 3.2.1.78)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1021 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 27;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                       POLY-GLU.
                                                                                                                                                                                                                                                                                                                                                                                                                                       ₩.
                                                                                                                                                                                                                                                                                          EMBL; S68467; AAC60568.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.1%;
83.3%;
                                                                                                                                                                                                                                                                                                       CAA93299.1; -.
                                                                                              SEQUENCE OF 72-720 FROM N.A.
                                                                                                                                                                                                                                                                                                              PIR; A48723; A48723.
PROSITE; PS00847; MCM_1; 1.
PROSITE; PS50051; MCM_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       80089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                    PFAM; PF00493; MCM; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhodothermus marinus
                                                                                                                                                                                                                                                                                                                                                                                                              372 3
461 4
720 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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MEDLINE; 94129084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                675 YRMLIR 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 YRLLIR 6
                                                                                                                                                                                                                                                                                                        EMBL; Z69369;
                                                                                                           STRAIN=972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MANA_RHOMR
                                                                                                                                                                                                                                                                                                                                                                                                              NP_BIND
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P49425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- FUNCTION: INVOLVED IN NONSENSE-MEDIATED DECAY OF MRNAS CONTAINING PREMATURE STOP CODONS. IT INTERACTS, VIA ITS C-TERMINUS, WITH NAM//UPF1. COULD BE INVOLVED IN DETERMINING THE PEFICIENCY OF TRANSLATIONAL TERMINATION OR REINITIATION OR PACTORS INVOLVED IN THE INITIAL ASSEMBLY OF AN INITIATION-AND TERMINATION-COMPETENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAINS-286C / AB972;
MEDLINE; 94378003.
MEDLINE; 94378003.
JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DOVER J.,
NU Z., FAVELLO A., FULTON L., GATTUNG S., GELSEL C., KIRSTEN J.,
KUCABA.T., HILLIER L., JIER M., JOHNSTON I.,
LATREILLE P., LOUIS E.J., MACRI C., MARDIE E., MENEZES S., MOUSER L.,
NHAN M., RIFKIN L., RILES L., ST PETER H., TREVASKIS E., VAUGHAN K.,
VIGNATI D., WILCOX L., WOHLDMAN P., WATERSTON R., WILSON R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDILINE, 95327692.

LEE S.I., UMEN J.G., VARMUS H.E.;

"A genetic screen identifies cellular factors involved in retroviral reameshifting.";

-I frameshifting.";

Proc. Natl. Acad. Sci. U.S.A. 92:6587-6591(1995).
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1995 (Rel. 31, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 33, Last annotation update)
NONSENSE-MEDIATED MRNA DECAY PROTEIN 2 (UP-FRAMESHIFT SUPPRESSOR 2).
NMDS OR UPP2 OR IFS1 OR SUA1 OR YHROV7C.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungl; Ascomycota; Hemiascomycetes; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CUI Y., HAGAN K.W., ZHANG S., PELTZ S.W.; "Identification and characterization of genes that are required for the accelerated degradation of mRNAs containing a premature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 95189083.
HE F., JACOBSON A.;
HIGHTLIGATION Of a novel component of the nonsense-mediated mRNA decay pathway by use of an interacting protein screen."; Genes Dev. 9:437-454(1995).
                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                          Length 1021;
                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                     EMBL; X90947; CAA62442.1; -.
Hydrolase; Glycosidase.
SEQUENCE 1021 AA; 115791 MW; DD4D2403 CRC32;
                                                                                                                                                                                                                                                                                                                          DB 1;
59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1089 AA.
                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                       Score 27;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translational termination codon.";
                                                                                                                                                                                                                                                                                                                          93.1%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genes Dev. 9:423-436(1995).
                                                                                                                                                                                                                                                                                                                       Query Match 93.1
Best Local Similarity 83.3
Matches 5; Conservative
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us-08-653-294-6.rsp

DOMAIN

Matches

EMBL;

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Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Bombycoidea; Bombycidae; Bombyx.
                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS PROTEIN BINDS 5S RNA (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE L18P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE-SILK GLAND;
YANG C.S., SEHNAL F.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
-1- FUNCTION: THIS PROTEIN BINDS 5S RNA (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE L18P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 26; DB 1;
Pred. No. 28;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WORMPEP; F54C9.5; CE02255.

PFAM; PF00861; Ribosomal_L18p; 1.

Ribosomal protein; FRNA-binding.

SEQUENCE 293 AA; 33386 MW, GFFECTEE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                            01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
PROBABLE 60S RIBOSOWAL PROTEIN LS.
                                    293 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            299 AA
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66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z49967; CAA90251.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 89.7
Best Local Similarity 66.7
Matches 4; Conservative
                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bombyx mori (Silk moth).
                                                                                                                                                                                                                                                        Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54
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49 YRLIVR
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076190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMS M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
RL5_BOMMO
RLS_CAREL
AC DT RELS_CAREL
AC DT 01-FE 
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                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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63;
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85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          843 975 ASP/GLU-RICH (HIGHLY ACIDIC).
2 2 D -> YQQ (IN REF. 3 AND 4).
1089 AA; 126746 MW; 4B6ADE8F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MATTHEWS L.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: STRONG, TO C.ELEGANS F54D1.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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15-JUL-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL 166.0 KD PROTEIN R09E10.5 IN CHROMOSOME IV.
      -!- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein; Transmembrane.
SEQUENCE 1459 AA; 165994 MW; 46E17445 CRC32;
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Pred. No. 63;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YFIM_CAEEL STANDARD;
Q21874;
15-JUL-1998 (Rel. 36, Created)
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83.3%;
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                                                                                                                                                                                                                                                                                                                    EMBL; U14974; AAA67724.1; -.
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83.3%;
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nes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Caenorhabditis elegans.
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SGD; L0001257; NMD2.
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
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580 YRILIR 585
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188 YRLLLR 193
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RESULT 13 YF1M\_CAEEL

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EMBL; AF008229; AAC24960.1; -

14

RESULT

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Gaps

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DR SQ

PFAM: PF00861; Ribosomal\_L18p; 1.
Ribosomal protein; rRNA-binding.
SEQUENCE 299 AA; 34378 MW; 7262D2FC CRC32;

Query Match

89.7%; Score 26; DB 1; Length 299;
Best Local Similarity 66.7%; Pred. No. 29;
Matches 4; Conservative 2; Mismatches 0; Indels

; 0

0; Gaps

1 YRLLIR 6 |||::| 49 YRLIVR 54 Op ò

Search completed: February 8, 2000, 00:59:48 Job time: 3777 sec

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Q82998 bunyavirus

09843 paramecium 0994mil aeropyrum p 062083 mus misculu 062083 mus misculu 022419 caenorhabdi 093507 bacteroides 093329 caenorhabdi 083607 treponema p P91066 caenorhabdi 048579 arabidopsis 061776 caenorhabdi 04879 arabidopsis P91094 caenorhabdi 048579 arabidopsis P91094 caenorhabdi 048579 arabidopsis 001767 caenorhabdi 08956 vaccinia vir 007047 variola vir 007047 variola vir 00705 escherichia 056838 vibrio chol

A Comment

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database :

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Caenorhabditis elegans.
Eukaryota, Metazoa, Nematoda, Secernentea, Rhabditia, Rhabditida,
Rhabditina, Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09Y942 PRELIMINARY; PRT; 325 AA.
09Y942;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
325AA LONG HYPOTHETICAL TRANSCRIPTION INITIATION FACTOR IIB.
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EMBL; 267395; CAA91946.1; -.
EMBL; 267737; CAA91946.1; JOINED.
EMBL; 267737; CAA91543.1; JOINED.
EMBL; 267995; CAA91543.1; JOINED.
SEQUENCE 2692 AA; 312318 MW; 9F782AC7 CRC32;
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Last sequence update)
Last annotation update)
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100.0%; Pred. No. 2e+02;
ive 0; Mismatches 0
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Archaea; Crenarchaeota; Aeropyrum
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q21547
Q21547, Q22086;
01-NOV-1996 (TEMBLEL 01, C1
01-MAY-1999 (TEMBLEL 10, L2
01-MAY-1999 (TEMBLEL 10, L2
101-M10, 8 PROTEIN
                                              Query Match 100.
Best Local Similarity 100.
Matches 6; Conservative
                                                                      416
445
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63
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  RESULT
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099942 aeropyrum p
056074 streptomyce
056074 streptomyce
09zml9 helicobacte
09ym1 thermotoga
045730 bacillus th
094887 homo sapien
094887 homo sapien
0951316 nostoc sp.
026858 methanobact
09006 myxine glut
09zki4 helicobacte
093496 treponema p
02115 bacillus th
06115 mas musculu
062849 rattus norv
016549 homo sapien
                                                                                            Search time 209.03 Seconds (without alignments)
1.990 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                                                                                        225878
                             Compugen Ltd
                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
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             GenCore version
Copyright (c) 1993 - 2000
                                                                                               February 8, 2000, 13:17:31
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    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Q9YML9
Q9Y18
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Q92XUH
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sp_bacteria:*
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1 YRLLIR 6
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sp_rodent: *
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126 YRLLLR 131
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                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 95290751.
MENTSMA A., DENERMA H., OKAMURA K., OKAMOTO R.,
TSUBERMA A., TSUBERMA H., OKAMURA K., OKAMOTO R.,
Nucleotide sequence analysis of the carbomycin blosynthetic genes
including the 3-0-acyltransferase gene from Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                             KAWARABAYSI Y., HINO Y., HORIKAWA H., YAMAZAKI S., HAIKAWA Y., JALNINO K., TAKAHASHI M., SEKINE M., BABA S., ANKAI A., KOSUGI H., HOSOYAWA A., FUKUI S., NAGAI Y., NISHIJIWA K., NAKAZAWA H., TAKAMIYA M., MASUDA S., FUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI A., AOKI K., KUBOTA K., NAKAMURA NOMURA N., SAKO Y., KIKUCHI H., AOKI K., KUBOTA K., NAKAMURA "Complete genome sequence of an aerobic hyper-thermophilic
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                                                                                                                                                                                                                   Length 325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 389;
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Last annotation update)
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96;
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EMBL: D30759; BAA06421.1; -.
Transferase; Acyltransferase.
SCOUENCE 389 AA; 42879 WW; 2282D0F7 CRC32;
                                                                                                                                                                  Initiation factor.
SEQUENCE 325 AA; 35735 MW; 4A3FCOC7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biosci. Biotechnol. Biochem. 59:582-588(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 27; DB;
Pred. No. 96;
1; Mismatches
                                                                                                                                                                                                                  Score 28; DB Pred. No. 47; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence
01-NOY-1998 (TrEMBLrel. 08, Last annotatic
MACROLIDE ANTIBIOTICS 3-O-ACYLTRANSFRANSE
                                                                                                                                crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
EMBL; AP000064; BAA81458.1; -.
                                                                                                                                                                                                                  96.6%;
ilarity 83.3%;
Conservative
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ilarity 83.3%;
Conservative
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Best Local Similarity
Matches 5; Conserv
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Matches 5; Conserv
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SEQUENCE FROM N.A.
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                                    MEDLINE; 99310339
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158 YRLLLR 163
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STRAIN-A3(2);
OLIVER K., HARRIS D.;
OLIVER C., HARRIS D.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-A3(2);

MEDLINE, 97000351.

REDENBACH M., KIESER H.M., DENAPAITE D., EICHNER A., CULLUM J.,

KINASHI H., HOPWOOD D.A.;

A set of ordered cosmids and a detailed genetic and physical map for

the 8 Mb Streptomyces coelicalor A3(2) chromosome.";

Mol. Microbiol. 21:77-96(1996).

EMBL; AL049841; CAB42785.1;

Hypothetical protein.

SEQUENCE 418 AA; 44560 MW; 9E269715 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALM R.A., LING L.-S.L., MOIR D.T., KING B.L., BROWN E.D., DOIG P.C., SMITH D.R., LING L.-S.L., CARMEL G., TUMMIND P.J., CARUSO A., URIA-NICKELSEN M., MILLS D.M., IVES C., TRUST T.J., MERBERG D., MILLS S.D., JIANG Q., TAYLOR D.E., VOVIS G.F., TRUST T.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori."; Nature 397:176-180(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Helicobacter pylori J99.
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
Helicobacter.
                                                                                                                                              Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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JAMES K.D., PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
                                       01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
HYPOTHETICAL 44.6 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TEMBLrel. 12, Last annotation update)
GLUCOSE INHIBITED DIVISION PROTEIN A.
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Pred. No. 1e+02;
418 AA
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  PRT;
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Conservative
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PROSITE; PS01280; GIDA_1; 1.
PRELIMINARY;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A. STRAIN-JEGATHESAN; MEDLINE; 96086008.
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548 YRLIIR 553
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HAFT D.H., HICKEY E.K., PETERSON J.D., NELSON W.C., KETCHUM K.A.,
MCDONALD L., UTTERBACK T.R., MALEK J.A., LINHER K.D., GARRET M.M.,
STEWART A.M., COTTON M.D., PRATT M.S., PHILLIPS C.A., RICHARDSON D.,
HEIDELBERG J., SUTTON G.G., FLEISCHMANN R.D., WHITE O., SALZBERG S.L.,
SMITH H.O., VENTER J.C., FRASER C.M.;
"Evidence for lateral gene transfer between Archaea and bacteria from
genome sequence of Thermotoga maritima.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NELSON K.E., CLAYTON R.A., GILL S.R., GWINN M.L., DODSON R.J.,
HAFT D.H., HICKEY E.K., PETERSON J.D., NELSON W.C., KETCHUM K.A.,
MCDONALD L., UTTERBACK T.R., MALEN,
STEWART A.M., COTTON M.D., PRATT M.S., PHILLIPS C.A., RICHARDSON D.,
HEIDELBEBERG J., SUTTON G.G., FLEISCHMANN R.D., WHITE O., SALZBERG S.L.,
SWIDMITTH H.O., VEWIER J.C., FRASER C.M.,
SWIDMITTH H.O., VEWIER J.C., FRASER C.M.,
SMITH H.O., VEWIER J.C., FRASER C.M.,
SMITH B.O., VEWIER J.C., FRASER C.M.,
PROSITE; PS01280; GIDA.1:
PROSITE; PS01280; GIDA.1:
PROSITE; PS01281; GIDA.2: 1.
                                                                                                                                                                             Gaps
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Pred. No. 1.5e+02;
1; Mismatches 0; Indels
                                                                                                                  Length 621;
                                                                                                            Score 27; DB 2; Length 621
Pred. No. 1.5e+02;
1; Mismatches 0; Indels
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Last annotation update)
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Last annotation update)
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Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DA_2; 1.
71039 MW; DA12D9CD CRC32;
                        928413A8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                            629 AA.
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01-NOV-1999 (TrEMBLrel. 12, Last anno
GLUCOSE-INHIBITED DIVISION PROTEIN A.
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Bacteria; Thermotogales; Thermotoga.
PS01281; GIDA_2; 1.
621 AA; 69691 MW;
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045730;
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83.3%;
                                                                                                               Query Match 93.1%;
Best Local Similarity 83.3%;
Matches 5; Conservative
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01-NOV-1998 (TrEMBLrel.
MOSQUITOCIDAL TOXIN.
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Best Local Similarity
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432 YRLLLR 437
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442 YRLLLR 447
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PROSITE;
SEQUENCE
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MEDLINE; DESCRIPTION OF THE SUTAMA M., KIKUNO R., MIYAJIMA N., TANAKA A., NAGASE T., ISHIKAWA K., SUTAMA M., KIKUNO R., MIYAJIMA N., TANAKA A., KOTANI H., NOMURA N., OHARA O.; "Prediction of the coding sequences of unidentified human genes. XI. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro."; DNA Res. 5:277-286(1998).
                                                                                                                                                                                                                                                                                                                                               Gaps
DELECTUSE A., ROSSO M.L., RAGNI A.; "Cloning and expression of a novel toxin gene from Bacillus thuringiensis subsp. jegathesan encoding a highly mosquitocidal protein.";
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                           Score 27; DB 2; Length 724;
Pred. No. 1.8e+02;
1; Mismatches 0; Indels
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SUN H., STONEKING T., LANGSTON Y., LAPLANT Y.;
"The sequence of Homo saplens BAC clone RG442F18";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
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Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AR018936; BAA34513.1; -.
EMBL; AR016194; AAD12224.1; -.
HSSP; P08567; 1PLS.
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Last sequence update)
Last annotation update)
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                                                                                                                                 Appl. Environ, Microbiol, 61:4230-4250(1995).
EMBL; X86902; CAA60504.1; -.
SEQUENCE 724 AA; 81343 MW; 8BB449D1 CRC32;
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Genome Res. 8:1097-1108(1998).
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                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-754 FROM N.A.
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DB 4; Length 1054;

Score 27;

93.18;

**09YF18** σ

RESULT Q9YF18

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ALDREDGE T., BASHTRADBH R., BLEUDGHERY C., LEE H.-M., DUBOIS ALDREDGE T., BASHTRADBH R., BLAKELY D., COOK R., GILBERT K., HARRISON D., HOANG L., KEAGLE P., LUMM W., POTHIER B., QIU D., SPADAPORA R., VICARE R., WANG Y., WIEKEADOWSKI J., GIBSON R., JIWANI N., CARUSO A., BUSH D., SAFER H., PATWELL D., PRABHAKAR S., MCDOUGALL S., SHIMER G., GOYAL A., PIETROVSKI S., CHURCH G.M., DANIELS C.J., MAO J.-I., RICE P., NOLLING J., REEVE J.N.; "Complete genome sequence of Methanobacterium thermoautotrophicum deltah: functional analysis and comparative genomics."; J. Bacteriol. 179:7135-7155(1997).

Bacteriol. 179:7135-7155(1997).

BRSD: P20625: JARR
                                                                                                                                                                                                                                                              Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
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Eukaryota; Metazoa; Chordata; Craniata; Myxini; Myxiniformes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF152472; AAD37804.1; -.
Ribosomal protein.
SEQUENCE 296 AA; 34296 MW; C3AB83EC CRC32;
                                                                                                                                              Last sequence update)
Last annotation update)
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01-NOV-1999 (TIEMBLEEL. 12, Last annotation update)
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Pred. No. 1.3e+02;
2; Mismatches 0;
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Pred. No. 1e+02;
1; Mismatches
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                                                                                                                   Created)
                                                         PRT;
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MEDLINE; 98037514.
SMITH D.R., DOUCETTE-STAMM L.A.,
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PFAM; PF00730; Endonuclease_3; 1.
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Local Similarity 66.7%;
les 4; Conservative
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Best Local Similarity 83.3%;
Matches 5; Conservative
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                                                         PRELIMINARY;
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46 YRVLIR 51
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49 YRLIVR 54
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SECUENCE 23
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                              Gaps
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JIN-NO K., TAKAHASHI M., SEKINE M., BABA S., ANKAI A., KOSUGI H.,
HOSOYAWA A., FUKUI S., NAGAI Y., NISHJUIMA K., NAKAZAWA H.,
TAKAMIXA M., MASUDA S., FUKUI T., TANKAT T., KUDOH Y.,
YAMAZAKI J., KUSHIDA N., OGUCHI A., AOKI K., KUBOTA K., NAKAMURA Y.,
NOMURA N., SAKO Y., KIKUCHI H.;
"Complete genome sequence of an aerobic hyper-thermophilic
crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999)
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01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
SSDNA REPLICATING PLASMID ENCODING A REPLICATION-ASSOCIATED PROTEIN
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Pred. No. 2.5e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WALTON D.K., GENDEL S.M., ATHERLY A.G.;
Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; M81381; AAA55516.1; -
SEQUENCE 173 AA; 19346 MW; B40B691A CRC32;
                                                                                                                                                                                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
116AA LONG HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNRA RES. 0:00 1241,17978.1; -.
EMBL. AP0000059; BAA79378.1; -.
SEQUENCE 116 AA; 12928 MW; 9D725285 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (REPA) AND THREE ORFS, COMPLETE CDS (REPA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89.7%; Score 26; ilarity 66.7%; Pred. No. Conservative 2; Mismatc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Archaea; Crenarchaeota; Aeropyrum
83.3%;
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=K1;
MEDLINE; 99310339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aeropyrum pernix
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164 YKLLIR 169
                                                                                                                            1 YRLLIR 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |||::|
3 YRLIVR 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YRLLIR 6
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Q51316 Q51316;

RESULT 10

Matches

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Gaps

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DUBOIS J.,

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Gaps

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Search completed: February 8, 2000, 13:17:33 Job time: 32482 sec
TIGR; TP0483; -.
PPRAM; PF00041, fn3; 1.
PROCHALICAL protein.
SEQUENCE 374 AA; 42126 MW;
                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-BRISTOL N2; MEDLINE; 94150718.
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STRAIN-BRISTOL N2;
WATERSTON R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
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48 YRVLIR 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||:|:|
72 YRILVR 77
                                                                                                                                                                                                                                                                                                                                                1 YRLLIR 6
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SEQUENCE
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MEDLINE; 98332770.
PRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G.,
DODSON R., GWINN M., HICKEY E.K., CLATTON R., KETCHUM K.A.,
SODERGREN E., HARDHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J.,
KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTTERBACK T.,
MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAND S.,
HATCH B., HORST K., ROBERTS K., WATTHEY L., WEIDMAN J., SMITH H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G.,
DODSON R., GWINN M., HICKEY E.K., CLAYTON R., KETCHUM K.A.,
SODERGREN E., HARDHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J.,
KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTTERBACK T.,
MCDONALD L., ARRIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAND S.,
HATCH B., HORST K., ROBERTS K., WAITHEY L., WEIDMAN J., SMITH H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALM R.A., LING L.-S.L., MOIR D.T., KING B.L., BROWN E.D., DOIG P.C., SMITH D.R., NOONAN B., GUILD B.C., DEJONGE B.L., CARMEL G., TUMMINO P.J., CARUSO A., URIA-NICKELSEN M., MILLS D.M., IVES C., TRUST R.Y., MERBERG D., MILLS S.D., JIANG Q., TAYLOR D.E., VOVIS G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genomic-sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
RMBL: AE001524; AAD06529.1; -.
HSSP; P21891; IAPP.
SEQUENCE 357 AA; 42379 MW; 931DB706 CRG32;
                                                                                                                                                                                                                                                                                          Helicobacter pylori J99.
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89.7%; Score 26; DB 2; Length 357; ilarity 83.3%; Pred. No. 1.5e+02; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases EMBL; AE001224; AAC65472.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Spirochaetales; Spirochaetaceae; Treponema
                                                                                                                                    01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
INTEGRASE/RECOMBINASE (XERCD FAMILY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAY-1999 (TrEMBLrel. 10, Last annotation update)
HYPOTHETICAL 42.1 KD PROTEIN.
                                                                       357 AA
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                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-J99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 99120557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216 YRLLIK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YRLLIR 6
                                                                   Q9ZKI4
Q9ZKI4;
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083496
AC 083496
AC 083496
DT 01-NOV
       RESULT 13
                                                                                                              ACCOCCOOR RAY REPRESENTED THE REPRESENTATION OF THE REPRESENTATION
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BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER M., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROPRIA A., SAUNDERS D., SHOWNKEEN R.,
SMALDON N., SMITH A., SONHHAMMER E., STAADEN R., GLISTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                     ö
                                                                           Length 374;
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Pred. No. 1.9e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BENTLEY D.;
Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U00052; AAA50712.1; -.
PFAM; PF00561; abhydrolase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 08, Last annotation update)
                                                                           Score 26; DB 2;
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        447 AA; 52991 MW; 399D289B CRC32;
D696A45B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                          447 AA.
                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TIEMBLIEL 01, C
01-NOV-1996 (TIEMBLIEL 01, L
01-NOV-1998 (TIEMBLIEL 08, L
SIMILAR TO EPOXIDE HYDROLASE.
                                                                           89.7%;
ilarity 83.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 66./-
                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                     Channa gachua.

ESM Mitochondrion Channa gachua

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;

Neopterygii; Teleostei; Eukaryota; Rercomorpha;

Derciformes; Channoidei; Channidae; Channa.

Perciformes; Channoidei; Channidae; Channa.

Chan, W.C. and Lee, P.G.

Systematics of southeast Asian snakeheads using molecular and morphological data

AL Unpublished

CE 2 (bases 1 to 306)

CR 3 (banission

Direct Submission

Submitted (08-JUL-1997) School of Biological Sciences, National

University of Singapore, 10 Kent Ridge Crescent 119260, Singapore
AC010371 Homo sapiens
U26736 Caenorhabditis
M61229 D.melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="FGSLLGLCLITQILTGLFLAMHYTSDISTAFSSVAHICRDVNYG
WLIRNLHANGASFFFICIYFHIGRGLYYGSYLYKETWNGGVVMLLLVMMTAFVGYVLP
                                                                                                                                 seg_documentation_block:
LOCUS
LOCUS
DEFINITION Channa gachua GAC4 cytochrome b (cytb) gene, mitochondrial gene
encoding mitochondrial protein, partial cds.
ACCESSION AF012770
VERSION AF012770.1 GI:2564448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF012771 306 bp DNA VRT 25-OCT-1997 Channa gachua GAC6 cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds.
AF012771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="from Nee Soon Swamp Forest, Singapore" <1. .>306
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Percent Identity: 100.000
  16637
18124
22663
5.1e+03
5.5e+03
6.9e+03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="cytb"
-1...>306
/gene="cytb"
/codon_start=1
/transl_table=2
/product="cytohrome b"
/protein_id="kab81733.1"
/db_xref="G1:2564449"
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/db_xref="taxon:33790"
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gb_htg3:AC010371
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1 U0078B Human neutrophil oxidas M76373 Human neutrophil oxidas M76373 Human neutrophil oxidas M76373 Human neutrophil oxidas M32011 Human neutrophil oxidas M32011 Human neutrophil oxidas M32011 Human neutrophil oxidas M500568 Oryzias latipes mRNA A723778B Salmonella typhimuriu AB009568 Oryzias latipes mRNA A723778B Salmonella enterica through M720178B Dumelanogaster myosin hills63 Petunia hybrida nitrate L11563 Petunia hybrida nitrate L11563 Petunia hybrida nitrate L11563 Petunia hybrida nitrate L11563 Escherichia coli fNSD gilly0084 Escherichia coli fNSD gilly0085                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X61658 B.brevis grsB gene for
AE001265 Treponema palifdum s
D29676 B. brevis grs2 gene en
AE000704 Aquifex aeolius seo
D90745 Escherichia coli genom
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AE002079 Deinococcus radiodur
AE000210 Escherichia coli K-1
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-MINMANCH-0.100 -LOOPCL-0.000 -LOOPEXT-0.000 -GAPOP-4.500

-QGAPEXT-0.050 -XGAPOP-10.000 -XGAPEXT-0.500 -FGAPOP-6.000

-FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500 -DELOP-6.000

-DELEXT-7.000 -START-1 -MATRIX-blosum62 -TRANS-human40.cd1

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-OUTFMT-pfs -NORM-ext -MINLEN-0 -MAXLEN-1000000 -USER-US08653294

-NCPU-6 -ICPU-3 -NO_XLPXY -WAIT -THREADS-1
                                                                                         About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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Database Inegth: -1518192014
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                          Mitochondrion Channa gachua
Bukaryota; Metazoa: Chordata; Craniata; Vertebrata; Actinopterygil;
Neopherygil; Teleostel; Euteleostel; Acanthopterygil; Percomorpha;
Perciformes; Channoidel; Channidae; Channa.

1 (bases 1 to 306)
Chan, W.C. and Lee, P.G.
Systematics of southeast Asian snakeheads using molecular and
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Mitochondrion Channa micropeltes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygil;
Neopterygil; Teleostel; Euteleostel; Acanthopterygil; Percomorpha;
Perciformes; Channoidel; Channidae; Channa.
                                                                                                                                                                                                                                     Submitted (08-JUL-1997) School of Biological Sciences, National University of Singapore, 10 Kent Ridge Crescent 119260, Singapore Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF012784 306 bp DNA VRT 25-OCT-1997
Channa micropeltes MIC1 cytochrome b (cytb) gene, mitochondrial
gene encoding mitochondrial protein, partial cds.
AF012784
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Chan, W.C. and Lee, P.G.
Systematics of southeast Asian snakeheads using molecular and
morphological data
Unpublished
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Gaps: 0
Percent Identity: 100.000
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Direct Submission
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US-08-653-294-6 x AF012771
              Channa gachua.
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Channa micropeltes.
Mitochondrion Channa micropeltes
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygil;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygil;
Boeberygil; Teleostei; Buteleostei; Acanthopterygil; Percomorpha;
Perciformes; Channoidei; Channidae; Channa.
I (bases I to 366)
Chan, W.C. and Lee, P.G.
Systematics of southeast Asian snakeheads using molecular and morphological data
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WLIRNLHANGASFFFICIYFHIGRGLYYGSYLYKETWNVGVVMLLLVMMTACVGYVLP
Chan,W.C. and Lee,P.G.
Direct Submission
Submission
Submitsed (08-JUL-1971) School of Biological Sciences, National
University of Singapore, 10 Kent Ridge Crescent 119260, Singapore
Location/Qualifiers
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Chan,W.C. and Lee,P.G.
Direct Submission
Submitted (08-JUL-1997) School of Biological Sciences, National
University of Singapore, 10 Kent Ridge Crescent 119260, Singapore
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF012785 306 bp DNA VRT 25-OCT-1997 Channa micropeltes MIC2 cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 6
Gaps: 0
Percent Identity: 100.000
                                                                                                                                              /organism="Channa micropeltes"/mitochondrion
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                                                                                                                                                                                                                                                                                                                                                                                                               /product="cytochrome b"
/protein_id="AAB81747.1"
/db_xref="G1:2564477"
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/isolate="MIC2"
/db_xref="taxon:64149"
/note="from Singapore"
<1. >>306
                                                                                                                                                                                             /isolate="MIC1"
/db_xref="taxon:64149"
/note="from Singapore"
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                                                                                                                                                                                                                                                                                                                                       /gene="cytb"
/codon_start=1
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                                                                                                                                                                                                                                                                                          /gene="cytb"
<1..>306
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Percent Similarity: 100.000
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US-08-653-294-6 x AF012784
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from: 1
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4.833
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Ratio: 4.833
Percent Similarity: 100.000
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US-08-653-294-6 x AF012786
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US-08-653-294-6 x AF012787
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Ratio:
Percent Similarity:
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KEYWORDS
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 ORIGIN
                                                                            /product="cytochrome b"
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WLIRNLHANGASFFFICIYFHIGRGLYYGSYLYKETWNVGVVMLLLVWMTACVGYVLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitochondrion Channa orientalis
Eukaryota; Metazoa, Chordata, Cranlata; Vertebrata; Actinopterygli;
Butearyota; Metazoa, Chordata; Dateleostei; Buteleostei; Buteleostei; Buteleostei; Perciformes; Channoidei; Channidae; Channa.

1 (Dases I to 306)
Chan W.C. and Lee, P.G.
Systematics of southeast Asian snakeheads using molecular and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             r 25-OCT-1997
gene, mitochondrial gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chan,W.C. and Lee,P.G.
Direct Submission
Submitted (08-UTL-1997) School of Biological Sciences, National
University of Singapore, 10 Kent Ridge Crescent 119260, Singapore
                                                                                                                                                                                                                                                             Quality: 29.00 Length: 6
Ratio: 4.83 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF012786 306 bp DNA VRT Channa orientalis ORII cytochrome b (cytb) gencoding mitochondrial protein, partial cds. AF012786 I GI:2564480
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1. 306
/organism="Channa orientalis"
/mitochondrion
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/note="from Sri Lanka"
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<1. .>306
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/codon_start=1
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US-08-653-294-6 x AF012785
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LOCUS AF012786
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to: 306

VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE

REFERENCE

JOURNAL REFERENCE

JOURNAL AUTHORS

TITLE

FEATURES

DEFINITION

ACCESSION

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Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha; Perciformes; Channoidei; Channidae; Channa.

1 (bases 1 to 306)
Lee, P.G. and Chan, W.K.
Methods for obtaining cytochrome b gene sequences from fresh and preserved tissues of snakehead fishes (Pisces; Channidae) using the polymerase chain reaction (PCR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha; Perciformes; Channoldei; Channidae; Channa.

1 (bases 1 to 306)
Lee, P.G. and Chan, W.K.
Methods for obtaining cytochrome b gene sequences from fresh and preserved tissues of snakebead fishes (Pisces; Channidae) using the polymerase chain reaction (PCR)
                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (21-FEB-1994) W. K. Chan, Zoology, National University of
Singapore, Lower Kent, Ridge Road, Singapore, S0511, Republic Of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (21-FEB-1994) W. K. Chan, Zoology, National University of Singapore, Lower Kent, Ridge Road, Singapore, S0511, Republic Of
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Gaps: 0
Percent Identity: 100.000
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/isolate="GAC/ISING"
/db_xref="taxon:3379"
/dev_stage="adult"
/tissue_type="muscle, skeletal"
/clone_lib="PCR Fragment"
a 78 c 48 g 105 t
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1. .306
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Chan, W.K.
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Percent Similarity: 100.000
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Channa gachua.
Channa gachua
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US-08-653-294-6 x CGMTCYB1
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Channa gachua.
Channa gachua
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                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                    Channa striata.
Mitochondrion Channa striata
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Actinopterygii;
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
Perciformes; Channoidei; Channidae; Channa.
1 (bases I to 306)
Chan, W.C. and Lee, P.G.
Chan, W.C. and Lee, P.G.
Systematics of southeast Asian snakeheads using molecular and morphological data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation-"FGSLLGLCLITQ1LTGLFLAMHYTSD1STAFSSVAH1CRDVNYG
WLIRNLHANGASFFFICIYFH1GRGLYYGSYLYKETWNVGVMLLLLVMMTAFVGYVLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (08-JUL-1997) School of Biological Sciences, National
University of Singapore, 10 Kent Ridge Crescent 119260, Singapore
Location/Qualifiers
                                                                                                                                                          Channa striata STR1 cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds.
AF012789
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C.gachua (GAC/1/SING) mitochondrial gene for cytochrome b.
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Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .306
/organism="Channa striata"
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/protein_id="AAB81752.1"
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/isolate="STR1"
/db_xref="taxon:64152"
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Chan, W.C. and Lee, P.G.
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                                                             84 TACCGCCTTCTCATCCGT 101
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                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: AF012789
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Percent Similarity: 100.000
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                     1 TyrArgLeuLeuIleArg
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US-08-653-294-6 x AF012789
                                                                                                                                             seq_documentation_block:
LOCUS AF012789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
LOCUS
                                                                                                     seq_name: gb_ov:AF012789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: gb_ov:CGMTCYB1
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gene

DEFINITION

ACCESSION VERSION

BASE COUNT

24-FEB-1994

BASE COUNT ORIGIN

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Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha; Perciformes; Channoldei; Channidae; Channa.

1 (bases i to 306)
Lee, P.G. and Chan, W.K.
Methods for obtaining cytochrome b gene sequences from fresh and preserved tissues of snakehead fishes (Pisces; Channidae) using the polymerase chain reaction (PCR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytochrome b.
Channa gachua.
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
Perciformes; Channoldei; Channidae; Channa.
I (bases 1 to 306)
Lee, P. G. and Chan, W. K.
Methods for obtaining cytochrome b gene sequences from fresh and
perserved tissues of snakehead fishes (Pisces; Channidae) using the
                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (21-FEB-1994) W. K. Chan, Zoology, National University
Singapore, Lower Kent, Ridge Road, Singapore, S0511, Republic Of
Singapore
                                                                              C.gachua (GAC/5/KUAL) mitochondrial gene for cytochrome b. 230270 GI:456644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGMTCTB5 306 bp DNA VRT 24-FEB-1 C.gachua (GAC/7/SING) mitochondrial gene for cytochrome b. 230271 GI:456645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:33790"
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/clone_lib=PCR_Ergment"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1. .306
/organism="Channa gachua"
/isolate="GAC/5/KUAL"
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                                                               306 bp
                                                                                                                                                                                                                                                                                                                                                               Unpublished
2 (bases 1 to 306)
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2 (bases 1 to 306)
Chan, W.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TyrArgLeuLeuIleArg 6
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Percent Similarity: 100.000
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US-08-653-294-6 x CGMTCYB4
                                                                                                                                                                  Channa gachua.
Channa gachua
                                         seg_documentation_block:
LOCUS CGMTCYB4
DEFINITION C.gachua (GAC
                                                                                                                                           cytochrome b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
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      seq_name: gb_ov:CGMTCYB4
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Ratio:
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                                                                                                                                         KEYWORDS
SOURCE
ORGANISM
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DEFINITION
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VERSION
                                                                                                                                                                                                                                                                                 AUTHORS
TITLE
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AUTHORS
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AUTHORS
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
Perciformes; Channoidei; Channidae; Channa.

1 (bases 1 to 306)
Lee, P.G. and Chan, W.K.
Methods for obtaining cytochrome b gene sequences from fresh and preserved tissues of snakehead fishes (Pisces; Channidae) using the Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (21-FEB-1994) W. K. Chan, Zoology, National University of
Singapore, Lower Kent, Ridge Road, Singapore, S0511, Republic Of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGMTCYB3 306 bp DNA VRT 24-FEB-1
Cgachua (GAC/3/SRIL) mitochondrial gene for cytochrome b.
230269.1 GI:456621
                                                                                                                                                                            Quality: 29.00 Length: 6
Ratio: 4.833 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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Gaps: 0
Percent Identity: 100.000
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/clone_lib="PCR Fragment"
80 c 48 g 103 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="Adult"
/tissue_type="Muscle, skeletal"
/clone_llb="PCR Fragment"
79 c 49 g 103 t
                                                                                                                                                                                                                                                                                                                          to: 306
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/organism="Channa gachua"
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/db_xref="taxon:33790"
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                                                                                                                                                                                                                                                                                                                        from: 1
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Ratio: 4.833
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                      to: CGMTCYB2
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Channa gachua.
Channa gachua
                                                                                                                                                                                                                                                          alignment_block: US-08-653-294-6 x CGMTCYB2
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US-08-653-294-6 x CGMTCYB3
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                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: gb_ov:CGMTCYB3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chan, W. K
                                                                                75
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                                                                                                                                                              alignment_scores
                                                                                                                                                                                                                                                                                                                    Align seg 1/1
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DEFINITION ACCESSION VERSION

KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

REFERENCE AUTHORS

JOURNAL

TITLE

FEATURES

JOURNAL

BASE COUNT

ORIGIN

Direct Submission

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/product="cytochrome b"
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ILTGLFLAMHYTSDISTAFSSVVHICRDVNYGWLIRNIHANGASFFFICIYLHIGRGL
YYGSYLKETWNYGILT=
77 c 56 g 128 t
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitochondrion Fundulus dispar
Sukaryote, Metazoa: Chordata; Craniata; Vertebrata; Actinopterygil;
Neopterygil; Teleostel; Euteleostel; Acanthopterygil;
Atherinomorpha; Cyprinodontiformes; Cyprinodontoidel; Fundulidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 357)
Shedotti, J., and Grose, M.J.
Phylogenetic relationships of the Fundulus nottii species group
(Fundulidae, Cyprinodontiformes) as inferred from the cytochrome-b
                                                                                                                                                                                                                                                                                            Submitted (04-NOV-1996) Natural History Museum, University Kansas, 502E Dyche Hall, Lawrence, KS 66045-2454, USA Location/Qualifiers
Length: 6
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps: 0
Percent Identity: 100.000

    .357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mitochondrion
/db_xref="taxon:34778"
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/note="individual 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copeia 4, 858-862 (1997)
2 (bases 1 to 357)
Ghedotti,M.J. and Grose,M.J.
Direct Submission
Submitted (04-NOV-1996) Natur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
/transl_table=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="cytb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="cytb"
                                                                                                                                                                                                                   101 TATCGCCTTCTCATACGT 118
                                                                                                                                                                             1 TyrArgLeuLeulleArg 6
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    29.00
                                          Percent Similarity: 100.000
                                                                                                                                       Align seg 1/1 to: PAU26956
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Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Fundulus dispar.
                                                                                alignment_block:
US-08-653-294-6 x PAU26956
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US-08-653-294-6 x FDU77119
                                                                                                                                                                                                                                                        seq_name: gb_ov:FDU77119
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    Quality:
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SOURCE
ORGANISM
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TITLE
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pristipomoides aquilonaris.
Mitochondrion Pristipomoides aquilonaris
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
Perciformes; Percodei; Lutjanidae; Pristipomoides.

1 (bases 1 to 340)
Sarver,S.K., Freshwater,D. and Walsh,P.J.
Phylogenetic relationships of western Atlantic snappers (Family Lutjanidae) based on mitochondrial DNA sequences
Submitted (21-FEB-1994) W. K. Chan, Zoology, National University of Singapore, Lower Kent, Ridge Road, Singapore, S0511, Republic Of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="SAWWNFGSLLGLCLAAQILTGLFLAMHYTSDISIAFSYVAHICR
DVNYGWLIRNLHANGASFFFICLYLHIGRGLYYGSYLYKETWNIGVVLFLLVWMTAFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (12-MAY-1995) David W. Freshwater, Center for Marine
Science Research, 7205 Wrightsville Avenue, Wilmington, NC 28403,
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prisipomoides aquilonaris cytochrome b gene, mitochondrial gene encoding mitochondrial protein, partial cds.
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    340
    /organism="Pristipomoides aquilonaris"

                                                                                                                                                                                                                                                                                                                Ouality: 29.00 Length: 6
Ratio: 4.833 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
                                                                                  1. .306
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//solate="cAc77/SING"
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//de_stage="adult"
//tissue_type="muscle, skeletal"
//clone_lib="PCR Fragment"
4 a 79 c 50 g 103 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102
                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mitochondrion
/db_xref="taxon:40511"
                                                                Location/Qualifiers
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104 c
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US-08-653-294-6 x CGMTCYB5
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LOCUS PAU26956
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                                            Singapore
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of

1 TyrArgLeuLeuIleArg

alignment_scores:

180 TACCGCCTTCTCATCCGT 197

us-08-653-294-6.rge

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Fundulus dispar.
Mitochondrion Fundulus dispar
Mitochondrion Fundulus dispar
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Actinopterygil;
Neopterygil; Teleostel; Euteleostel; Acanthopterygil;
Atherinomorpha; Cyprinodontiformes; Cyprinodontoidel; Fundulidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product-"cytochrome b"
/protein_id-"AAC12590.1"
/d_xref="G1:232959"
/translation-"MANIRKTHPLEKIVNNALVDLPAPVNISVWWNFGSLLGLCLISO
ILTGLFLAMHYTSDISTAFSSVVHICRDVNYGWLIRNIHANGASFFFICIYLHIGRGL
                                                                                                                                                                                                                                                                                                 (bases 1 to 357)
Ghedotti, M.J. and Grose, M.J.
Phylogenetic relationships of the Fundulus nottil species group
(Fundulidae, Cyprinodontiformes) as inferred from the cytochrome-b
                                      seq_documentation_block:
LOCUS FDU77120 357 bp DNA VRT 07-APR-1998
DEFINITION Fundulus dispar cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds.
ACCESSION U77120
VERSION U77120.1 GI:2329958
                                                                                                                                                                                                                                                                                                                                                                                                         Copeia 4, 858-862 (1997)
2 (bases 1 to 357)
Ghedotti,M.J. and Grose,M.J.
Direct Submitssion
Submitted (04-NV-1996) Natural History Museum, University of Kansas, 502E Dyche Hall, Lawrence, KS 66045-2454, USA
Location/Qualifiers
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Percent Identity: 100.000
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    .357
    /organism="Fundulus dispar"

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/tissue_type="muscle"
/note="individual 2"
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/codon_start=1
/transl_table=2
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Ratio: 4.833
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US-08-653-294-6 x FDU77120
seq_name: gb_ov:FDU77120
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Polycistronic maize U14.1 D Polycistronic maize U14.1 D Rat tumour necrosis factor Drosophila semaphorin I cDN

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New polynucleotides encoding human secreted proteins - derived from
PT e.g. human blood, kidney, foetal lung, placente, testes, brain,
PT e.g. human blood, kidney, foetal lung, placente, testes, brain,
PT e.g. human blood, kidney, foetal lung, placente, testes, brain,
PT ovary, pituitary, retina and colon CDNA libraries
Claim 1: Page 119; 633pp; English
CC claim 1: Page 119; 633pp; English
CC claim 2: Sequence represents an expressed sequence tag (EST), and is a
polynucleotide of the invention. The polynucleotides of the invention are
call secreted EST sequences insolated from a variety of human tissue
cources: The EST sequences and proteins encoded by them are predicted to
have useful biological activitities which would make them suitable for
treating, preventing or ameliorating medical conditions in humans and
animals, although no supporting data is given. Suggested activities
conditional activity, immune stimulating or suppressing activity,
hammatopolesis regulating activity, tissue growth activity,
activity, nactivity, receptor/ligand activity, and ti-inflammatory
cativity, cabherin/tumour invasion suppressor activity, tumour inhibition
controlly the EST sequences are also stated to be useful for gene
                                                                                                                                                                                                                                                  EST clone D310.

EST clone D310.

Expressed sequence tag; secreted protein; haematopoiesis regulator;

Expressed sequence tag; secreted protein; haematopoiesis regulator;

Expressed sequence tag; secreted protein suppressor; EST; human; chemotaxis; chemotaxis; haemostaxis; gene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
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Polynucleotide sequence from the genome of Treponema pallidum.
Treponema pallidum infection; syphilis; Borrelia infection; animal; enzyme production; ds.
                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
W09845435-A2.
15-0CT-1998.
10-APR-1997; US-835913.
(GEMY ) GENETICS INST INC.
Agostino MJ, Jacobs K, Lavallie ER, MCCOy JM, Merberg !
WPI; 99-070076/06.
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ID X20560 standard; DNA; 8467 BP.
AC X20560;
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V86097;
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US-08-653-294-6 x V86097/rev
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                                                                                                                   seq_name: N_Geneseq_36:V86097
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Ratio: 4.833
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Treponema pallidum.
W0985034-A2.
30-DEC-1998.
                                                                                                                                                                seq_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 506 BP;
  N_Geneseq_36:T08745
N_Geneseq_36:T14849
N_Geneseq_36:Q05328
N_Geneseq_36:Q87444
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                                                                                                                                                                                          POWER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tree Len | Documentation | 1. New polynucleot | 1. ST clone Dillo | 1. Stabholococus                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Acya gene. Gene encoding 3-acy
Human secreted protein gene 15
Helicobacter pylori dapE gene
DNA encoding a gidAl protein.
Nonsense-mediated mRNA decay 2
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Staphylococcus aureus contig S
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-Q=/cgn1_1/USPTO_spool/US08653294/runat_04022000_160701_15807/app_query.fasta.1
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-GAPEXT=4 0.00 -MINMATCH=0.100 -LOOPEXT=0.000
-QGAPOP=4.500 -QGAPEXT=0.000 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THK_SCORE=pct
-ALIGN=15 -MODE=LCCAL -OUTFWT=Pfs -NORM=ext -MINLEN=0.
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                                                                                           About: Results were produced by the GenCore software, version Copyright (c) 1993-2000 Compugen Ltd.
    out_format : pfs
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OM of: US-08-653-294-6 to: N_Geneseg_36:*
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Database sequences: 311585
Database length: 125096042
search time (sec): 590.520000
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Query: US-08-653-294-6
Query length: 6
                                                                                                                                                              Command line parameters:
                                               Date: Feb 8, 2000 1:27
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N_Geneseq_36:V31189
N_Geneseq_36:T22714
N_Geneseq_36:T22714
N_Geneseq_36:T23714
N_Geneseq_36:Y75248
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N_Geneseq_36:V64557
N_Geneseq_36:V52296
N_Geneseq_36:V5570
N_Geneseq_36:Q27321
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N_Geneseq_36:x39936
N_Geneseq_36:v59910
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N_Geneseq_36:V58937
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N_Geneseq_36:V74488
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N_Geneseq_36:T17044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :T84061
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N_Geneseq_36:
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N_Geneseq_36
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N_Geneseq_36
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Sequence
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N_Geneseq_3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _Genesed_
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136 T;

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alignment_block:
US-08-653-294-6 x V31189/rev
                                                                                                                                                                                                            This sequence represents a E. coli nucleotide sequences - used to develop products for the detection of pathogenic E. coli and to develop products for the detection of pathogenic E. coli and to alicit an immune response to pathogenic E. coli and 21; Page 84-88; 250pp; English.

This sequence represents a E. coli strain J96 contig containing pathogenicity island (PAI) sequences, and represents a nucleic acid molecule of the invention. PAIs are large fragments of DNA which comprise pathogenicity determinants. The sequences of the invention are taken from PAII V and PAII V. PAII IV is located at approximately 64 min (near pheV) con the E. coli chromosome and is greater than 170 kb. PAI V is located at approximately 94 min (at pheR) on the E. coli chromosome and is specific to the proteins encoded approximately 160 kb in size. Antibodies specific to the proteins encoded detect uropathogenic E. coli. The proteins are used in vaccines to elicit approach immune response in an animal to the uropathogenic E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0cT-1998 (first entry)
E. coli J96 pathogenicity island contig #3.
E. scli J96 pathogenicity island; uropathogenic E. coli detection; PAI IV; pheR; PAI V; pheV; pheV; accine; protective immune response; ds.
Escherichia coli.
                                                        New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis claim 1, Page 523-527; 1150pp; English.

X20500-21243 represent polynucleotide sequences from the genome of Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detecting diseases related to Borrella infections in animals, and for the production of blosynthetic products such as enzymes.
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                                                                                                                                                                                                                                                                                      Quality: 29.00 Length: 6
Ratio: 4.833 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2222 C;
                                                                                                                                                                                                                                                                                                                                                                                                      to: 8467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-NOV-1997; U21347.
21-NOV-1997; U21347.
22-NOV-1996; US-061953.
(HUMA-) HUMAN GENOME SCI INC. (UVMI-) UNIV WISCONSIN.
Choi GH, Dillon PJ, Welch RA; WPI; 98-312461/27.
                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: X20560 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2212 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
ID V31189 standard; DNA; 8752 BP.
             (HUMA-) HUMAN GENOME SCI INC. Fraser CM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality: 29.00
Ratio: 4.833
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TyrArgLeuLeuIleArg 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: N_Geneseq_36:V31189
24-JUN-1997; US-050667
                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-08-653-294-6 x X20560
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                                             WPI; 99-081273/07
                                                                                                                                                                                                                                                                          alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a protective strain J96.
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synthetase like activity
Claim 6; Page 17-41; 93pp; English.
This sequence encodes an enzyme which has cyclosporin synthetase-
like activity. This sequence was isolated from Tolypocladium niveum
like activity. This sequence was isolated from Tolypocladium niveum
(formerly known as T. inflatum GAMS). The enzyme encoded by this
sequence catalyses the peptide blosynthesis of cyclosporins and
structurally related molecules. This sequence may be used for the
production of cyclosporin by transforming a vector containing this
sequence in to a recombinant host. This allows effective production
of antibiotic cyclosporin or its derivatives.
Sequence 46899 BP; 10651 A; 13513 C; 12509 G; 10226 T;
                                                                                                                                                                                                                                                                                      054386;
08-JUL-1994 (first entry)
T. niveum Cyclosporin synthetase gene.
Enzyme: cyclosporin; synthetase-like activity; Tolypocladium niveum;
T. inflatum GAMS; blosynthesis; vector; cyclosporin synthetase; ss.
Tolypocladium niveum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated DNA sequence - which codes for enzyme having cyclosporin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            885. 46730
/*tag a //frag a 40230
/*tag b //frag f //frag f //frag d //frag d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Sall restriction fragment, preferred fragment, Claim 5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-MAR-1993; AT-000437.
29-ARR-1993; CH-001310.
04-MAY-1993; CH-001310.
(5-MAY-1993; CH-001375.
(SANO ) SANDOZ LID.
(SANO ) SANDOZ PATENT GMBH.
(SANO ) SANDOZ-ERFINDUNGEN VERW GES MBH.
Leitner E, Schneider E, Schoergendorfer K, Weber G; P-PSDB; R44929.
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Gaps: 0
Percent Identity: 100.000
to: 8752
   from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
to reverse of: V31189
                                                                                                                                                                                                                            seq_documentation_block:
ID Q54386 standard; DNA; 46899 BP
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                                                                                                                   8544 TACAGACTTTTGATACGT 8527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TyrArgLeuLeuIleArg 6
                                                            1 TyrArgLeuLeuIleArg 6
                                                                                                                                                                         seq_name: N_Geneseq_36:Q54386
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Ratio: 4.833
Percent Similarity: 100.000
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US-08-653-294-6 x Q54386
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05-JUL-1993; 810474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
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Align seg 1/1
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This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (RAM), read-only memory (RAM) or CD-RAM. Homology searches using the S. aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be obtained. Secureus infection. The be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of Saureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food polsoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 iocation/Qualifiers
361. 420
/*tag= a
/note= "these bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus config SEQ ID #937.
Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelld infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
                                                                        Example 5: Page 63; 79pp; English.
A DNA clone (T43366) was generated by 5'RACE using primers (see also T43364-56) based on FbLate2 clone All (T43362), a partial CDNA clone corresponding to mRNA prevalent in the late development of cotton fibre. The RACE product showed 91.6% similarity at the nucleotide level to the genomic clone, FbLate2-82A (see also T43360). The homology of the RACE product started from nucleotide position 2269 of the FbLate2-28A gene. The ATG initiation codon was identified at position 2315 of the gene.
Sequence 519 BP; 191 A; 127 C; 87 G; 114 T;
Plant fibre-specific, developmentally regulated FbLate promoter · useful for producing transgenic plants, esp. cotton, with altered fibre properties
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUL-1997.
07-JAN-1997; 100117.
05-JAN-1996; US-009861.
(HUMA-) HUMAN GENOME SCI INC.
Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality: 28.00 Length: 6
Ratio: 4.667 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 83.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to reverse of: T43366 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      V75248 standard; DNA; 615 BP. V75248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 TACCGATTATTAGTGAGA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-08-653-294-6 x T43366/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: N_Geneseq_36:V75248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 97-374922/35.
                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
Quality:
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     A single-stranded DNA (or its complementary strand or the corresp. A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences of given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed CDNA libraries prepared from various human tissues; synthesis of CDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-ent of mRNA by using poly(T) as the sole primer. Since the 3'-ent of mRNA by using poly(T) as the sole primer since the 3'-ent of mRNA by using poly(T) as the sole primer. Since the 3'-ent of mRNA by using poly(T) as the sole primer of the section of all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different from the GS sequences) as a means of diagnosing abnormal cell function or for sequence 15 BP; 80 A; 23 C; 43 G; 67 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matsubara K, Okubo K;
WPI: 95-206931/27.
Identifylng gene signatures in 3'-directed human cDNA library - e.g.,
for diagnosis of abnormal cell function, by preparing cDNA that
reflects relative abundance of corresp. mRNA in specific human
                                                                                                                            14-AUG-1996 (first entry)
Human gene signature HUMGSO4372.
Gene signature; messenger RNA; mRNA; relative abundance; frequency;
Human; cloning; mapping; non-biased library; diagnosis; detection;
cell typing; abnormal cell function; ss.
HOMO sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-MAR-1997 (first entry)
Cotton Fblate 2-82A gene cDNA clone All amplified fragment.
Fblate; promoter; fibre; transgenic plant; cotton;
Gossyplum hirsutum; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity: 100.000 Percent Identity: 83.333
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                                                                                 F22714 standard; cDNA to mRNA; 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
ID T43366 standard; DNA; 519 BP.
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                                                                                                                                                                                                                                                                                                                                                   11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
Matsubara K, Okubo K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-6 x T22714/rev
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  seq_name: N_Geneseq_36:T22714
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06-JUN-1996; U09449.
06-JUN-1995; US-4675
                                                       seg_documentation_block:
                                                                                                                                                                                                                                                                                                     WO9514772-A1.
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WPI; 97-042726/04.

John ME;

Synthetic.

T43366;

to: 519

tissues

NAME OF THE PROPERTY OF THE PR

to: 684

from: 1

8888888

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Align seg 1/1 to reverse of: T84061
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                                                                                                                                                                                                                                                                                                                                                                                                                       WO9730070-A1.
                                                                                                                                                                                                                    27-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                          1-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SMIK)
                                                                                                                                                                                DNA encoding a Staphylococcus aureus protein of unknown function. Staphylococcus aureus protein; ribozyme; antisense sequence; control; Staphylococcal gene; regulatory element; bacterial gene expression; vaccine; staphylococcal infection; food poisoning; scaled skin syndrome; toxic shock syndrome; se.
syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the computer readable medium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence encodes a Staphylococcus aureus protein of unknown function. The present sequence was isolated from a library of clones of S. aureus WCUH 29 in Escherichia coll. The DNA sequence can be used in the construction of ribozymes and antisense sequence to control the expression of Staphylococcal genes. The DNA sequence is also useful as a source of regulatory elements for the control of bacterial agene expression. The encoded protein may be used to produce vaccines to enable a host to produce specific antibodies with antibacterial action. These vaccines and antibodies would protect a host against invasion by S. aureus, and conditions relating to Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled skin syndrome, and toxic shock syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 to isolate antimicrobial compounds, and in vaccines against S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Black MT, Burnham MK, Hodgson JE, Knowles DJC, Nicholas RO,
Pratt JM, Reichard RW, Rosenberg M, Ward JM;
                                                                                                 163 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps: 0
Gaps: 0
Percent Identity: 83.333
                                                                                                                                                                            Length: 6
Gaps: 0
Percent Identity: 83,333
                                                                                                 83 G;
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2
                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to reverse of: V75248 from: 1
                                                                                                 102 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus aureus.
Location/Qualifiers
CDS 125. 436
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 9; Page 853; 989pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                 202 A;
                                                                                                                                                                                                                                                                                                                                                                                    122 TATAGATTGCTGGTTCGC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-AUG-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T84061 standard; DNA; 684
                                                                                                                                                                            Quality: 28.00
Ratio: 4.667
Percent Similarity: 100.000
                                                                                                                                                                                                                                                           alignment_block:
US-08-653-294-6 x V75248/rev
                                                                                                                                                                                                                                                                                                                                                               1 TyrArgLeuLeulleArg 6
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US-08-653-294-6 x T84061/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: N_Geneseq_36:T84061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio: 4.667
Percent Similarity: 100.000
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19-FEB-1997; UO2318.
20-FEB-1996; US-011888.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
                                                                                                 615 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 97-424969/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
Quality:
Ratio: 4
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Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; W28135
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                                                                                                   Seguence
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NEW TENDER OF THE PROPERTY OF

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DNA encoding a Staphylococcus aureus protein of unknown function. Staphylococcus aureus protein: ribozyme; antisense sequence; control; staphylococcal gene; regulatory element; bacterial gene expression; vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome; toxic shock syndrome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aureus injection.

Claim 9; Page 874; 989pp; English.

Claim 9; Page 874; 989pp; English.

The present sequence encodes a Staphylococcus aureus protein of maknown function. The present sequence was isolated from a unknown function. The present sequence was isolated from a sequence can be used in the construction of ribozymes and antisense sequences to control the expression of Staphylococcal genes. The DNA sequence is also useful as a source of regulatory elements for the control of bacterial gene expression. The encoded protein may be used to produce vaccines to enable a host to produce specific antibodies with antibacterial action. These vaccines and antibodies would protect a host against invasion by S. aureus, and conditions relating to Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled skin syndrome, and toxic shock syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - nseq
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ID T13048 standard; cDNA; 1283 BP.

AC T13048

DE 27-MAY-1996 (first entry)

DE Cotton fibre-specific cDNA clone E9.

KW Cotton; fibre; promoter; transgenic plant; crop improvement; ds.

OS Gossypium hirsutum strain Coker 312.

PN US5495070-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 to isolate antimicrobial compounds, and in vaccines against S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Black MT, Burnham MK, Hodgson JE, Knowles DJC, Nicholas RO,
Pratt JM, Reichard RW, Rosenberg M, Ward JM;
WPI; 97-424969/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coulity: 28.00 Length: 6
Ratio: 4.667 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 83.333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus.
Location/Qualifiers
CDS 253. 537
/*tag- a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from: 1
                                                                                                                                                                                    seq_documentation_block:
ID T84095 standard; DNA; 1032 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  349 A;
655 TATAGACTATTAGTCCGA 672
                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                           seq_name: N_Geneseq_36:T84095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-FEB-1996; US-011888.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TyrArgLeuLeuIleArg
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US-08-653-294-6 x T84095
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seq_documentation_block:
ID T70055 standard; cDNA; 1283 BP.
                                                                                                                                                                                                                                                                                                     118 TACCGATTATTAGTGAGA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 TACCGATTATTAGTGAGA 101
                                                                                                                                                                                                                                                                  1 TyrArgLeuLeuIleArg 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JAN-1997.
04-OCT-1988; 253243.
04-OCT-1988; US-253243.
21-NOV-1990; US-617239.
18-OCT-1993; US-138814.
20-SEP-1995; US-530797.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 28.00
Ratio: 4.667
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-08-653-294-6 x T62624/rev
                                                                                                                                                                             alignment_block:
US-08-653-294-6 x T30265/rev
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                                                                                                                                                                                                                                                                                                                                    seq_name: N_Geneseq_36:T62624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seg_name: N_Geneseg_36:T70055
                                                                                                     Quality: 28.00
Ratio: 4.667
Percent Similarity: 100.000
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                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
 ပ္ပ်ပ္ပ်ပ္လ
                                                                                                                                                                                                                                                                                                                                                                                           Cotton fibre cell-specific pronoter sequences were isolated by cotton fibre cell-specific pronoter sequences were isolated by differential screening of a cotton plant cDNA ibrary. Of 4788 clones from a 10 day cell library screened with leaf cDNAs, 800 clones not present in the leaf were isolated. These were screened with cDNAs from ovule, root and flower mRNAs and resulted in 79 clones isolated. PCR analysis was then used to remove cross-hybridising clones. This resulted in the isolation of 18 cDNA clones specifically expressed in cotton fibre cells (T30242-4 and T30253-67). These cDNAs were then used to screen for homologous genomic sequences (T30245-53 and T30268) in order to obtain the corresp. promoter sequences.

This cDNA clone contains an insert of 1283 bp which is highly expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The promoters isolated from the fibre cell-specific clones can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cotton fibre cell-specific cDNA clone CKFB10-E9.
Cotton fibre; promoter; differential screening; leaf; ovule; root;
flower; PCR; polymerase chain reaction; homology; transgenic plant; ds.
GOSSYPium hirsutum.
US5521078-A.
                                                                                                                                    New isolated fibre-specific promoters - used for introducing altered fibre-specific Characteristics into plants, partic. cotton. Example 3; Column 45-46; 48pp; English.
Cotton cDNA clone E9 (T13048) was isolated from a cDNA library of cotton var. Coker 312 15-day-old boll cells using a subtractive hypridization procedure. The clone hybridises strongly to fiber RNA and weakly to pettal RA. E9 and other fibre-specific cDNA clones (see T13033-47 and T13049-T13050) were used to screen cotton genomic libraries, leading to the isolation of genomic clones (see T13025-53) contg. sequences capable of promoting gene expression in fibre cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolation of fibre-specific cotton promoter sequences - using selected DNA probes to screen genomic DNA fragments, for production of cotton fibres with improved characteristics

Examples; Column 45-46; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps: 6
Gaps: 0
Percent Identity: 83,333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to reverse of: Tl3048 from: 1 to: 1283
                                                                                                                                                                                                                                                                                                                                      251 G;
                                                                                                                                                                                                                                                                                                                                      233 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in fibres and weakly in petal tissues.
                                                                                                                                                                                                                                                                                                                                    509 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T30265 standard; DNA; 1283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 TACCGATTATTAGTGAGA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-DEC-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-08-653-294-6 x Tl3048/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TyrArgLeuLeuIleArg 6
                                                                                                                                                                                                                                                                                                                                                                                                     Ouality: 28.00
Ratio: 4.667
Percent Similarity: 100.000
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04-007-1988; 253243.
04-007-1988; US-253243.
21-NOV-1990; US-617239.
18-MAY-1992; US-8885970.
19-007-1994; US-298687.
(CFTU ) AGRACETUS INC.
                                                   21-NOV-1990; US-617239.
18-MAY-1992; US-885970.
27-FEB-1996.
04-OCT-1988; 253243.
04-OCT-1988; US-253243.
                                                                                    (CETU ) AGRACETUS INC.
John M;
WPI; 96-139095/14.
                                                                                                                                                                                                                                                                                                                                  1283 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 96-267794/27
                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                          Sequence
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Example 4; Column 53-54; 33pp; English.
T162609-24 are cotton fibre-specific cDNA clones which can be used to identify genomic clones. This clone, CKFB15-E9, is expressed in fibre cells, but is also expressed at low levels in petal. (CK = Coker; FB = Fibre; 10, 15 or 23 = age in days of fibre cells; Al and the last character and number stand for clone identity). The fibre-specific genes were identified by differential cDNA library screenings. Coding sequences from these isolated genes are used in sense or antisense orientation to alter the fibre characteristics, e.g. strength, of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 97-108326/10.
Produced fransgenic cotton plants - by transformation with the H6 coding sequence or E6 anti-sense sequence, produces fibre of altered strength
generate transgenic cotton plants and lines producing fibres having altered quantity and quality.

Sequence 1283 BP; 509 A; 233 C; 251 G; 290 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-MAY-1997 (first entry)
Cotton fibre specific cDNA clone CKFB15-E9.
Cotton, fibre-specific, strength; transgenic plant; anthesis;
developmentally regulated; E6; H6; antisense; sense; SS.
Gossypium hirsutum strain Coker 312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           290 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 6
Gaps: 0
Percent Identity: 83.333
                                                                                                                                                                                        Length: 6
Gaps: 0
Percent Identity: 83.333
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                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to reverse of: T30265 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
ID T62624 standard; cDNA to mRNA; 1283 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transgenic fibre-producing plants.
Sequence 1283 BP; 509 A; 2
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P-PSDB; W81744.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1
                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                  primers.
DNA constructs contg. truncated promoter sequence - for fibre-specific gene expression in cotton plants
Example 3; Column 45-48; 48pp; 14911sh.
T70040-57 are cotton fibre-specific cona clones which can be used to obtain genomic clones containing fibre-specific promoters. Claimed DNA constructs comprise a truncated promoter sequence (from one of T70031-38) that promotes preferential gene expression in plant fibre cells, a protein coding sequence not naturally associated with the promoter sequence and a 3' termination sequence. The DNA constructs are useful for expressing foreign genes in fibre-producing plants, esp. to produce transgenic cotton plants with varied cotton fibre characteristics and quality. The present sequence comprises B9 cDNA isolated from clone CKFB15-E9 (CK = Coker; FB15 = 15 day old bolls).
Sequence 1283 BP; 509 A; 233 C; 251 G; 290 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated Mycobacterium tuberculosis polypeptides and DNA - use to develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11a; Page 207-209; 250pp; English.
This DNA sequence codes for an antigenic portion (see W64377) of
                        20-AUG-1997 (first entry)
Cotton fibre specific cDNA clone E9.
cotton: E6; fibre; promoter; transgenic plant; truncated; heterologous gene expression; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-NOV-1998 (first entry)
Mycobacterium tuberculosis antigen RDIF7 DNA.
Tuberculosis; infection; diagnosis; antigen; RDIF7; ss.
Mycobacterium tuberculosis strain Erdman.
Location/Qualifiers
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07-CCT-1997; U18214.
113-WAR-1997; U2-218111.
11-CCT-1996; US-729622.
(CORI-) CORIXA CORP.
Campos-Neto A, Dillon DC, Houghton R, Lodes M
Reed SG, Skeiky YAW, Twardzik DR, Vedvick TS;
WPI; 98-251292/22.
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                                                                                                                          Gossypium hirsutum strain Coker 312.
US5620882-A.
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ID V44448 standard; DNA; 2367 BP.
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US-08-653-294-6 x T70055/rev
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24-OCT-1988; US-253343.
21-NOV-1990; US-617239.
18-MAY-1992; US-885970.
19-OCT-1994; US-298829.
                                                                                                                                                                                                                                                                                                                                             (CETU ) AGRACETUS INC
                                                                                                                                                                                                                                                                                                                                                                                              WPI; 97-235185/21
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CONTRACTOR DESCRIPTION OF THE PROPERTY OF THE
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Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - used to develop products for the detection of M. tuberculosis infection and for disgnosis, treatment and prevention of tuberculosis infection Claim 4; Page 194-195; 230pp; English.

This sequence encodes an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M. tuberculosis immunogenic polypeptide RDIF7 DNA.
Tuberculosis; immunogenic; soluble; antigen; protective immunity; TB;
vaccine; pharmaceutical; infection; diagnosis; ss.
Mycobacterium tuberculosis antigen RDIF7. It was isolated from a M. tuberculosis strain Erdman genomic DNA expression library using rabbit anti-sera raised against M. tuberculosis fractionated proteins. Phage plaques expressing immunoreactive antigens were purified. The invention relates to compositions and methods for diagnosing tuberculosis. It provides Polypeptides (see W64291-W64379) comprising antigenic or immunogenic portions of M. tuberculosis antigenic or immunogenic portions of M. polypeptides, recombinant expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using these polypeptides, antibodies or oligonucleotide probes and
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Gaps: 0
Percent Identity: 83.333
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Gaps: 0
Percent Identity: 83.333
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ID V64557 standard; DNA; 2367 BP.
AC V64557;
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07-OCT-1997; U18293.
13-MAR-1997; US-818112.
11-OCT-1996; US-730510.
(CORI-) CORIXA CORP.
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US-08-653-294-6 x V44448/rev
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US-08-653-294-6 x V64557/rev
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Ratio: 4.667
Percent Similarity: 100.000
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AQ790119 HS_3247_A1_E06_MR
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In Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 14 286 1810
Fax: 14 286 1810
Fax: 1524
High quality sequence starts: 1 High quality sequence stops: 1
Source: IMAGE Consortium, LINI This clone is available royalty-free through LLML: contact the IMAGE Consortium (info@image.llnl.gov)
for further information. Trace considered overall poor quality
Insert Length: 2224
Seq primar: -21mil3
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/organism="Homo sapiens"
/db_xref="GBB174520"
/db_xref="Taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:121975"
/clone="Lb="Soares fetal liver spleen INFLS"
/clone="IMAGE:121975"
/clone="IMAG
                                                                                                                                           197779 70 bp mRNA EST 29-MAR-1995
ye58h04.sl Soares fetal liver spleen INFLS Homo sapiens cDNA clone
IMAGE:121975 3' similar to qb:M32011 NEUTROPHIL CYTOSOL FACTOR 2
HUMAN); mRNA sequence.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M. Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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High quality sequence stop: 1.
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LOCUS T97779
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gb_gss10:AQ180569
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                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                              ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
COMMENT
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AA470910 ne62a0.s1 NoI_CGAP_A1
AA670909 af34c01.s1 Soares_tote
AA671099 af34c01.s1 Soares_tote
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AV24866 AV26198 Mus musculus
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AV26198 AV026198 Mus musculus
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AV443803 AV43803 Mus musculus
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AA458948 aa26h11.x1 Zebrafish W
AA58853 HS_C608 X1 NCI_CGAP_K1
AN068853 HS_C605_T7A_RPC
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AQ821027 HS_4756_A1_G09_SP6E_C1
AQ059883 CIT-HSP-2348L22_TR_CIT
AQ061442 CIT-HSP-2348011.TR_CIT
AW025732 Wu05902.x1 NCI_CGAP_GC
AQ671287 HS_452_A2_L04_SP6E_RF
AQ055230 CITEL_E1-2534H15.TF_CI
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Search time (sec): 8553.360000
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OM of: US-08-653-294-6 to:
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                                                                                                                                                                 Command line parameters:
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                                               Date: Feb 8, 2000 4:02
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gb_est13:AA751293
gb_est16:AA564601
gb_est10:AV026198
gb_est30:AV026198
gb_est47:AU0782706
gb_est43:AU0782706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gb_gss1:CNS00Y83
gb_est19:AA738876
gb_est5:H93368
gb_est19:AA751483
gb_est30:AI642616
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gb_est20:AA872097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gb_gss4:AQ671287
gb_gss12:AQ355230
gb_gss15:AQ644952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gb_est23:AI076270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gb_est15:AA458948
gb_est24:AU029860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gb_est38:AW025732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gb_est44:AW173025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gb_est38:AW058842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gb_gss10:AQ221577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gb_gss13:AQ468537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_gss8:AQ059883
gb_gss8:AQ061642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gb_gss8:AQ061283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gb_gss9:AQ145722
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gb_est2:T97779
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63108

DEFINITION

ACCESSION VERSION KEYWORDS ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

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seg_documentation_block: 209 bp mRNA EST 26-MAY-1999
LOCUS A1679465 209 bp mRNA CLONE IMAGE:2256774 3'
DEFINITION tu14c04.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2256774 3'
similar to gb:M14219 BONE PROTEOGLYCAN II PRECURSOR (HUMAN);, mRNA
MAGE:1033536 3' similar to gb:M27492 INTERLEUKIN-1 RECEPTOR, TYPE
                                                                                                                                         Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhin1; Hominidae; Homo.

1 (Dases 1 to 203)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Ladry,M., Le.N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashD-NCI human EST Project
Unpublished (1977)

On Sep 12, 1996 this sequence version replaced gi:1407372.

Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
Trace Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 841 Std Error: 0.00
Seq primer: -40m13 fwd. Er from Amersham
High quality sequence stop: 1.
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                by Bento Soares and M. Fatima Bonaldo. 32 g 69 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Scares_total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 6
Gaps: 0
Percent Identity: 100.000
            I PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to: 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/clone="IMAGE:1033536"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from: 1
                                                                      AA621099.1 GI:2525038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TyrArgLeuLeuIleArg 6
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Percent Similarity: 100.000
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US-08-653-294-6 x AA621099
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                                            ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
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                                                                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                       REFERENCE
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                                                                                                                                                                      AA470910 197 bp mRNA EST 14-AUG-1997 ne62a07.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:908820, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGPP clone distribution information can be
found through the I.M. G.E. Consortium/LLNL at:
www-blo.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  !issue Procurement: Lee Helman, M.D., Michael R. Emmert-Buck, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pAMP10; mRNA made from alveolar rhabdomyosarcoma, cDNA made by oligo-dr priming.
Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."
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LOCUS AA621099 203 bp mRNA EST 02-MAR-1998
DEFINITION af34c01.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 197)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1394316.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: David B. Krizman, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:908820"
/clone_lib="NoI_cGAP_Alv1"
/tlssue_type="alveolar rhabdomyosarcoma"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps: 0
Percent Identity: 100.000
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Seq primer: -41ml3 fwd. ET from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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AA470910.1 GI:2198219
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                                         50 TATAGGTTACTCATAAGG 33
1 TyrArgLeuLeuIleArg 6
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Percent Similarity: 100.000
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US-08-653-294-6 x AA470910
                                                                                          seq_name: gb_est15:AA470910
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                                                                                                                                            seq_documentation_block:
LOCUS AA470910
                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                       sequence
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FEATURES

alignment_scores

BASE COUNT

ORIGIN

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Quality:
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                TITLE
JOURNAL
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COMMENT
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TITLE
      AUTHORS
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                                                                                                        COMMENT
                                                                        Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Mammalia; Eukheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (Dassa 1 to 209)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

I mior Gene Index

Tumor Gene Index

Tumor Gene Index

To 1998 this sequence version replaced gi:2948836.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausbergenh, gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.69 kb. Life Technologies catalog #: 11549-011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST 20-JAN-1998 ISSU0105 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa AA751293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa.
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; Lillopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/do_xref="teaxon:9606"
/clone="IMAGE:2256774"
/clone_lib="NCI_CGAP_Gas4"
/tissue_type="poorly differentiated adenocarcinoma with
/signet ring cell features"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to: 209
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Gaps: 0
Percent Identity: 100.000
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Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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  GI:4889647
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US-08-653-294-6 x A1679465/rev
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Ratio: 4.833
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
LOCUS AA751293
                                                                Homo sapiens
AI679465.1
EST.
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ORGANISM
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                                                           ORGANISM
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AUTHORS
TITLE
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KEYWORDS
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                                                                                                                                                                                                         JOURNAL
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KEYWORDS
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/ 45 g 61 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 221)

8 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

8 NATIONAI Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

1 (pubblished (1997)

1 (pubblished (1997)

1 (contact: Robert Strausberg, Ph.D.

1 (201) 496-1550

2 Emmil: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Emmil: Robert Strausbergenih.gov

Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                Email: myeun@sun20.asti.re.kr
Submitted by Back Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: Mi3 Reverse primer.
Nahm, B. H., Kim, J. K., Cheong, J. J., Kim, S. I., Hahn, T. R., Moon, E. P., Kim, W. T., Kim, W. Y., Yang, M. S., Park, R. D., Sohn, U. I., Kang, K. Y., Lee, M. C. and Eun, M. Y.
Leach, M. C. and Eun, M. Y.
Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)
On Sep 12, 1996 this sequence version replaced gi:1404701.
Contact: Eun M. Y.
Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kynnggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:

LOCUS AA564601 221 bp mRNA EST 04-SEP-1997

LOCUS AA564601 CARP_Pr21 Homo sapiens cDNA clone IMAGE:985186 3'

DEFINITION n102e06.s1 NCI_CGAR_Pr21 Homo sapiens cDNA clone IMAGE:985186 3'

SIMILAR to 9b:M27492 INTERLEUKIN-1 RECEPTOR, TYPE I PRECURSOR ACCESSION AA564601

VERSION AA564601 GI:2336240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: M. Bento Soares, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps: 0
Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-08-653-294-6 x AA751293/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173 TATAGACTACTCATAAGA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TyrArgLeuLeulleArg 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio: 4.833
Percent Similarity: 100.000
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us-08-653-294-6.rst

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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Dassa 1 to 238)
1 (Dassa 1 to 238)
1 (Ansaa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishiawa, T., Kawai, J., Kikuchi, N., Izawa, M., Kadota, K., Kagawa, T., Kai, C., Kawai, J., Kikuchi, N., Mika, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Namura, M., Oda, H., Okazaki, Y., Shiata, Y., Shiach, T., Sato, K., Shibata, K., Shiata, T., Yakhashi, F., Tateno, M., Tominaga, N., Taunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTS (Konno, H., et al.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viote—"Organ: prostate; Vector: pT773D-Pac (Pharmacia)
with a modified polylinker; 1st strand cDNA was prepared
from normal prostate bulk tissue, and was then primed with
a Not I - oligo(dI) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT773 vector. Library is not normalized. Library
was constructed by Bento Scares and M. Fatima Bonaldo. "
30 c 53 g 65 t
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/Link at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AV274866 RIKEN full-length enriched, adult male testis (DH10B) Mus macaculus cDNA clone 4932422P17 3', mRNA sequence.
AV274866.1 GI:6262903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-NOV-1999
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Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps: 0
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                          Trace considered overall poor quality Insert Length: 797 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 1. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio: 4.833
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                           1, .221
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US-08-653-294-6 x.AA564601
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LOCUS AV274866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73
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VERSION
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Transcriptional sequencing: A method for DNA sequencing using RNA Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) ItOh.M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Oxazaki,Y. and Hayashizaki,Y., Ozawa,Y., Muramatsu,M., Oxazaki,Y. and Hayashizaki,Y. Automated filtration-based high-throughput plasmid preparation system Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: Sall; 3' end: BamHI."
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ORL:http://genome-rtc.riken.go.jp,
Sasakt,N., Izawa,M., Matahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
                  Genome Science Laboratory
The Institute of Physical and Chemical Research (RIKEN), Genomic
Senome Exploration Research Group, Life Science Tsukuba Center,
                                                                                           3-1-1 Koyadal, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 6
Gaps: 0
Percent Identity: 100.000
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US-08-653-294-6 x AV274866/rev
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                                                                                                                                                                                                                                                                              Hayashizaki, Y.
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LOCUS

ACCESSION VERSION KEYWORDS ORGANISM

AUTHORS REFERENCE

TITLE JOURNAL COMMENT

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Eutheria: Rodentia; Craniata; Vertebrata: Mammalia; Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus. Eto 256; Sciurognathi; Mara, Mara, M., Radota, M., Hara, M., Hayatsu, N., Hiozane, T., Hori, F., Ishikwa, T., Itch, M., Izawa, M., Radota, M., Ragawa, I., Katuchi, N., Majima, Y., Koya, S., Kusakabe, M., Mats, C., Rawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Matsu, Ganoto, Y., Saito, H., Saro, M., Sato, K., Shibata, K., Shibata, Y., Saito, H., Sano, M., Sato, K., Shibata, Y., Saito, H., Saro, M., Sato, K., Shibata, Y., Saito, H., Sano, M., Sato, K., Sugahara, Y., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Suzuki, H., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Tsundda, Y., Watahiki, A., Watanabe, S., Tamamura, T., Yasunishi, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Nobeliide Hayashizaki, Genome Exploration Research Group, Life Science Tsukuba Center, Genome Exploration Research Group, Life Science Tsukuba Center, Contact: Toshinde Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Rawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci,P. and Hayashizaki,Y. Garninci,P. and Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center
3.1-1 Kopadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9018
Email: genome-res@ttc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp,
MAL:http://genome.rtc.riken.go.jp/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="11 days pregnant, adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'tissue_type="ovary and uterus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adult female ovary and uterus"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             further details.
Location/Qualifiers
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                                   house mouse
   KEYWORDS
SOURCE
ORGANISM
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JOURNAL
COMMENT
                                                                                                                                                                       REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                    Carning, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Owa, C., Sato, K., Shibata, Y., Matsuyama, T., Mitsuma, H., Oda, H., Suaki, T., Shipata, Y., Shibata, Y., Shipata, H., Tateno, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Toshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. Ingublished (1999)

Con Apr 7, 1998 this sequence version replaced g1:3034511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length CDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing. A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
LOCUS AV285786 256 bp mRNA EST 09-NOV-1999
DEFINITION AV285786 RIKEN full-length enriched, 11 days pregnant adult female
ovary and uterus Mus musculus cDNA clone 5031414A18 similar to
AF030402 Mus musculus KH domain RNA binding protein QKI-5A mRNA,
AVO26198 251 bp mRNA EST 31-AUG-1999
AVO26198 Mus musculus adult C57BL/6J lung Mus musculus cDNA clone
1200018M16, mRNA sequence.
                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 251)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="1200018M16"
/clone_lib="Mus musculus adult C57BL/6J lung"
/tissue_type="lung"
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Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: genome-res@rtc.riken.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
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54 c 95 a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Senome Science Laboratory
                                                                                                   AV026198
AV026198.1 GI:4803190
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AV285786
AV285786.1 GI:6296290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 81-298-36-9145
Fax: 81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-6 x AV026198/rev
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Percent Similarity: 100.000
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                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                       house mouse
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BASE COUNT

ORIGIN

FEATURES

ACCESSION VERSION

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 274)
S Ronno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T.,
S Fukuda, S., Eukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F.,
Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I.,
Rai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koga, S., Kusakabe, M.,
Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
Shibata, Y., Saligemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y.,
Suzuki, H., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N.,
Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A.,
Yokota, T., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTS (Konno, H., et al.)
On Dec 20, 1995 this sequence version replaced gi:1134368.
Genome Exploration Research Group, Life Science Tsukuba Center,
Genome Exploration Research Group, Life Science Tsukuba Center,
The Institute of Physical and Chemical Research (RIKEN), Genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh.M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y. Ozawa,Y., Muramatsu,M., Atomated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
Email: genome-res@ftc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
                                                                           seq_documentation_block:
LOCUS AV218201 274 bp mRNA EST 30-OCT-1999
DEFINITION AV218201 RIKEN full-length enriched, adult male hippocampus Mus
musculus cDNA clone 29000087E03 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
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/clone="2900087E03"
/clone_lib="RIKEN full-length enriched, adult male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="hippocampus"
/dev_stage="adult"
/lab_host="SOLR"

    .274
    /organism="Mus musculus"
    /strain="C57BL/6J"

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                                                                                                                                                                                                     AV218201.1 GI:6159042
EST.
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                        seq_name: gb_est39:AV218201
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                                                                                                                                                                                                                                                                                    Mus musculus
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                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                        VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                  ACCESSION
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S12251_12Z, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 110 267)
Yamamoto, K. and Sasaki, T.
Rice CDNA from green shoot
Unpublished (1996)
On May 18, 1998 this sequence version replaced gi:3137393.
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program
2-1-2 Kannondai, Tsukuba
Ibaraki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
Locus AU078270 267 bp mRNA EST
DEFINITION AU078270 Rice green shoot Oryza sativa cDNA clone
                                                                                                                                                  Length: 6
Gaps: 0
Percent Identity: 100.000
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/clone_lib="Rice green shoot"
/note="Green shoot (8 days old)"
39 c 61 g 87 t
                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to reverse of: AV285786 from: 1
                        104
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    .267
    /organism="Oryza sativa"
    /strain="Nipponbare"

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Tel: 0298 38-7441
Fax: 0298-38-7468
Email: tsssaki@abr.affrc.go.jp
PROJECT = 'RGP'.
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Location/Qualifiers
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US-08-653-294-6 x AV285786/rev
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                  48
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Percent Similarity: 100.000
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Percent Similarity: 100.000
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BamHI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: gb_est37:AU078270
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US-08-653-294-6 x AU078270
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Ratio:
                     69
                                                                                                                            alignment_scores
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                  BASE COUNT
ORIGIN
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VERSION
KEYWORDS
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AUTHORS
TITLE
JOURNAL
COMMENT
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FEATURES

ORIGIN

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alignment_block:
US-08-653-294-6 x AV143803
                                                                                                                                                                                                                                                                                                                             seq_name: gb_est20:AA872097
                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS AA872097
                                                                  Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human.
                                              alignment_scores:
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VERSION
KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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AUTHORS
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COMMENT
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EMERYORACHUS.

ENERYORACH METAZOR: Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

E 1 (bases 1 to 284)

Carninol, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Alzawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Nitsuma, H., Oda, H., Gwa, C., Sato, K., Shibata, Y., Shigamoto, Y., Shiraki, T., Sogabe, Y., Sugamera, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.

RIKEN Mouse ESTS

In Opublished (1999)

On May 18, 1998 this sequence version replaced g1:3136837.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: genome-resertc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
Trenanostabilization and thermoactivation of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
AV143803 Mus musculus C57BL/6J 10-11 day embryo Mus musculus CDNA clone 2810432E15, mRNA sequence.
AV143803
EST
C155347798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="2810432E15"
/clone_lib="Mus musculus C57BL/6J 10-11 day embryo"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                       to: 274
                                                                                                                                                                                                        Length: 6
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="10-11 day embryo"
80 c 43 q 99 t
                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to reverse of: AV218201 from: 1

    .284
    /organism="Mus musculus"

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RIKEN
                                                                                                                                                                                                                                                                                           alignment_block:
US-08-653-294-6 x AV218201/rev
                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio: 4.833
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                             1 TyrArgLeuLeulleArg 6
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                                                                                                                                                                                                            29.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: gb_est34:AV143803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
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                                                                                                                                                                                                              Quality:
Ratio:
                                                                                                          57
                                                                                                                                                                                         alignment_scores:
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ORIGIN
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ORIGIN
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JOURNAL
COMMENT
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KEYWORDS
SOURCE
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="INAGE:1476318"
/clone=INAGE:1476318"
/clone=INAGE:1476318"
/clone=INAGE:1476318"
/clone=INAGE:1476318"
/clone=INAGE:1476318"
/clone=InAge:"Pooled germ cell tumors.
/lab_host="Anthone"
/note="Vector: p77730-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - ollgo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7773 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "A Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor Gene Index
Uppublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1404743.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nlh.gov
Iissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Email: Robert_Strausbergenth.gov
Issue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Email: Robert_Strausbergenth.gov
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Sequencing Arrayed by: Greg Lennon, Ph.D.
Clone distribution: WCI-GGAP clone distribution information can be found through the I.M.A.G.E., Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA872097 297 bp mRNA EST 17-WAR-1998 oil2e04.sl NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1476318 3' similar to gb:M32011 NEUTROPHIL CYTOSOL FACTOR 2 (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 297)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP of the content of 
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trace considered overall poor quality
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: AV143803 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 TACCGCCTCCTTATTCGA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TyrargLeuLeullearg 6
                                                                             Ratio: 4.833
Percent Similarity: 100.000
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us-08-653-294-6.rst

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house mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
  SOURCE
ORGANISM
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JOURNAL
COMMENT
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                                                                               REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 300)
Salanoubat, M., Choisne, N., Artiguenave, F., Brottier, P., Wincker, P., Samson, D., Saurin, W., Weissenbach, J. and Quetier, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                              thale cress.
Arabidopsis thallana
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (25-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRX cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr | Location/Qualifiers
                                                                                                                                                                                                                                                                                                     CNSOOT83 300 bp DNA GSS 29-JUN-1999
Arabidopsis thaliana genome survey sequence SP6 end of BAC T15N20
of TAMU library from strain Columbia of Arabidopsis thaliana,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:

LOCUS AA738876 338 bp mRNA EST 14-JAN-1998
DEFINITION VV62b01.r1 Soares 2NbMT Mus musculus cDNA clone IMAGE:1226953 5',
ACCESSION AA738876
VERSION AA738876.1 GI:2776128
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Gaps: 0
Percent Identity: 100.000
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/strain="Columbia"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref-"taxon:3702"
/clone_l1b="TAMU"
                                                                                                                      Align seg 1/1 to reverse of: AA872097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="end : SP6'
                                                                                                                                                                                                                                                                                                                                                               genomic survey sequence.
AL095841
AL095841.1 GI:5303996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="T15N20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-08-653-294-6 x CNS00Y83/rev
                                                            alignment_block:
US-08-653-294-6 x AA872097/rev
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                                                                                                                                                                                                     50 TATAGGTTACTCATAAGG 33
                                                                                                                                                              1 TyrArgLeuLeuIleArg 6
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  Ratio: 4.833
Percent Similarity: 100.000
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                                                                                                                                                                                                                                           seq_name: gb_gss1:CNS00Y83
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TITLE
JOURNAL
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AUTHORS
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 338)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p17T3 vector. RNA provided by Dr. Bartrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Fathma Bonaldo."
                                                                                                                                                                                                                                           Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashIngton University School of MedicineP
WashIngton University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseesf@watson.wustl.edu
Email: mouseesf@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:652545
ukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps: 0
Percent Identity: 100.000
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High quality sequence stop: 337.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Soares 2NbMT"
/sex="male"

    .338
    /organism="Mus musculus"
    /strain="C57BL/6J"

                                                                                                                                                                                                                       The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
/clone="IMAGE:1226953"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'tissue_type="Thymus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-08-653-294-6 x AA738876/rev
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Ratio: 4.833
Percent Similarity: 100.000
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Sequence:

Run on:

Searched:

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W33781 standard; peptide; 6 AA.
W33781;
19-JUN-1998 (first entry)
Peptide #2 used in immunomodulating dimer peptide.
Immunomodulating dimer; immunosuppressant drug; CTL activation; transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                             22-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Homo sapiens.
WO9744351-A1.
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RESULT
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Peptide #2 used in
Immunomodulatory p
Immunomodulatory p
HLA-B2702 84-79-84
Peptide B2702,84-7
Immunomodulating d
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Peptide B2702.84-7
HSV-2 strain SB5 C
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Immunomodulatory p
Peptide #4 used in
Immunomodulatory p
Immunomodulatory p
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HLA-B2702 CTL modu
HLA-B2702 CTL modu
HLA-B2702 84-75-84
HLA-B2702 84-751/7
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HLA-B2702 CTL modu
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Peptide B2702.84-7
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Canine 32K alveola
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quence encoded b
                                                     February 8, 2000, 01:29:36; Search time 122.56 Seconds (without alignments) 1.160 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                    Description
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                                                                                                                                                              188963
                Compugen Ltd
                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                              188963 seqs, 23686106 residues
       GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                           SUMMARIES
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                                        - protein search, using sw model
                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
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W47270
R95429
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R92909
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R95430
W33778
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W72145
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W71513
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R92908
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R04210
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P70483
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Listing first 45
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29
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Perfect score:
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Result No.

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Enzyme Q36. DNA en
Human thioredoxin
Human thioredoxin
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Manduca sexta BT t
Mouse DEC-205. Lig
                                             Human KM-102-deriv
                                                                      Bacillus thuringie
Human thioredoxin
KM31-7 precursor
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23-ARR-1997.
23-ARR-1997. U06705.
22-MAY-1996. US-651650.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM;
WPI; 98-018220/02.
NOVel immunomodulatory peptide-type compound - useful for inhibiting
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Claim 10; Page 36; 41pp; English.
The present sequence is an immunomodulatory peptide, which
comprises a Class I HAA-B alpha-1 domain sequence. It can be used
in a pharmaceutical composition together with a subtherapeutic dose
of an immunomosuppressant, to extend the period of acceptance of a
transplant from a major histocompatibility complex (MHC) unmatched
donor, i.e. to inhibit transplant rejection. It can also be used in
the treatment of autoImmune diseases.
Peptides using the D-form amino acids are more effective
immunomodulators than their diastereomers or enantiomers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .6
/note= "at least one of the amino acids is the D-isomer
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Immunomodulator; Class I HLA-B alpha-1 domain; inhibition;
transplant rejection; treatment; autoimmune disease.
Homo saplens.
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100.0%; Pred. No. 1.5e+05;
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  W83401
W83404
W83404
R79949
R739949
W83402
W83403
W90183
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                                                                                                                                                                      claim 15; Page 35: 41pp; Engilsh.

Claim 15; Page 35: 41pp; Engilsh.

Claim 15; Page 35: 41pp; Engilsh.

Cof the immunomodilating dimer peptides of the invention. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal advised and/or C-terminal antidated or including the N-terminal and/or C-terminal amidated or compound or variant is claimed which has immunomodulating activity, including the N-terminal and/or C-terminal amidated or comprises the formula: A-B. where A, B = (R aa76-77L) (aa79-84) or C camparises the formula: A-B. where A, B = (R aa76-77L) (aa79-84) or C camparises the formula: A-B. where A, B = (R aa76-77L) (aa79-84) or C camparises the formula: A-B. where A: aa77 = D, S or N; aa79 = R or G; camparises the formula: A-B. where A: aa79 = R or G; camparises the formula: A-B. where A: aa79 = R or G; camparises the peptide type bond or L; aa83 = G or R; and aa represents amino acid. The sequence in the brackets. The compounds comprise amino acid sequences related to brackets may optionally be absent or truncated at any peptide type bond within the brackets. They cam also be used in combination with antigenic peptides or proventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosis. The products can also be used for detection and diagnosis.
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The present sequence is an immunomodulatory peptide, which comprises a Class I HLA-B alpha-1 domain sequence. It can be used in a pharmaceutical composition together with a subtherapeutic dose of an immunosuppressant, to extend the period of acceptance of a transplant from a major histocompatibility complex (MHC) unmatched donor, i.e. to inhibit transplant rejection. It can also be used in
              22-MAY-1997; U08689.
24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STAMFORD JUNIOR.
Beulow R, Clayberger C, Krensky AM;
WPI; 98-086530/08.
New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or
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Immunomodulator; Class I HLA-B alpha-1 domain; inhibition;
transplant rejection; treatment; autoimmune disease.
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100.0%; Pred. No. 1.5e+05;
iive 0; Mismatches 0;
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23-APR-1997.
22-MAY-1996; UG-651650.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W47266 standard; peptide; 10 AA.
                                                                                                                                                                treating autoimmune diseases
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Best Local Similarity 100.
Matches 6; Conservative
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  27-NOV-1997
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HIA-B2702 84-79-84 palindrome.
HIA-B2702 84-79-84 palindrome.
HIA- p74; alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic I lymphocyte; CTL; differentiation;
                                                                                                                                                                                                     Gaps
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Novel immunomodulatory peptide-type compound - useful for inhibiting
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Immunomodulator; Class I HLA-B alpha-1 domain; inhibition;
transplant rejection; treatment; autoimmune disease.
                                                                                                                             100.0%; Score 29; DB 1; Length 10; 100.0%; Pred. No. 0.25; 1ve 0; Mismatches 0; Indels
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immunomodulators than their diastereomers or enantiomers.
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22-APR-1996; US-651650.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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                                                                                                                                                                                                     6; Conservative
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10-NOV-1993; US-150493.
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                                                                                                                                 Query Match
Best Local Similarity
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Best Local Similarity
Matches 6; Conserv
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Synthetic.
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WO9513288-Al
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R95429
ID R9
AC R9
DT 122
DE HI
KWW T-1-
KWW B
CYWW B
PD CS
SY
OS SY
PD 116
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Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                     remains and R95415-R55431 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the result of 1974 from a T-cell lysate. P74 is a T-cell surface membrane of protein associated with T-cell activation mammalian T-cells, and is also immunologically cross reactive with the heat shock protein HSC70. P74 is found in a limited number of cell types, but is particularly corpusessed on B and T cells. P74 can be isolated by lysis of a sultable column containing a covalently bound HLA-B270 palindromic peptide. CC column containing a covalently bound HLA-B270 palindromic peptide. CC compositions comprising the extracellular fragment of p74 combined with the HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits compounds can be screened for their effect on the cytolytic activity of compounds can be screened for their effect on the cytolytic activity of determining them with the extracellular portion of p74 and determining T-cells and antigen presenting cells (APCS), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete with p74 for the binding of the p74 ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New liminomodulating dimer peptide(s) - based on a Class I HLA-B mupl; 98-086530/08.

New liminomodulating dimer peptide(s) - based on a Class I HLA-B mupl; 98-086530/08.

New liminomodulating dimer peptide(s) - based on a Class I HLA-B mupl alpha-1 domain, used for preventing rejection of transplants or treating autoimmune diseases

Example 1; Page 19; 41pp; English.

Example 2; A peptide 1; Page 2; Page 2
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                                                                                           Compsns. comprising lymphoid surface membrane proteins - which may hibbit cytolyric activity and differentiation of CTLS. Example: Page 12; 29pp; English. R95413, and R95415-R95431 represent palindromes and fragments of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUN-1998 (first entry)
Peptide B2702.84-79/79-84 tested for immunomodulating activity.
Immunomodulating dimer: Immunosuppressant drug; CIL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 29; DB 1
100.0%; Pred. No. 0.3;
Live 0; Mismatches
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22-MAY-1997.
24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
STRD ) UNIV LELAND STANFORD JUNIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W33798 standard; peptide; 12 AA.
                               Clayberger C, Krensky AM;
WPI; 95-194027/25.
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Best Local Similarity
Matches 6; Conserv
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1 YRLAIR 6
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                                          activate CILS. They can also inhibit the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosis. The products can also be
used in combination with antigenic peptides or proteins of interest to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Immunomodulating dimer peptide #3.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autolimmune disease; Class I HLA-B alpha-1 domain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 29; DB 1; Length 12; 100.0%; Pred. No. 0.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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                                                                                                                                                                                                                                                 used for detection and diagnosis.
Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W33799 standard; peptide; 12 AA.
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Best Local Similarity
Matches 6; Conserv
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Score 29; DB 1; Length 12; Pred. No. 0.3; Mismatches 0; Indels

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Conservative
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Best Local Similarity
for 6; Conserva
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Best Local Similarity
Matches 6; Conserv
of the patient.
Sequence 20 AA;
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16-MAY-1996
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R95428
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 15; Page 36; 80pp; English.

R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HLA-B2702.

These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherrapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (comparate to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLS)
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                  16-MAY-1996 (first entry)

HLA-B2702 CTL modulating peptide (B2702.84-75/75-84(T)).

Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
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R83061-R83085, R83090 and R92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to administration of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HLA-B2702 CTL modulating peptide (B2702.84-75/84-75). Cytotoxic I lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                    Extension of acceptance period of transplants from MHC unmatched donor hosts – using Class I B75-84 MHC antigen of the recipient
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                                                                                                                                                                                                                                                                    05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM, Parham P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clayberger C, Krensky AM, Parham P; WPI; 95-358582/46.
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(STRD ) UNIV LELAND STANFORD JUNIOR.
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     standard; peptide; 20 AA
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05-APR-1995; U04349.
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05-APR-1995; U04349.
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Best Local Similarity
Matches 6; Conserv
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| YRLAIR 6
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R83061-R83085, R83090-R83096 and R92207-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLS)
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HLA-B3702 84-75-84 palindrome.
HLA-B3702 84-75-84 palindrome.
HLA-B3702 194-75-84 palindrome.
That, PV4, alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic I lymphocyte; CTL; differentiation;
Synthetic.
W09513288-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIA-B2702 CTL modulating peptide (B2702.84-75/75-84). Cytocoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                                                                               Gaps
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12-OCT-1995.
05-APR-1995; U04349.
05-APR-1995; UN-222851.
05-APR-1995; UNIV LELAND STANFORD JUNIOR.
(STRD ) UNIV LELAND STANFORD JUNIOR.
CLAYBERGET C, Krensky AM, Parham P;
WPI; 95-358562/46.
Extension of acceptance period of transplants from MHC unmatched Extension of acceptance period of transplants from the recipient "---- hosts - using Class I B75-84 MHC antigen of the recipient "---- hosts - using Class I B75-84 MHC antigen of the recipient
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100.0%; Score 29; DB 1; Length 20; 100.0%; Pred. No. 0.52;
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                                                                           0; Indels
                                                                           Mismatches
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10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRO ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                   R92907 standard; peptide; 20 AA.
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Sequence
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                                                            Whis yolytic activity and differentiation of CTLS.

Example: Page 12: 29pp: English.

PS Example: Page 12: 29pp: English.

R95413, and R95415-R9543 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the human-leucocyte-associated antigens. This sequence represents the human-leucocyte-associated antigens. This sequence represents the the Protein Py4 from a T-cell lysate. Py4 is a T-cell surface membrane protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein HSC70. This is found in a limited number of cell types, but is particularly expressed on B and T cells. Py4 is found in a limited number of cell types, but is particularly coll with an amphoteric detergent, and then passed through an affinity coll with an amphoteric detergent, and then passed through an affinity coll with an amphoteric detergent, and then passed through an affinity coll with an amphoteric detergent, and the passed through an affinity coll with an amphoteric detergent, and the passed through an affinity coll with an amphoteric detergent of the extracellular fragment of p74 combined with the HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits compounds can be screened for their effect on the cytolysis. Candidate compounds can be screened for their effect on the cytolysis. Candidate compounds the amount of binding between the candidate composition of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APC8), by adding to the containing T-cells and antigen presenting cells (APC8), by adding to the containing T-cells and antigen presenting cells (APC8), by adding to the containing T-cells and antigen presenting cells (APC8), by adding to the containing T-cells and antigen presenting cells (APC8), by adding to the containing T-cells and antigen presenting cells (APC8), by adding to the containing T-cells and antigen presenting cells (APC8), by adding to 
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Example: Page 12: 29pp: English.

Example: Page 13: 29pp: English.

Example: Page 13: 29pp: English.

Example: Page 13: 20pp: English.

Example: Page 13: 20pp: English.

Example: Page 13: 20pp: English.

Example: Page 14: 20pp: English.

Example: Page 15: 20pp: English.

Example: Page 25: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-NOV-1996 (first entry)
HLA-B2702 84-75T/75-84T palindrome.
HLA-B2702 84-75T/75-84T palindrome.
HLA-B2702 84-75T/75-84T palindrome.
The property of the protein that an annual the protein that the protein Hsc70; APC;
B cell, calcium influx, cytotoxic T lymphocyte; CTL; differentiation; cytolysis; antigen presenting cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Candidate compounds can be screened for their effect on the cytolytic activity of T-cells, by combining them with the extracellular portion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             differentiation or cytolysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 29; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 0.52; Matches 6; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-MAY-1995.
10-NOV-1994; U12985.
10-NOV-1993; US-150493.
GERD ) UNIV LELAND STANFORD JUNIOR.
CLAYDERGE C, Krensky AM;
WPI; 95-194027/25.
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Krensky AM;
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W09513288-A1.
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R95430;
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Will ye used tor preventing rejection of transplants or treating autofinanting dimer peptide(s) - based on a class I HLA-B alpha-1 domain, used for preventing rejection of transplants or treating autofinmune diseases.

Claim 16, Page 35; 41pp; English.

Profile of the invention. A peptide type compound or variant is claimed which has immunomodulating activity, including the N-terminal activity, where the peptide type compound comprises the formula; A-B, where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or N; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84-a a represents amino acid; The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid; sequences related to a class I HLA-B alphal domain (positions 79-84). They can be used to inhibit cytotoxic of 1-1ymphocytes (CTL) from undesirably attacking cells in a host or in tructions of interest to activate CTLS. They can also be used in combination with antigenic peptides or proliferation of T cells in response to anti-CD3. The peptide can be cused for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosis.
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p74 and determining the amount of binding between the candidate compound and p74. Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCs), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete with p74 for the binding of the p74 ligand. Sequence 20 AA:
                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunomodulating dimer peptide #1.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
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                                                                                                                                                                                                                                                   100.0%; Score 29; DB 1; Length 20; larity 100.0%; Pred. No. 0.52; Conservative 0; Mismatches 0; Indels
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22-NAY-1997.
24-NAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beulow R, Clayberger C, Krensky AM;
WPI; 98-086530/08.
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W33779
ID W33779 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W33778 standard; peptide; 20 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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WO9744351-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YRLAIR
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19-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rejection.
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This sequence represents a specifically claimed immunomodulating dimer peptide of the invention. A peptide-type compound or variant is claimed which has immunomodulating activity, including the W-terminal activated and/or C-terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B er R a76-77L) (a270-84) or (a284-70; (lasa7)-68); a276 = E or visca7) = D, S or N; a29 = R or G; a280 = I or N; a281 and a captacesents annion acid; a282 = R or L; a283 = G or R; and as represents annion acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a class I HLA-B absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a class I HLA-B absent or Trumcated at any peptide type bond within the brackets.

Tymphocytes (CTL) from undesirably attacking cells in a host or in the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune the products can also be used for detection and diagnosis.

The products can also be used for detection and diagnosis.
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New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or treating autoimmune diseases.

Example 1: Page 19: 41pp; English.

Peptides W33784-98 and W33778-9 were assayed for their immunomodulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                           Immunomodulating dimer peptide #2.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New immunomodulating dimer peptide(s) - based on a class I HLA-alpha-1 domain, used for preventing rejection of transplants or treating autoimmune diseases
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(STRD ) UNIV LELAND STANFORD JUNIOR.
Beulow R. Clayberger C, Krensky AM;
WPI; 98-086530/08.
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(STRD ) UNIV LELAND STANFORD JUNIOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 16; Page 35; 41pp; English.
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                                (first entry)
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Best Local Similarity
Matches 6; Conserv
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| YRLAIR 6
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WO9744351-A1.
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                          19-JUN-1998
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                                                                                                                                                                 rejection.
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cc activity. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or cc immunomodulating activity, including the N-terminal acylated and/or cc c-terminal amidated or esterified forms of up to 60 amino acids, where creaming the peptide-type compound comprises the formula; A-B, where A, B = cc (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V: aa77 = cc (R aa76-77L) (aa89 = R or L); aa83 = G or R; and aa represents amino acid. The sequence in the brackets may optionally be absent or truncated cat any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a class I HLA-B alphal domain (positions 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from cused in combination with antiqenic peptides or proteins of interest to used in combination with antiqenic peptides or proteins of interest to cresponse to anti-cD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, creamatoid arthritis and lupus erythematosis. The products can also be consent for detection and diagnosis.

Query Match

Dest Local Similarity 100.0%; Pred. No. 0.52; DB 1; Length 20; Best Local Similarity 0; Mismatches 0; Indels 0; Gaps 0; INRLAIR 6.
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Search completed: February 8, 2000, 01:29:37 Job time: 1749 sec

Wed Feb

	Ltd.
4.5	Compugen
version	- 2000
GenCore	(c) 1993
•	Copyright

OM protein - protein search, using sw model

February 7, 2000, 11:54:18; Search time 117.7 Seconds (without alignments) 2.405 Million cell updates/sec Run on:

US-08-653-294-7 29 1 YRLAIR 6 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

142080 seqs, 47169319 residues Searched:

142080 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

Database :

pirl:* pir2:* pir3:* pir4:* PIR_62:* 1: pir1: 2: pir2: 3: pir3: 4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		æ			SOMMANIES	
Result		Query				
No.	Score	Match	Match Length	88	ΩI	Description
1	29	100.0	г	7	503	hypothetical prote
7	28	96.6	388	7	2	-4
m	28	96.6	579	7	236	oligopeptide ABC t
4	27	93.1	185	~	S74416	hypothetical prote
ī	27	93.1	309	7	G70882	oxic
9	27	93.1	404	7	F71324	probable gcpE prot
7	26	89.7	96	~	B69327	conserved hypothet
œ	26	89.7	105	~	T10473	molt-inhibiting ho
6	26	89.7	255	~	H71963	fumarate reductase
10	26	89.7	255	~	A64544	fumarate reductase
11	26	89.7	291	~	F72660	
12	26		545	ď	JN0448	t-complex polypept
13	26	89.7	883	7	S31175	hypothetical prote
14	25		148	~	B69960	3-dehydroquinate d
15	25		190	7	B42957	iron-sulfur protei
16	25	86.2	195	~	F64955	fliz protein - Esc
17	25		223	~	D49804	
18	25		256	Н	S10164	
19	25	86.2	368	~1	F72281	hypothetical prote
20	25	86.2	380	~	H70590	
21	25	86.2	381	~	T06293	yisob
22	25	86.2	463	~	B72500	probable seryl-tRN
23	25	86.2	545	N	T00485	probable phosphori
24	25	86.2	629	~	560385	mem
25	25	86.2	744	~	T10035	hypothetical prote
56	25	86.2	747	~	D70802	
27	25	86.2	783	~	JC6136	н
28	25	86.2	785	~	S64706	subtilisin-like pr
29	25	86.2	σ	~	T16911	thetical pro
30	25	86.2	1603	-	BVASA1	c

probable cell-surf hypothetical prote hypothetical prote	hypothetical prote probable membrane hypothetical prote	probable membrane ribosomal protein hypothetical prote	hypothetical prote hypothetical prote trans-zeatin secre	probable adenylate trans-zeatin secre cellobiose phospho
152 101 154	192 168 144	192 150 177	122 147 332	.22 198
\$2785; G6480; PC2054	S76792 S64368 D72544	\$69292 \$14050 D64577	A75022 S63647 JJAG32	S06738 S03122 D49898
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3 3 3 3 5 5 5	33.4 35.8	37 38 39	444 012	4 4 4 6 4 6 0

## ALIGNMENTS

hypothetical protein b2549 - Escherichia coli (strain K-12).
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: L2-8ep-1997 #sequence_revision 17-Sep-1997 #text_change 14-Nov-1997
C;Accession: D65032
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
C;A.; Rose, D.J.; Mau, B.; Shao, Y.
S.A.; Rose, D.J.; Mau, B.; Shao, Y.
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Recession: D65032
A;Accession: D65032
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1124 CBLAT>
A;Cross-references: GB:AEO00341; GB:U00096; NID:g1788899; PID:g1788900; UWGP:b2549
A;Experimental source: strain K-12, substrain MG1655

Gaps ö 100.0%; Score 29; DB 2; Length 1124; 100.0%; Pred. No. 24; tive 0; Mismatches 0; Indels ( Query Match 100.
Best Local Similarity 100.
Matches 6; Conservative 1 YRLAIR 6

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111111 412 YRLAIR 417 g ò

RESULT 2
\$15593
hypothetical protein (insertion sequence ISH27-3) - Halobacterium halobium C;Species: Halobacterium halobium C;Species: Halobacterium halobium C;Species: Halobacterium halobium C;Species: Halobacterium halobium C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 30-Jun-1998 C;Accession: \$15593
R;Pfeider: F: Blasselo, U.
Nucleic Acids Res. 18, 6921-6925, 1990
A;Title: Transposition burst of the ISH27 insertion element family in Halobacterium hA;Title: Transposition burst of the ISH27 insertion element family in Halobacterium hA;Accession: \$1559; MUID:91088266
A;Accession: \$15593
A;Status: preliminary
A;Accession: \$15593
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-388 cPFE>
A;Cross-references: EMBL:X54434
A;Note: the authors translated the initiation codon GTG for residue 1 as Val
C;Genetics:
A;Mobile element: insertion sequence ISH27-3
A;Start codon: GTG

Gaps ö Query Match 96.6%; Score 28; DB 2; Length 388; Best Local Similarity 83.3%; Pred. No. 15; Matches 5; Conservative 1; Mismatches 0; Indels

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93.18;
83.38;
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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|121 YRLALR 126
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A;Gene: Rv2776c
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                                                                                                                                                                                            C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C;Accession: A72367
R;Nelson, KE.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                                              A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316
A;Accession: A72367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Species: Synechocystis sp.
A; variety: PCC 6803
C; Date: 25-Apr.1997 #sequence_revision 25-Apr.1997 #text_change 21-Aug-1998
C; Accession: 574416
R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Tasuda DNA Res. 3, 109-136, 1996
A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                  periplasmic oligopeptide-binding protein - Thermotoga mari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S74416
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-185 < KANN
A; Residues: 1-185 < KANN
A; Cross-references: EMBL: D64001; GB: AB001339; NID: g1001102; PID: d1010985; PID: g1001190
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
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probable oxidoreductase - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: J-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 29-Sep-1999
C;Accession: G70882
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE001728; GB:AE000512; NID:g4981027; PID:g4981044; TIGR:TM0531 A;Experimental source: strain MSB8 C;Genetics: A;Gene: TM0531 A;Gene: TM0531
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1; Mismatches
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ilarity 83.3%;
Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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A;Molecule type: DNA
A;Residues: 1-579 <ARN>
                                             154 YRLAVR 159
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| 168 YRLAVR 173
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i Connor, R.; Davies, R.; Deviln, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Nature 393, 537-544, 1998
A; Authors: Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Oliver, S.; Osborne, J.; Qua, Tatlylor, R.; Whitehead, S.; Barrell, B.G.
A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A; Reference number: A70500; MUID:98295987
A; Accession: G70882
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-309 <COL>
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C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Jun-1998
C;Accession: B69127
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
;;Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A.Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes,
Smith, H.O.; Woese, C.R.; Venter, J.C.
A.Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
A;Reference number: A69250; MUID:98049343
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                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AL008967; GB:AL123456; NID:g3261491; PIDN:CAA15591.1; PID:e129
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable gcpE protein (gcpE) - syphilis spirochete
C; Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C; Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C; Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 17-Mar-1999
C; Accession: F1324
R; Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A; Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A; Reference number: A71250; MUID:98332770
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A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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A;Residues: 1-404 <COL>
A;Cross-references: GB:AE001221; GB:AE000520; NID:g3322720; PID:g3322731
A;Eross-reference: strain Nichols
C;Genetics:
A;Gene: TP0446
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Pred. No. 29;
1; Mismatches
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Pred. No. 22;
1; Mismatches
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Cipecies: Aeropyrum pernix
Cipecies: Aeropyrum pernix
Cipecies: Aeropyrum pernix
Cipecies: Aeropyrum pernix
Cipecies: Pacession: F72660
Rikawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Ta awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J. ATILIA: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero A; Reference number: A72450; MUID: 99310339
A; Reference number: A72450; MUID: 99310339
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-291 < KAW>A; Residues: 1-292 < KAW>A; Residues: 1-291 < KAW>A; Residues: 1-291 < KAW>A; Residues: 1-201 < KAWAB; Residues: 1-201 <
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C;Superfamily: fumarate reductase cytochrome b
                                                                                                                                                                                                                                       C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 11-Jun-1999
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 11-Jun-1999
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 11-Jun-1999
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKe son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, Mature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Accession: A64520; MUID:97394467
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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Pred. No. 33;
1; Mismatches
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Mismatches
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Pred. No.
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Best Local Similarity
Matches 5; Conserv
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188 YRLAIK 193
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188 YRLAIK 193
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         1 YRLAIR 6
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A;Variety: strain J99
G;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 11-Jun-1999
C;Accession: H71963
C;Accession: H71963
B;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71800; MUID:99120557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zool. Sci. 14, 785-789, 1997
A; Title: Molecular cloning of a molt-inhibiting hormone cDNA from the kuruma prawn Penae
A; Reference number: 217038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GB:AE001439; NID:g4154689; PIDN:AAD05763.1; PID:g415469
A; Accession: B69327
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-96 < KLE>
A; Residues: 1-96 < KLE>
A; Cross-references: GB: AE001062; GB: AE000782; NID: 92689385; PID: 92650002; TIGR: AF0618
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C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T10473
R;Ohira, T.; Watanabe, T.; Nagasawa, H.; Aida, K.
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C.Keywords: hormone; neuropeptide
F.1-28/Domain: signal sequence #status predicted <SIG>
F:29-105/Product: molt-inhibiting hormone #status predicted <MAT>
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A;Cross-references: EMBL:AB004652; NID:d1107174; PID:d1021266
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Pred. No. 14;
1; Mismatches
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13;
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;Superfamily: fumarate reductase cytochrome
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Pred. No.
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Pred. No.
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 5; Conserv
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A; Residues: 1-255 <ARN>
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51 YRLAIK 56
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2 YRLAMR 7
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C; Genetics:
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A;Gene: yqhS
C;Superfamily: catabolic 3-dehydroquinate dehydratase
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R.Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Broni, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997

A.; Authors: Foulger, D.; Fritz, C.; Fullta, M.; Fullta, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hopono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Ochlyama,
A.; Winters, P.; Widpat, A.; Yamamoto, H.; Yamane, K.; Yasamoto, K.; Yata, K.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Voshida, R
A.; Hitle: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Title: Cloning of a cDNA encoding the Tcp-1 (t complex polypeptide 1) homologue of Ara
A:Reference number: JN0448; MUID:93138412
                                                                                A:Molecule type: mRNA
A:Residues: 1-545 <MOR>
A:Cross-references: DDBJ:D11351; NID:g217870; PIDN:BAA01955.1; PID:d1002434; PID:g217871
C:Superfamily: molecular chaperone t-complex-type
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A;Experimental source: strain 168
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Chironomus thummi
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 29-Jan-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Bacillus subtilis
C;Date: 05-Dec_1997 #sequence_revision 05-Dec-1997 #text_change 22-Jun-1999
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R;Blinov, A.G.; Sobanov, Y.V.; Bogachev, S.S.; Donchenko, A.P.; Filippova Mol. Gen. Genet. 237, 412-420, 1993
A;Title: The Chironomus thummi genome contains a non-LTR retrotransposon. A;Reference number: S31174; MUID:93247556
A;Accession: S31175
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A;Residues: 1-883 <BLI>
A;Cross-references: GB:S59870; NID:g299960; PID:g299962
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Pred. No. 1.1e+02;
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Pred. No. 69;
                                                                                                                                                                                                                                                                                                                       1; Mismatches
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A; Accession: B69960
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Best Local Similarity 83.33
Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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A: Residues: 1-148 < KUN>
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| 803 YKLAIR 808
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characterization of the Rhodospirillum rubrum carb
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                                                                                                                                                                                                                                                                                                                                                  R; Kerby, R.L.; Hong, S.S.; Ensign, S.A.; Coppoc, L.J.; Ludden, P.W.; Roberts, G.P. J. Batteriol, 174, 2284-5294, 1992
A; Title: Genetic and physiological characterization of the Rhodospirillum rubrum ce A; Reference number: A42957; WuID:92355502
A; Cession: B42957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Superfamily: nrfC protein; ferredoxin 2[4Fe-4S] homology
C; Keywords: 4Fe-4S; iron-sulfur protein; metalloprotein
F:10-85/Domain: ferredoxin 2[4Fe-4S] homology *FERI>
F:89-162/Domain: ferredoxin 2[4Fe-4S] homology *FERI>
F:17, 20, 23, 77/Binding site: 4Fe-4S cluster (Cys) (covalent) *status predicted
F:27, 65, 68, 73/Rinding site: 4Fe-4S cluster (Cys) (covalent) *status predicted
F:96,99;102,154/Binding site: 4Fe-4S cluster (Cys) (covalent) *status predicted
F:96,99;102,154/Binding site: 4Fe-4S cluster (Cys) (covalent) *status predicted
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                                                                                                                                                                                                                                                                                                                 Species: Rhodospirillum rubrum
.Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 11-Jun-1999
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Length 148;
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44;
DB
35;
                                                      2; Mismatches
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Pred. No.
Score 25;
Pred. No.
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86.2%;
66.7%;
Query Match 86.2
Best Local Similarity 66.7
Matches 4; Conservative
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Matches 4; Conserv
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                                                                                                                                                    132 YKLAVR 137
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Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
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412 YRLAIR 417
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bacillus su
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canis famil
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schizosacch
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P95649 rhodobacter
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P552677
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                          Compugen Ltd.
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           GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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PSPA_CANFA
PSPA_MOUSE
PSPA_PIG
RL5_DCNSA
RL5_SCHPO
RL5B_SCHPO
ARCC_ECOLI
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PABB_LACLA
MIH_PENJP
FRDC_HELPY
TCPA_ARATH
TCPA_ARATH
FLIZ_ECOLI
COOF_RHORU
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COAT_CTV36
FRDC_WOLSU
FRE7_YEAST
ARO1_EMENI
YF65_SYNY3
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RM25_YEAST
IPT2_AGRT7
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OMPP_ECOLI
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    protein search, using sw model

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RL5_NEUCR
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Gapop 10.0 , Gapext 0.5
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Listing first 45
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29
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Match Length DB
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length: 1000000
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                                          streptomyce
hemigrapsus
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schizosacch
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mycobacter1
    drosophila
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STRAIN-K12 / MG1655;
MEDLINE; 97426617.
MEDLINE; 97426617.
MELATYRER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V., RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F., GREGN J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J., "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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0
P06002
P28678
P27903
Q25158
P52851
P46387
Q50790
Q00813
Q009718
Q097753
Q16881
                                                                                                                                                                                                                                                                                                                                             YPHG_ECOLI

ID YPHG_ECOLI

ID YPHG_ECOLI STANDARD; PRT; 1124 AA.

AC P7658;

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DF HYPOTHETICAL 127.3 KD PROTEIN IN CSIE-GLYA INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match

100.0%; Score 29; DB 1; Length 1124;
Best Local Similarity. 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels
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Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE000341; AAC75602.1; -.
ECGENE; EG13468; yphG.
Hypothetical protein.
SEQUENCE 1124 AA; 127284 WW; 0A06B4C6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
CBBY PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           230 AA.
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                 OPSI_DROPS
DP3B_STRCO
OPSZ_HENSA
DP3B_MYCLE
DP3B_MYCLU
TYSQ_MYCTU
TYSQ_MYCTU
TYSQ_MYCTU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AREDINE: 94014976.
ARHIN F.F., VINING L.C.;
"Cloning, nucleotide sequence and expression in Streptomyces lividans and Escherichia coli of pabB from Lactococcus lactis subsp. lactis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCDO 496.";
J. Gen. Microbiol. 139:1785-1793(1993).
-!- FUNCTION: CATALYZES THE BIOSYNTHESIS OF 4-AMINO-4-DEOXYCHORISMATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ADC) FROM CHORISMATE AND GLUTAMINE.

-!- PATHWAY: FOLATE BIOSYNTHESIS PATHWAY. FIRST STEP IN THE BIOSYNTHESIS OF P-AMINOBRNZOATE (PABA).

-!- SUBUNIT: CONSISTS OF TWO NONIDENTICAL CHAINS: COMPONENT I CATALYZES THE FORMATION OF ADC. BY BINDING CHORISMATE AND AMMONIA; COMPONENT II PROVIDES THE GLUTAMINE AMIDOTRANSFERASE ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-CT-1996 (Rel. 34, Last annotation update)
PARA-AMINOBENZOATE SYNTHASE COMPONENT I (EC 4.1.3.-) (ADC SYNTHASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                               ö
                                        STRAIN=HR;
MEDLINE; 97158658.
GIBSON J.L., TABLIA F.R.;
"Analysis of the cbbxxz operon in Rhodobacter sphaeroides.";
                                                                                                                                                                                                                                                                                                                   Score 27; DB 1; Length 230;
Pred. No. 8.9;
                                                                                            J. Bacteriol. 179:663-669[1997].
-!- SIMILARITY: BELONGS TO THE CBBY/CBBZ/GPH/YIEH FAMILY
                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                               EMBL: U67781; AAC44828.1; -.
PFAM; PF00702; Hydrolase; 1.
SEQUENCE 230 AA; 25118 MW; 54A55A59 CRC32;
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PFAM; PF00425; chorismate_Dind; 1.
Lyase; Folate biosynthesis.
SEQUENCE 470 AA; 50970 WW; 41AC304B CRC32;
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                                                                                                                                                                                                                                                                                                                     93.1%;
83.3%;
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Best Local Similarity 83.3
Matches 5; Conservative
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                           SEQUENCE FROM N.A.
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Rhodobacter
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P27629;
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YANG W.-J., A IDDA K., TERAUCHI A., SONOBE H., NAGASAWA H.;

YANG W.-J., A IDDA K., TERAUCHI A., SONOBE H., NAGASAWA H.;

YANG W.-J., A IDDA K., TERAUCHI A., SONOBE H., NAGASAWA H.;

*Amino acid sequence of a peptide with molt-inhibiting activity from the kuruma prawn Penaeus Japonicus.";

Peptides 17:197-202(1996).

-I TISTORIAN TO THE TY-ORGANS WHERE MOLTING HORMONE (ECDYSTEROID) IS SECRETED. A MOLTING CYCLE IS INITIATED WHEN MIH SECRETION DIMINISHES OR STOPS. HAS LITTLE OR NO HYPERGLYCEMIC ACTIVITY.

-I TISSUE SPECIFICITY: PRODUCED BY THE MEDULIA TERMINALIS X-ORGAN IN THE EYESTALKS AND TRANSPORTED TO THE SINUS GLAND WHERE IT IS STORED AND RELEASED.

-I SIMILARITY: BELONGS TO THE ARTHROPOD CHH/MIH/GIH/VIH FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISOURDELLINE: 98112189.

OHIRA T., WATANABE T., NAGASAWA H., AIDA K.;

OHIRA T., WATANABE T., NAGASAWA H., AIDA K.;

"Molecular cloning of a molt-inhibiting hormone cDNA from the kuruma
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Penaeus japonicus (Kuruma prawn).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeidae;
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                                                                                                                                                                                                                                                                                                   MIH_PENJP STANDARD; PRT; 105 AA.
P55847; 002379;
01-NOV-1997 (Rel. 35, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
MOLT-INHIBITING HORMONE PRECURSOR (MIH) (PEJ-SGP-IV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLT-INHIBITING HORMONE.
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Score 27; DB 1;
Pred. No. 19;
1; Mismatches
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Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS01250; CHH_MIH_GIH; 1.
PFAM; PF01147; Crust_neurohorm; 1.
Signal; Neuropeptide; Hormone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prawn Penaeus japonicus.";
Zool. Sci. 14:785-789(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL: AB004652: BAA20432.1;
                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Conservative
                      Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                 411 YRIAIR 416
                                                                                                              1 YRLAIR 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HORMONES.
        Query Match
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TCPA_ARATH
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                                                                                                                                                                                                                                                                                                   TOMB J.-F., WHITE O., KERLAVAGE A.R., CLAYTON R.A., SUTTON G.G., FLEISCHMANN R.D., KETCHUM K.A., KLENK H.-P., GILL S., DOUGHERTY B.A., NELSON K., QUACKENBUSH J., ZHOU L., KIRKNESS E.F., PETERSON S., LOFTUS B., RICHARDSON R., KHALAK H.G., GLODEK A., MCKENNEY K., FITZGERALD L.M., LEE N., ADAMS M.D., HICKEY E.K., BERG D.E., GOCAYNE J.D., UTTERBACK T.R., PETERSON J.D., KELLEY J.M., COTTON M.D., WEIDMAN J.M., FUJII C., BOWMAN C., WATTHEY L., WALLIN E., VENTER J.C., SMITH H.O., FRASER C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 388:539-547(1997).
-!- FUNCTION: DI-HEME CYTOCHROME OF THE FUMARATE REDUCTASE COMPLEX (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY).
SUBUNIT: FUNDAMENTE DEHYDROGENASE FORMS PART OF AN ENZYME COMPLEX CONTAINING THREE SUBUNITS: A FLAVOPROTEIN, AN IRON-SULFUR, AND CYTOCHROME B-556 (BY SIMILARITY).
SIMILARITY: TO CYTOCHROME B-558 FROM B.SUBTILIS SUCCINATE DEHYDROGENASE.
                                                                                                                                                              Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                 "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane; Electron transport; Heme.
                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-UA802 / NCTC 11639;
GE 2., JIANG Q., KALISIAK M.S., TAYLOR D.E.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L -> V (IN REF. 1).

L -> V (IN REF. 1).

V -> A (IN REF. 1).

E -> D (IN REF. 1).

AECA224C CRC32;
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HEME (POTENTIAL).
HEME (POTENTIAL).
HEME (POTENTIAL).
HEME (POTENTIAL).
I -> V (IN REF. 1).
                                                                                                                 01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
FUMARATE REDUCTASE CYTOCHROME B SUBUNIT.
                                                                              255 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U78101; AAC46063.1; -.
EMBL; AE000539; AAD07260.1; -.
                                                                                                    (Rel. 35, Created)
(Rel. 35, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28886 MW;
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=26695 / ATCC 700392;
MEDLINE; 97394467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tricarboxylic acid cycle;
                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              255 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY)
                                                                                                                                                   FRDC OR HP0193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HP0193;
                                                                                                                                                                                      Helicobacter.
            2 YRLAMR
1 YRLAIR
                                                                                                    01-NOV-1997
                                                                                                                01-NOV-1997
01-NOV-1997
                                                                            FRDC_HELPY
O06912;
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TRANSMEM
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                                                                  FRDC_HELPY
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-!- FUNCTION: MOLECULAR CHAPERONE; ASSIST THE FOLDING OF PROTEINS UPON ATP HYDROLYSIS. KNOWN TO PLAY A ROLE, IN VITRO, IN THE FOLDING OF ACTIN AND TUBULIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
Wakryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermarophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -! SUBUNIT: HETERO-OLIGOMERIC COMPLEX OF ABOUT 850 TO 900 KD THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
MORI M., KUNO N., MURATA K., KUBOTA H., FURUYA M., MATSUSHIRO A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning of a cDNA encoding the Tcp-1 (t complex polypeptide 1) homologue of Arabidopsis thaliana."; Gene 122:381-382(1992).
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                                                                                                                                                                                                                                                                                                                                                        01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FORMS TWO STACKED RINGS, 12 TO 16 NM IN DIAMETER.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- SIMILARITY: BELONGS TO THE TCP-1 CHAPERONIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE; 93138412.
MORI M., MURATA K., KUBOTA H., YAMAMOTO A., MATSUSHIRO A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 26; DB 1; Length 545;
Pred. No. 40;
L; Mismatches 0; Indels
                     Length 255;
                                                                         Indels
                                                                         ö
                Score 26; DB 1;
Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P48424; 1ASX.
PROSITE; PS00750; TCP1_1; 1.
PROSITE; PS00751; TCP1_2; 1.
PROSITE; PS00995; TCP1_3; 1.
PRAM; PF00118; Cpn60_TCP1; 1.
Chaperone; AIP-binding; Multigene family.
SEQUENCE 545 AA; 59229 MW; 0E52A94B CRC32;
                                                                                                                                                                                                                                                                                                          545 AA
                                                                      Mismatches
89.7%; Sc.
83.3%; Pred
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llarity 83.3%;
Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D11351; BAA01955.1; -. EMBL; D11352; BAA21772.1; -.
                                                                         Conservative
                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JN0448.
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Best Local Similarity
Matches 5; Conserv
                  Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                     188 YRLAIK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||||:|
124 YRLAMR 129
                                                                                                                       1 YRLAIR 6
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                                                                                                                                                                                                                                                                                                    TCPA_ARATH
P28769;
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MEDLINE; 97426617
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P31894;
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COOF_RHORU
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                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the between the Swiss Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                       STRAIN-168 / JH642;
KOBAYASHI Y., MIZUNO M., MASUDA S., TAKEMARU K., HOSONO S.,
SATO T., TAKEUCHI M.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: 3-DEHYDROQUINATE = 3-DEHYDROSHIKIMATE + H(2)O.
-!- PATHWAY: SECOND STEP OF THE QUINIC ACID CATABOLIC PATHWAY.
-!- SIMILARITY: BELONGS TO THE TYPE-II 3-DEHYDROQUINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                01-OCT-1996 (Rel. 34, Created)
1-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
PUTATIVE CATABOLIC 3-DEHYDROQUINATE DEHYDRATASE (EC 4.2.1.10) (3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86.2%; Score 25; DB 1; Length 148; 66.7%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                            Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                  l protein; Quinate metabolism; Lyase.
148 AA; 16431 MW; B2DOF289 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLIZ_ECOLI STANDARD; PRT; 183 AA. P52627; P76317; 01-0c7-1996 (Rel. 34, Created) 01-0c7-1996 (Rel. 34, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                   SUBTILIST; BG11707; YQHS.
PROSITE; PS01029; DERHYDROUINASE_II; 1.
PRAM; PF01220; DHQUINASE_II; 1.
Hypothetical protein; Quinate metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-RP437;
MEDLINE: 96125225.
MYTELKA D.S., CHAMBERLIN M.J.;
"Escharichia coli fliazy operon.";
J. Bacteriol. 178:24-34(1996).
                                                                                                                                                                                                                                                                                                                                                                            EMBL; D84432; BAA12556.1; -. EMBL; Z99116; CAB14378.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                Bacillus subtilis
                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                             DEHYDROQUINASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 YKLAVR 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FLIZ PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia.
                                          3DHO_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                              3DHQ_BACSU
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BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V., RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F., GREDOR J., DAVIS N.W., KIRRPATRICK H.A., GOEDEN M.A., ROSE D.J., MAU B., SHAO Y.; "The complete genome sequence of Escherichia coli K-12."; science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=K12;
MEDLINE; 96060842.
LIU X, MATSUMURA P.;
"An alternative signa factor controls transcription of flagellar class-III operons in Escherichia coli: gene sequence, overproduction, purification and characterization.";
Gene 164:81-84(1995).
-i- FUNCTION: MAY REGULATE SIGMA FACTOR ACTIVITY.
                                                                                                                                                                                                                                                                                                                        ITOH T., AIBA H., BABA T., FUJITA K., HAVASHI K., INADA T.,
IISONO K., KASAI H., KIMURA S., KITAKANA M., KITAGANA M.,
MAKINO K., MIKI T., MIZOBUCHI K., MORI H., MORI T., MOTOMURA K.,
NAKADE S., NAKANURA Y., NASHIMOTO H., NISHIO Y., OSHIMA T.,
SAITO N., SAMPEI G., SEKI Y., SIVASUNDARAM S., TAGAMI H.,
TAKEDA J., TARKENOTO K., WADA C., YANAMOTO Y., HORIUCHI T.,
"A 460-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 40.1-50.0 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; alpha subdivision; Rhodospirillaceae;
Rhodospirillum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86.2%; Score 25; DB 1; Length 183; 66.7%; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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01-JUL-1993 (Rel. 26, Last sequence update)
01-NOV-1997 (Rel. 25, Last annotation update)
IRON-SULFUR PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 AA
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STRAIN-URL;
MEDLINE; 92355502.
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EMBL; AE000285; AAC74988.1; ALT_INIT.
EMBL; D90832; CAB21661.1; --
EMBL; L36677; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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SEQUENCE 183 AA; 21
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                             MEDLINE; 97251358.
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SEQUENCE FROM N.A.
MEDITINE; 94160579.
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SEQUENCE FROM N.A.
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Best Local Similarity
Matches 4; Conserv
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SEQUENCE 23
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P17413;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Citrus tristeza virus (isolate T36) (CTV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Closteroviridae;
                                   "Genetic and physiological characterization of the Rhodospirillum rubrum carbon momoxided dehydrogenage system.";
J. Bacteriol. 174:5284-5294(1992).
I. PONCTION: CODH MAY OXYDATE CARBON MONOXYDE COUPLED, VIA COOF, TO REDUCTION OF HYDROGEN CATTON BY AN HYDROGENASE (POSSIBLA COOH).
COOF IS REQUIRED IN STOICHIOMETRIC AMOUNTS IN VITRO FOR ANCHORING CODH TO THE MEMBRANE AS WELL AS FOR CONVEYING THE ELECTRONS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEKIYA M.E., LAWRENCE S.D., MCCAFFERY M., CLINE K.;
"Molecular cloning and nucleotide sequencing of the coat protein gene
of citrus tristeza virus."
J. Gen. Virol. 72:1013-1013-1091).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
   HONG S.S., ENSIGN S.A., COPPOC L.J., LUDDEN P.W.,
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24:
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Last annotation update)
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IRON SULFUR I
IRON SULFUR 2
IRON SULFUR 2
IRON SULFUR 2
IRON SULFUR 3
IRON SULFUR 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Iron-sulfur; Electron transport; 4Fe-4S.
METAL 17 17 IRON-SULFUR 1
METAL 20 20 IRON-SULFUR 1
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MEDLINE; 91237334.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; B42957; B42957.
HSSP: P00208; JEGU.
PROSITE: PS00108; 4F64S_FERREDOXIN; 1.
PFAM: PF00037; fer4; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last seq
01-FEB-1996 (Rel. 33, Last ann
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66.7%;
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                                                                                                                                                                           THE HYDROGENASE.
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Best Local Similarity
Matches 4; Conserv
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| 167 YRIALR 172
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ID COAT_CTV36
%C Q00686;
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SEQUENCE
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PAPPU H.R., KARASEV A.V., ANDERSON E.J., PAPPU S.S., HILF M.E., FEBRES V., ECKLOFF R.M.G., MCCAFFERY M., BOYKO V., GOWDA S., DOLJA V.V., KOONIN E.V.; "Nucleotide sequence and organization of eight 3' open reading frames of the citrus tristera closterovirus genome.";
                                                                                                                                                                                                      Virology 199:35-46(1994).
-!- PIM: CONSISTS OF AT LEAST TWO SIZE VARIANTS, CP1 AND CP2, WHICH RESULT OF POST-TRANSLATIONAL PROTECLYSIS AT SITES APPROXIMATIVELY 12 TO 15 AND 26 AA FROM THE N-TERMINOS RESPECTIVELY.
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Submitted (JUL-1997) to the EMBL/Genbank/DDBJ databases.
-!- FUNCTION: DI-HEME CYTOCHROME OF THE FUMARATE REDUCTASE COMPLEX.
-!- SUBUNT: PARE OF AN ENZYME COMPLEX CONTAINING THREE SUBUNTS:
A FLAVOPROTEIN, AN IRON-SULFUR PROTEIN AND A CYTOCHROME B.
-!- SIMILARITY: TO CYTOCHROME B-558 FROM B.SUBFILIS SUCCINATE
DEHYDROGENASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wolinella succinogenes.
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
Wolinella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.2%; Score 25; DB 1; Length 223; 66.7%; Pred. No. 28;
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01-AUG-1990 (Rel. 15, Last sequence update)
01-5UL-1998 (Rel. 36, Last annotation update)
FUMARAIE REDUCTASE CYTOCHROME B SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       256 AA
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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE; 90355847.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-S28BC / FY1679;
MEDLINE; 96132030.
ACSAMANOR A., CASAS C., HERRERO E., GAMO F.J.,
LAFUENTE M.J., GANCEDO C., ARINO J.;
LAFUENTE M.J., GANCEDO C., ARINO J.;
PARA Sequence analysis of a 13 kbp fragment of the left arm of yeast chromosome XV containing seven new open reading frames.";
Peast 11:1281-1288(1995).
-!-COFACTOR: FAD (FROBABLE).
                                                                                                                                                                                                                                                Gaps
EMBL; X51509; CAA35874.1; -.
EMBL; AJ000662; CAA04213.1; -.
PIR; S10164; S10164.
Tricarboxylic acid cycle; Transmembrane; Electron transport; Heme.
                                                                                                                                                                                                                                                                                                                                                                                                                                            FRE7 OR YOL152W.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungi: Ascomycota: Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-i- SIMILARITY: BELONGS TO THE FRE / CYBB FAMILY.
                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane; Iron transport; FAD; NAD
                                                                                                                                                                                                                      Length 256;
                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
FERRIC REDUCTASE TRANSMEMBRANE COMPONENT 7 PRECURSOR.
                                                                                                                                                                                                                      DB 1;
32;
                                                                                                                           HEME (POTENTIAL).
HEME (POTENTIAL).
HEME (POTENTIAL).
HEME (POTENTIAL).
                                                                                                                                                                                C3AB8928 CRC32
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POTENTIAL.
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Pred. No. 32;
2; Mismatches
                                                                         POTENTIAL.
POTENTIAL.
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                                                                                                                  POTENTIAL
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                                                                                                                                                                                29723 MW;
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66.7%;
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                                                                                                                                                                                                                                                Conservative
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128
188
215
225
286
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Electron transport;
                                                                                                                                                                                256 AA;
                                                                                                                                                                                                                      Query Match
Best Local Similarity
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108
168
195
238
266
                                                                                                                                                                                                                                                                                                   188 YRLAVK 193
                                                                                                                                                                                                                                                                          1 YRLAIR 6
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Q12333;
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BINDING
SEQUENCE
                                                                            TRANSMEM
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FRE7_YEAST
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15-DEC-1999 (Rel. 39, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
15-DEC-1999 (Rel. 39, Last annotation update)
PENTARONCTIONAL ARON POLYPEPTIDE (INCLUDES: 3-DEHYDROQUINATE SYNTHASE
(EC 4.6.1.3): 3-DEHYDROQUINATE DEHYDROGENASE (EC 4.2.1.10)
(3-DEHYDROQUINASE); SHIKIMATE 5-DEHYDROGENASE (EC 11.1.1.25); SHIKIMATE
KINASE (EC 2.7.1.71); EPSP SYNTHASE (EC 2.5.1.19)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: ADP + SHIKIMATE - ADP + SHIKIMATE 3-PHOSPHATE. CATALYTIC ACTIVITY: PHOSPHOENOLEYRUATE + 3-PHOSPHOSHIKIMATE - ORTHOPHOSPHATE + O(5)-(1-CRBOXYVINIXL)-3-PHOSPHOSHIKIMATE - PATHWAX: SECOND TO SIXTH STEP IN THE BIOSYNTHESIS FROM CHORISMATE OF THE AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAX)
                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=R153;
MEDLINE: 86176723.
CHARLES I.G., REYLE J.W., BRAMMAR W.J., SMITH M., HAWKINS A.R.;
"The isolation and nucleotide sequence of the complex AROM locus of Aspergillus nidulans.";
                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHARLES I.G., KEYTE J.W., BRAMMAR W.J., HAWKINS A.R.; "Nucleotide sequence encoding the biosynthetic dehydroquinase function of the penta-functional arom locus of Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                       Emericella nidulans (Aspergillus nidulans).
Eukaryota; Fungi; Ascomycota; Euascomycetes;
Eurotiales; Trichocomaceae; Emericella.
                                                                                                       Length 629;
                                                                                                                                    Indels
                                                                                                       DB 1;
84;
                                          POTENTIAL.
AC37EFC2 CRC32;
                                                                                                                                                                                                                                                                         PRT; 1586 AA.
                                                                                                                                    2; Mismatches
                                                                                                       Score 25;
Pred. No. 8
              POTENTIAL. POTENTIAL.
   POTENTIAL
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313 PC
442 PC
330 PC
541 PC
71996 MW;
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                                                                                                     86.2%;
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                                          541 :
629 AA;
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Job time: 3778 sec
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Best Local Similarity
Matches 5; Conservat
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YG2E_YEAST
ID YG2E_YEAST
AC P53247;
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KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
MIYAJIMA N., HIROSAMA M., SUGIURA M., SASAMOTO S., KIMURA T.,
MIYAJIMA N., HIROSAMA M., BUGIURA M., NARAZAKI N., NARUO K.,
OKUMURA S., SHIMPO S., TAKEUCHI C., WADA T., WATANABE A.,
YAMADA M., YASUDA M., TABATA S.;
Sequence analysis of the genome of the unicellular cyanobacterium
Synechocystis sp. strain PCC6803. II. Sequence determination of the
entire genome and assignment of potential protein-coding regions.";
DNA Res. 3:109-136(1996).

-I - SIMILARITY: BELONGS TO THE HESB/XADR/YFHF FAMILY.
                                                                                                                                                                                                 PFAM; PF01202; SKI; 1.
PFAM; PF01488; DHquinate_I; 1.
PFAM; PF01488; Shikimate_DH; 1.
Aromatic amino acid blosynthesis; Multifunctional enzyme;
Aromatic amino acid blosynthesis; Multifunctional enzyme;
Aromatic I, yase; Transferase; Kinase; NADP; ATP-binding.
384 3-DEHYDROQUINATE SYNTHASE.
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BY SIMILARITY.
BY SIMILARITY.
FORMS A SCHIFF-BASE INTERMEDIATE
(BY SIMILARITY).
W; 279EFF15 CRC32;
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Pred. No. 2.2e+02;
0; Mismatches 1; Indels
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Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                              EPSP SYNTHASE.
SHIKIMATE KINASE.
3-DEHYDROQUINASE.
SHIKIMATE DEHYDROGENASE.
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PFAM; PF01521; HesB-like; 1.
PYPOCTHERIAL PIOCEALD.
SEQUENCE 113 AA; 12520 MW; 927AED62 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 12.5 KD PROTEIN SLR1565.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 AA
                                                                   PROSITE; PSO0104; EPSP_SYNTHASE_1; 1.
PROSITE; PSO0885; EPSP_SYNTHASE_2; 1.
PROSITE; PS01028; DEHYDROQUINASE_1; 1.
PROSITE; PS01128; SHIKIMATE_KINASE; 1.
PFAM; PF00275; EPSP_SYNTASE; 1.
PFAM; PF01202; SKI; 1.
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  CAA28836.1;
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Matches 5; Conservative
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                       PIR; A24962; BVASA1.
PIR; A24042; A24042.
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|1141 YRLAFR 1146
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P74596;
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NP_BIND
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ACT_SITE
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YF65_SYNY3
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Gaps

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                                                       ö
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
                                                       ö
                                                                                                                                                                                                                                                                                                                               01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-1996 (Rel. 34, Last annotation update)
HYPOTHETICAL 14.1 KD PROTEIN IN UPF3-SMD1 INTERGENIC REGION.
  Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
WEDLER H., SCHARFE M., WEDLER E., WAMBUTT R.;
Submitted (WAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z72858; CAAy/u/J.,
Hypothatical protein; Transmembrane.

1 21 POTENTIAL.
TRANSMEM 103 123 POTENTIAL.
TRANSMEM 103 123 POTENTIAL.
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100.0%; Pred. No. 27;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                       123 AA
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Query Match
Best Local Similarity 66.7
Matches 4; Conservative
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                                                                                                                                                       26 FRLAVR 31
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"Sequence analysis of 43A9 fosmid clone of Zymomonas mobilis ZM4.";
"Sequence analysis of the EMBL/GenBank/DDBJ databases.
-1- CATALYTIC ACTIVITY: 5,10-METHYLENETERTRAHYDROFOLATE + DUMP -
DIHYDROFOLATE + DTMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zymomonas mobilis.
Bacteria; Proteobacteria; alpha subdivision; Zymomonas group;
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-!- SUBUNIT: HOWDIMER (BY SIMILARITY).
EMBL: AF10.2543; AAD19406.1; ---
HSSP; P00470; IAN5.
HSSP; P00091; THYMIDYLATE_SYNTHASE; 1.
Transferase; Methyltransferase; Nucleotide biosynthesis.
ACT_SITE 143 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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100.0%; Pred. No. 14;
Live 0; Mismatches
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01-MAY-1999 (TYEMBLEEL 1 1
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THYMIDYLATE SYNTHETASE.
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Best Local Similarity
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    56
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21 YRLAIR
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    Zymomonas.
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094501 schizosacch
P72467 streptomyce
045803 caenorhabdi
P84475 herpes simp
Q9x201 thermotoga
Q55192 synchocyst
Q5248 streptomyce
085467 mycobacteri
0893460 treponema p
001914 caenorhabdi
Q9933 gailus gall
Q29637 archaeoglob
Q25637 archaeoglob
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Q07995 chironomus
O11376 molluscum c
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caenorhabd1
                                                                                                                                                                 Search time 209.03 Seconds (without alignments)
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                           GenCore version
Copyright (c) 1993 - 2000
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Q07995
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Gapop 10.0 , Gapext 0.5
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sp_invertebrate:*
sp_mammal:*
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MEDLINE: 87111457.
MCGEOCH D.J., MOSS H.W., MCNAB D., FRAME M.C.;
"DNA sequence and genetic content of the Hindill 1 region in the short unique component of the herpes simplex virus type 2 genome: identification of the gene encoding glycoprotein G, and evolutionary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WILLSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONTFIELD J. BURTON J., CONNELL M., COPERY T., COOPER J., COULSON A.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTHING J., LLOYD C., MCMURRAY A., MONTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., SOOPRA A., SAUNDERS D., SHOWNKEEN R.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WAITENSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
LLOYD C., WILKINSON J.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
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Viruses; dSDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
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Last annotation update)
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Pred. No. 34;
1; Mismatches
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83.3%;
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01-MAY-1997 (TrEMBLEEL.
01-NOV-1998 (TrEMBLEEL.
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Best Local Similarity
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LABESEE G., VIDAL-GROS A., CHOMILIER J., GAUDRY M., MORNON J.;

Structural comparisons lead to the definition of a new superfamily of
NAD(P)(H) accepting oxidoreductases: the single-domain
reductases/epimerases/dehydrogenases (the 'RED' family).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   using an ampC beta-lactamase promoters in Streptomyces lividans by Mol. Gen. Genet. 210:23-32(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Amplification of a Streptomyces lividans 4.3 kb DNA element causes overproduction of a novel hypha- and vesicle-associated protein."; Microbiology 143:1243-1252(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
12-COMPLEX PROTEIN 1, ALPHA SUBUNIT HOMOLOG, CHAPERONIN FAMILY.
SPBC12D12.03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 29; DB 3; Length 556; llarity 100.0%; Pred. No. 31; Conservative 0; Mismatches 0; Indels
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Pred. No. 33;
                                                                                                                                                                                                                                                                                                               STRAIN-972H-;
STRAIN-972H-;
STUDE M. RAJANDREAM M.A., BARRELL B.G., XIANG Z., AVES S;
Submitted (JAW-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL035085; CAA22677.1;
HSSP; P48425; 1A6E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01 FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
                                                                                                                                           Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota: Archiascomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE: PS00750; TCPL_1; 1.
PROSITE; PS00751; TCPL_2; 1.
PROSITE; PS00995; TCPL_3; 1.
SEQUENCE 556 AA; 60047 MW; 27F285FA CRC32;
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MEDLINE; 88121703.
FORSMAN M., JAURIN B.;
Chromogenic identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z70724; CAA94732.1; -. SEQUENCE 343 AA; 36846 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             304:95-99(1994).
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83.38;
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                                                                                                                                                                                                                                    Schizosaccharomyces
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
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MEDLINE; 97286540.
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01-FEB-1997
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RESULT P72467

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Length 350; Indels.

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MEDLINE; 92356101.
BARNETT B.C., DOLAN A., TELFORD E.A.R., DAVISON A.J., MCGEOCH D.J.;
"A novel herpes simplex virus gene (UL49A) encodes a putative membrane protein with counterparts in other herpesviruses.";
J. Gen. Virol. 73:2167-2171(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NELSON K.E., CLAYTON R.A., GILL S.R., GWINN M.L., DODSON R.J.,
HAFT D.H., HICKEY E.K., PETERSON J.D., NELSON W.C., KETCHUM K.A.,
MCDONALD L., UTTERBACK T.R., MALEK J.A., LINHER K.D., GARRETT M.M.,
STEWART A.M., COTTON M.D., PRATT M.S., PHILLIPS C.A., RICHARDSON D.,
HEIDELBERG J., SUTTON G.G., FLEISCHMANN R.D., WHITE O., SALZBERG S.L.,
SMITH H.O., VENTER J.C., FRASER C.M.,
"Evidence for lateral gene transfer between Archaea and bacteria from
genome sequence of Thermotoga maritima.";
                                                  MEDLINE, 20278430.
MEDLINE, FORWICK M.;
EVERETT R., FENWICK M.;
"Comparative DNA sequence analysis of the host shutoff genes of different strains of herpes simplex virus: type 2 strain HG52 encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                           MEDLINE; 92113549.

MCGEOCH D.J., CUNNINGHAM C., MCLNIYRE G., DOLAN A.;

"Comparative sequence analysis of the long repeat regions and adjoining parts of the long unique regions in the genomes of herpes simplex viruses types 1 and 2.";

J. Gen. Virol. 72:3057-3075(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9W201;
01-NOV-1999 (TTEMBLrel. 12, Created)
01-NOV-1999 (TTEMBLrel. 12, Last sequence update)
01-NOV-1999 (TTEMBLrel. 12, Last annotation update)
01:GOPEPTIDE ABC TRANSPORTER, PERIPLASMIC OLIGOPEPTIDE-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
NELSON K.E., CLAYTON R.A., GILL S.R., GWINN M.L., DODSON R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                               Length 545;
                                                                                                                                                                                                                                                                                                                                                                     Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; 286099; CAB06715.1; -.
SEQUENCE 545 Aa; 59309 MW; 99AB4CDD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                     truncated UL41 product.";
Gen. Virol. 71:1387-1390(1990).
comparisons.";
J. Gen. Virol. 68:19-38(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                96.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 399:323-329(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 96.6
Best Local Similarity 83.3
Matches 5; Conservative
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299 YRLAVR 304
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HAFT D.H., HICKEY E.K., PETERSON J.D., NELSON W.C., KETCHUM K.A., MCDONALD L., UTTERBACK T.R., MALEK J.A., LINHER K.D., GARRETT M.M., STEWART A.M., COTTON M.D., PRATT M.S., PHILLIPS C.A., RICHARDSON D., SHENBERG J., SUTTON G.G., FLEISCHWANN R.D., WHITE O., SALZBERG S.L., SUBTER J.C., FRASER C.M.; SWITH H.O., VENTER J.C., FRASER C.M.; SALZBERG S.L., ERBL, GENBL, RAD35516.1; - ERBL, REO1128; ARD35516.1; - SEGUENCE 579 AA; 66508 MW; BF5C4AB3 CRC32;
                                                                                                                                                                                                                                                                                                  Gaps
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KANEKO I., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y., MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T., HOSOUCHI I., MATSUNO A., MURAKI A., NAKAZAKI N., NAKUO K., OKUMURA SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M., TABATA S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-PCC6803;
MEDILNE; 96127529.
MEDILNE; 96127529.
SUGIURA M., TANARA A., SATO S., KOTANI H., SAZUKA T., MIYAJIMA N., SUGIURA M., TABATA S.;
SUGIURA M., TABATA S.;
Suguence analysis of the genome of the unicellular cyanobacterium "Sequence analysis of strain PCC6803. I. Sequence features in the 1 MD region from map positions 64% to 92% of the genome.";
DNA Res. 2:153-166(1995).
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                                                                                                                                                                                                                                             Length 579;
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Bacteria; Cyanobacteria; Chroococcales; Synechocystis
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0
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Pred. No. 57;
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Pred. No. 31;
1; Mismatches
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83.3%;
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055192;
01-NOV-1996 (TIEMBLIEL).
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Submitted (AUG-1995)
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Best Local Similarity
Matches 5; Conservat
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                                                                                                                                                                                                                                                                                                                                                                                           168 YRLAVR 173
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SEQUENCE FROM N.A. STRAIN-H37RV;
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|65 YRIAIR 70
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MEDLINE; 99051446.
ICHINOSE K., BEDFORD D.J., TORNUS D., BECHTHOLD A., BIBB M.J.,
REVILL W.P., FLOSS H.G., HOPWOOD D.A.;
"The granaticin biosynthetic gene cluster of Streptomyces
violaceoruber Tu22: sequence analysis and expression in a heterologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Structure and deduced function of the granaticin-producing polyketide synthase gene cluster of Streptomyces violaceoruber Tu22."; EMBO J. 8:2717-2725(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-H37RV;
MEDLINE; 9829597.
COLE S.T., BROSCH R., PARKHILL J., GARNIER T., CHURCHER C., HARRIS D., GONDON S.V., EIGLMEIER K., GAS S., BARRY III C.E., TEKAIA F.,
BADCOCK K., BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R.,
BADCOCK K., BASHAM D., FELTWELL T., GENTILES S., HAMLIN N., HOLROYD S.,
HORNESY T., JAGELS K., KROGH A., MCLEAN J., MOULE S., MURPHY I.,
OLIVER S., OSBORNE J., QUAIL M.A., RAJANDREAM M.A., ROGERS J.,
RUTTER S., SEEGER K., SKELTON S., SQUARES S., SQARES R., SULSTON J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BECHTHOLD A., SOHNG J.K., SMITH T.M., CHU X., FLOSS H.G.; "Identification of Streptomyces violaceoruber Tu22 genes involved in the biosynthesis of granaticin."; MMOl. Gen. Genet. 248:610-620(1995).
EMBL: AJ011500; CAA09630.1; -.
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                                                                                                                                                                                                                                                                                                 Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-TU22;
MEDLINE; 90060034.
SHERMAN D.H., MALPARTIDA F., BIBB M.J., KIESER H.M., BIBB M.J.,
HOPWOOD D.A.;
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                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                  Last sequence update)
Last annotation update)
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01-NOV-1998 (TIEMBLrel. 08, Last sequence update)
01-NOV-1999 (TIEMBLrel. 12, Last annotation update)
HYPOTHETICAL 33.5 KD PROTEIN.
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   283 AA
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                                                                                                                                                                PATHWAY-SPECIFIC TRANSCRIPTIONAL ACTIVATOR.
                                                                    Created)
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chem. Biol. 5:647-659(1998).
                                                         01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis.
                                                                                                                                                                                                                                    Streptomyces violaceoruber
PRELIMINARY;
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Best Local Similarity
Matches 5; Conserv
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SEQUENCE FROM N.A.
FRASER C.M., TONORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G.,
DODSON R., GWINN M., HICKEY E.K., CLAYTON R., KETCHUM K.A.,
SODERGREN E., HARDHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J.,
KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTTERBACK T.,
MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAND S.,
HATCH B., HORST K., ROBERTS K., WAITHEY L., WEIDMAN J., SMITH H.O.,
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MEDILINE; 98332770.
FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G.,
DODSON R., GWINN M., HICKEY E.K., CLAYTON R., KETCHUM K.A.,
SODERGREN E., HARDHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J.,
KHALAK H., RICHARDSON D., HOWELJ J.K., CHIDAMBARAM M., UITERBACK T.,
MACDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAND S.,
HATCH B., HORST K., ROBERTS K., WATTHEY L., WEIDMAN J., SMITH H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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TAYLOR K., WHITEHEAD S., BARRELL B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 27; DB 2; Length 404;
Pred. No. 70;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                  PARKHILL J.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AL008967; CAA15591.1; -.
EMSP; P31164; 2PIA.
PROSITE; PS00197; 2FEZS_FERREDOXIN; 1.
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EMBL; AE001221; AAC65433.1; -.
TIGR; TP0446; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treponema pallidum.
Bacteria; Spirochaetales; Spirochaetaceae; Treponema
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Last sequence update)
Last annotation update)
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PFAM: PF00115; oxidored_fad; 1.
Hypothetical protein; Iron-sulfur.
SEQUENCE 309.AA; 33517 MW: B152B590 CRC32;
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Pred. No. 53;
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83.3%;
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Best Local Similarity 83.3%;
Matches 5, Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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STRAIN-WHITE LEGHORN; TISSUE-BRAIN;
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1008 YRLALR 1013
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01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
NEURON-GLIA CELL ADHESION MOLECULE (NG-CAM) PRECURSOR (NG-CAM).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                   WILLSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPER J., COULSON A.,
BONFIELD J., BURTON J., CONNELL M., COPER J., COLLSON A.,
GARDNER A., GREEN P., HAWINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
PARSONS J., PERCY C., RIFKEN L., ROPPRA A., SAUNDERS D., SHOWNKEEN R.,
THIERRY MIEG J., THOMAS K., VADUIN M., VADGHAN K., WATERSTON R.,
WATENSTON A., WEINSTOCK L., WILKINSON-SFROAT J., WOLLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=BRISTOL N2;
ROHLETING T., WOLLDMANN P.;
"The sequence of C. elegans cosmid F23H11.";
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
WATERSTON N. Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WATERSTON R.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                            Last sequence update)
Last annotation update)
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Pred. No. 1.5e+02;
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83.3%;
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                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 368:32-38(1994).
                                                                                                                                                                                                                         Caenorhabditis elegans.
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN-BRISTOL N2; MEDLINE; 94150718.
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SEQUENCE FROM N.A.
                                                                                                                                                                                    F23H11.2 PROTEIN.
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                                  RESULT 11
001914
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XX MEDLINE, 98049343.

X KLENK H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E.,

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XA KLENK H.-P., CLAYTON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,

XA KICHARDSON D.L., KERLAYNGE A.R., GRAHAM D.E., KYRFIDES N.C.,

XA RICHARDSON D.L., MONGKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,

XA KIRKNESS E.F., DOUGHERTY B.A., MOKENNEY K., ADAMS M.D., LOFTUS B.,

XA KIRKNESS E.F., DOUGHERTY B.A., MOKENNEY K., ADAMS M.D., LOFTUS B.,

XA COTTON M.D., SPRIGGS I., ARTIACH P., KAINE B.P., SYKES S.M.,

XA ADOWN P.W., D'ANDRER K.P., BOWMAN C., FUJII C., GARLAND S.A.,

XA MASON I.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
                                                                                                                                                                                                                                           Gaps
                                                                       'Cell adhesion molecules NgCAM and axonin-1 form heterodimers in the
MEDLINE; 97133428.
BUCHSTALLER A., KUNZ S., BERGER P., KUNZ B., ZIEGLER U., RADER C.,
SONDEREGGER P.;
                                                                                       neuronal membrane and cooperate in neurite outgrowth promotion."; J. Cell Biol. 135:1593-1607(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
NEURON-GLIA CELL ADHESION MOLECULE
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Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 27; DB 13; Length 12 Pred. No. 2.4e+02; 1; Mismatches 0; Indels
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Last annotation update)
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1280 AA; 138432 MW; A72DEE34 CRC32;
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                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-WHITE LEGHORN; TISSUE-BRAIN;
MEDLINE; 91154306
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96 AA; 10892 MW;
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ilarity 83.3%;
Conservative
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EMBL; AE001062; AAB90622.1;
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1280
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Best Local Similarity
Matches 5; Conserv
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Length 96;

DB 1;

Score 26;

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Nature 397:176-180(1999).
BENBL; AE001456; AAD057631: -.
SEQUENCE 255 AA; 28872 MW; 04B2EB82 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helicobacter pylori J99.
Bacteria: Proteobacteria: epsilon subdivision; Helicobacter group;
Helicobacter.
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                                               0; Indels
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
291AA LONG HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                         255 AA.
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83.3%; Pred. No. 28;
tive 1; Mismatches
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Archaea; Crenarchaeota; Aeropyrum
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092MN9;
01-MAY-1999 (TrEMBLrel. 10, C;
01-MAY-1999 (TrEMBLrel. 10, Ls
01-MAY-1999 (TrEMBLrel. 10, Ls
FUMARATE REDUCTASE.
Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity
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188 YRLAIK 193
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51 YRLAIK 56
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Best Local Similarity 83.3%; Pred. No. 88;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps
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11.1:1
Db 66 YRLAMR 71
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Search completed: February 8, 2000, 13:17:35 Job time: 32484 sec

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AC008807 Drosophila melano
AC008807 Homo sapiens chro
AC008681 Homo sapiens chro
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TION PLEUTOLUS OSTICATUS MRNA for hydrophobin 1.

IN Y14656.1

N Y14656.1

N Y14656.1

N Y14656.1

N Y14656.1

Syster mushroom.

IISM Pleurotus ostreatus
Eukaryota; Fung1; Basidiomycota; Hymenomycetes; Aphyllophorales;
Lentinacaes; Pleurotus.

CE 1 (bases 1 to 342)

RS Asgeirsdottir,S.A., de Vries,O.M. and Wessels,J.G.

Identification of three differentially expressed hydrophobins in Pleurotus ostreatus (oyster mushroom)

NL Microbiology 144 (Pt 11), 2961-2969 (1998)
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/VLGCSPIAALGVLSGIASLIGEVGLDCSPLQVIGVGANSCSSQAACCTGNTFNGA
                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 342)
Asgeirsdottir,S.A.
Direct Submission
Submitted (22-AdG-1997) S.A. Asgeirsdottir, Department of Plant
Biology, University of Groningen, Kerklaan 30, 9751 NN Haren,
NETHERLANDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
LOCUS G46114 485 bp DNA STS 23-MAR-1999
DEFINITION 26550_1 Zebrafish AB Danio rerio STS genomic clone 26550 5',
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58456
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1. 342
7. organism="Pleurotus ostreatus"
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/dev_stage="fruiting"
/tissue_type="fruit body"
 8.6e+03
1.1e+04
1.2e+04
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'gene="POH1"
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US-08-653-294-7 x PORNAH1
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LOCUS PORNAH1
                                                                 seq_name: gb_pl2:PORNAH1
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 gb_htg7:AC018207
gb_htg3:AC008807
gb_htg3:AC008681
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AUTHORS
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MEDLINE
REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 Y14656 Pleurotus ostreatus mRNP (4614 2650_1 Zebrafish AB Dan (AL25500 Pleurotus ostreatus PC (A15954 Lactobacillus influenzae (A15954 Lactobacillus plantarum (A15954 Lactobacillus (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC009604 Leishmania major chr
273969 Caenorhabditis elegans
281576 Caenorhabditis elegans
U71217 Human Clone c15H12, 24
AF102543 Zymomonas mobilis ZW
280902 Human DNA sequence frd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           277665 Caenorhabditis elegans
270286 Caenorhabditis elegans
                                                                                                             Command line parameters:
-MODEL-frame+_p2n.model -DEV-xlp
-MODEL-frame+_p2n.model -DEV-xlp
-O-/cgnl_1/USPFO_spool/US08653294/runat_04022000_160701_15779/app_query.fasta.1
-DB-GenEmbl -QEMT=fastap -SUFFIX-rge -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -GAPOP=4.500
-GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -BELOP=6.000
-GAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -BELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX-blosmm62 -TRANS-human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -ALIGN=15 -MODE=LOCAL
-OUTFWT=pfs -NORM=ext -MINLEN=0 -MAXLEN=1000000 -USER-US08653294
-NCPU=6 -ICPU=3 -NO_XLPXY -WAIT -THREADS=1
                                                                   About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4832
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   out_format : pfs
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313.26
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86.84
   OM of: US-08-653-294-7 to: GenEmbl:*
                                                                                                                                                                                                                                                                                                                                                                   Database: GenEmbl:*
Database sequences: 821193
batabase length: -1518192014
Search time (sec): 11370.480000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strd Orlg
                                  Date: Feb 8, 2000 4:37 PM
                                                                                                                                                                                                                                                                                                                  Search information block:
Query: US-08-653-294-7
Query length: 6
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9b_ini:AFC020343

9b_ini:AFC020343

9b_ini:AFC020343

9b_ini:AFC020343

9b_pi:AFC020343

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9b_pi:YSZBGLUA

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9b_pi:SPCDC7

9b_bai:BSCDC07

9b_bai:BSCDC07

9b_bai:BSCBC07

9b_bai:BSCBC0341

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9b_bai:AEC000312

9b_bai:AEC000312

9b_bai:AEC000312

9b_bai:BSCBC1

9b_bai:AEC014909

9b_ini:CEK02E11

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gb_ba2:AF109102
gb_ba1:LPY15954
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gb_pl2:PORNAH1
gb_sts:G46114
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'trans la tion-"mesiristyvilaasallava ipmintetpocnygpiocnsvos
ktssaaagplaalgylsgiasllgevgldcsployigyganscssqaacctgntfnga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (19-MAR-1998) Asgeirsdottir S.A., Molecular Plant
Biology, University of Groningen, Kerklaan 30, 9751 NN Haren, THE
NETHERLANDS
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Aphyllophorales;
Lentinaceae; Pleurotus.
1 (bases 1 to 518)
Asgeirsdottir, S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Asgeirsdottir,S.A., de Vries,O.M. and Wessels,J.G. identification of three differentially expressed hydrophobins in
                                                                                                                                                                                                                                                                                01-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .420,474. .515)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oin(1. .90,155. .199,259. .420,474. .518)
gene="POH1"
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Gaps: 0
Percent Identity: 100.000
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                                                                                                            to: 485
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Microbiology 144 (Pt 11), 2961-2969 (1998)
99061188
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'gene="POH1"
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protein_id="CAA12391.1"
db_xref="G1:2982618"
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/db_xref="taxon:5322"
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                                                                                                            from: 1
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Locds PoAJS066 518 bp DNA
LOCHS POAJS060 Streatus POH1 gene.
ACCESSION AJ225060
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1. .518
                                                                                                            to reverse of: G46114
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oyster mushroom.
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/gene="POH1"
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/gene="POH1"
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                                                      alignment_block:
US-08-653-294-7 x G46114/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submission
Ratio: 4.833
Percent Similarity: 100.000
                                                                                                                                                                                                                          seq_name: gb_pll:POAJ5060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="Adult"
/lab_host="DH5alphaF'IQ"
/note="Vector: ml3MP19 with added BstXI site; V-type:
Phote="Vector: ml3MP19 with added BstXI site; V-type:
Phote="Vector: ml3MP19" with adult Zebrafish of AB
strain was digested with Alui, Cac81, HaeIII, NlaVI, or
Rsal. Fragments in the range of 250-500 bp were gel
purified and a BstXI linker was added. The fragments were
cloned into a modified Ml3mp19 vector and transformed
into E. Coli DH5alpha. Microsatelllite sequences were
                                                                                         Danio rerio

Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Actinopterygil;
Neopterygil: Teleostel: Euteleostel: Ostarlophysi: Cypriniformes:
(Sprinoidea: Cyprinidae: Rasborinae; Danio.
1 (bases 1 to 485)
Shimoda, N., Knapik, E.W., Ziniti, J., Sim, C., Yamada, E., Kaplan, S. and Fishman, M.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               into E. Coli DH5alpha. Microsatelllite sequences were screened with labeled d(CA)15 and d(GT)15 oligonucleotide
                                                                                                                                                                                                                                                                                              Contact: Mark C. Fishman
Cardiovascular Research Center
Massachusetts General Mospital
Mail code 1494100A, 149 13th Street, Charlestown, MA 02129, USA
Fax: 6177565806
Bmail: fishman@mgh.cvrc.harvard.edu
http://zebrafish.mgh.harvard.edu
Primer A: TGTTTCCTGATTCGCTGTTG
Primer B: GCCTACTGTTCTGATTCGTCCATTG
STS size: 157
PCR Profile:
                                                                                                                                                                                                                        genetic linkage map of the zebrafish with 2000 microsatellite
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50 mM
10 mM
8.3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="z6550"
/clone_lib="zebrafish AB"
/sex="F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55. .211
55. .74
complement(191. .211)
83 c 124 g
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/db_xref="taxon:7955"
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Polymerization: 7
PCR Cycles: 2
Thermal Cycler: M
 sequence tagged site
                     G46114
G46114.1 GI:4492405
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Total Vol:
                                                                                                                                                                                                                                                               Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Denaturation:
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55
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alignment_block:
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                                                            Ouality: 29.00
Ratio: 4.833
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                  seq_name: gb_bal:LPY15954
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                                                alignment_scores:
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-10_signal
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   ORIGIN
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EDAELQKLMQEQDKKVQEFQAQNEKRQAEERGKLLDSIQTATNNLAKAKGYTYVLDAN
SVVFAVEGKDITEEVLKSIPASEKAAARAEEKK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="ALALGIALASGYAAAEEKIAFINAGYIFQNHPDRQAVADKLDAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2. (bases 1 to 585)
El-Adhami, W., Kyd, J.M., Bastin, D.A. and Cripps, A.W.
El-Adhami, W., Kyd, J.M., Bastin, D.A. and Cripps, A.W.
El-Adhami, W., Kyd, J.M., Bastin, D.A. and Cripps, A.W.
Elect Submission of Canberra, ACT 2601, Australia
Location/Qualifiers
1. 585
/organism="Haemophilus influenzae"
/strain="UCI8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haemophilus influenzae.
Haemophilus influenzae
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
1 (bases I to 585)
El-Adhami,W., Kyd,J.M., Bastin,D.A. and Cripps,A.W.
Characterization of the gene encoding a 26 kilodalton protein (OMP26) from nontypeable Haemophilus influenzae and immune responses to the recombinant protein infect. Immun. 67 (4), 1935-1942 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="outer membrane protein 26"
/protein_id="AAD23984.1"
/db_xref="G1:4574280"
                                                                                                                                                                                                                                                     Gaps: 0
Percent Identity: 100.000
                                                                                                                                                          132 t
                                                                                                                                                                                                                                                                                                                                                to: 518
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/gene="skp"
<1. .582
/gene="skp"
/note="oMp26; skp"</pre>
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/number=2
259. 420
/gene="poH1"
/mumber=3
421. 473
/gene="poH1"
/mumber=3
/qt. .>518
                                                                                                                                                                                                                                                                                                                                                                                              309 TATCGCCTCGCTATTAGG 326
                                                                                                                                           /number=4
168 c
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Ratio: 4.833
Percent Similarity: 100.000
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US-08-653-294-7 x POAJ5060
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FARTILIRYASKVKYWMTFNEINSAVHFPVMGGGLVLSTGANDKKNVFQAWHNQFVAS
AKAVKIAHELRDDIQVGCMILYATSYAYDSNPVNQLANLQHNQDFNFFCADVQVRGAY
PTYRKRLLAEYNLTFDDLETTDGDLALLQQYFYDY GGFSYYMSSAVETTGSYTDTVAG
NLMGGVKNPFLKASDWGWDTDFTGLRIALNELHDRYQKPLFVVENGLGAIDKPDKNFY
VEDDY RIDYLKQHIEMARAJIDDGVDLMGYTPWGCIDLVSASTGEMSKRYGFIYVDLD
DQGHGTLARYPKKSFYWYQDVIKHNGLIKK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     beta-glucosidase; bglT gene.
Lactobacillus plantarum.
Lactobacillus plantarum
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
Lactobacillus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation-"MSEFPEGFLWGGATAANQLEGGYQEGGRGLSIADRLPGGKDRFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (17-DEC-1997) M. Sacco, Istituto Internazionale di
Genetica e, Biofisica, via Marconi 10, I- 80125, Napoli, ITALY
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                 02-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Expression of the bglH gene of Lactobacillus plantarum is controlled by carbon catabolite repression J. Bacteriol. 180 (13), 3400-3404 (1998) 98317280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 1797)
Marasco,R., Muscariello,L., Varcamont1,M., De Felice,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190. .203
/note="cyclic-AMP responsive element (CRE)"
235. .1677
235. .1677
                                                                                                                                                                        to: 585
Length: 6
Gaps: 0
Percent Identity: 100.000

    1797
    /organism="Lactobacillus plantarum"
/strain="B21"

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                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
Locus LPY15954 1797 bp DNA
DEFINITION Lactchacillus plantarum bglT gene.
VERSION X15954.1 GI:3288505
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/db_xref="G1:3288506"
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/transl_table=11
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/gene="bglT"
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Sacco, M.
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1047 TATCGCCTAGCGATAAGA 1064
                                                   seq_name: gb_in1:AF020343
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TYSYSAGLLSHFLGIGGKLRFRVHSTSSCLLTSKLRVFLWEHSQPQCRRPKFHTLTLM
GLDWRAVIOACCATANFGDSGARFWIMPLSAPRAPQTVETKFEFY IRLIGIDYIPDL
CRQINYKORFGWFLISTRYTTELFBYRIBSTIGVKTRKVNFTNAFAIKCATTG
MHWGRCILHFTWSWHRNTEAGKNAREISQSRLEWVITVLQHIILGIRGILVYDNAKSEF
FEFGSFAGPVISGGTPNEAENWRVQSTSWQWIHAVTVSIEVLPGFREYGRSAGPWTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rgyvdrnilmvshlftspylgmaiwyvfdayghiptdvtttvelesirhlsphvhilk
                                                                                                                                                                                                                                                                                                                                                                                                                         artichoke italian latent virus.
artichoke italian latent virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Comoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (05-MAY-1995) F. Grieco, Univ. of Bari, Dipt Protezione
Piante, via Amendola 165/A, 70126 Bari, ITALY
Location/Qualifiers
                                                                                                                                                                                                                                                                                                              seq_documentation_block:
LOCUS AILV1828 1828 bp mRNA VRL 19-FEB-1996
DEFINITION Artichoke italian latent virus mRNA unknown function (1828bp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation-"NGDFAFSQRITYPAARTVGTVIGTLDIFALIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  italian latent virus"
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                                Quality: 29.00 Length: 6
Ratio: 4.833 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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Gaps: 0
Percent Identity: 100.000
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db_xref="GI:1199792"
db_xref="SPTREMBL:Q64959"
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    1828
    1828
    organism="artichoke idd_xref="taxon:46075"

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2 (bases 1 to 1828)
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1 (bases 1 to 1828)
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US-08-653-294-7 x LPY15954/rev
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Ratio: 4.833
Percent Similarity: 100.000
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US-08-653-294-7 x AILV1828
                                                                                                                                                                                                                                                                            seq_name: gb_vi:AILV1828
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                 alignment_scores
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WVINDDAKPGRNPRERERSWTIETTTKAQLEKSRRCAKKRIKERALMGSLHSTLNGN
SIAGSIQTISHDLYDDDSMGGAFDNVPSSFRPRTGSNLSIPGSSRVSPAIGSDIYDD
LEFPSWYGSSYPAIPSDIYDRTDQMALDATHIGGYOLKOESKRIKTEBIAPPSSYHE
LUSYRGSCAQNPLLANDRYRDAPLAAXGNYONGGTTPINMLSTSNSPLPGI
GSCGIVAAQHTVASSSALPIDLENLILDDQPLMDTMOVDALIRHELSQAGGHIHFDL
                                                                                                                                                                                                          Caenorhabditis elegans.
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 2565)
1 (bases 1 to 2565)
1 (bases 1 to 2665)
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EPIPRDRCNWFWMRRPQLEPPLNSSPIIHEQIPEEDADLYGSNEQCQGLGGASSNUGST
APLIPPGSNSHQTSFPSRESPDDTVSGRKITTRRNAGNASYELIITAIMASPE
RRLILAGVYEMAVQOVPEFRDKGSSNGSMKNSIRHILGLHSRFMRIQNGGAGKSSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="fork head-related transcription factor DAF-16a2"
/protein_id="AABB4391.1"
/db_xref="G1:2618979"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (21-AUG-1997) Molecular Biology, MGH, 50 Blossom St., Boston, MA 02114, USA
Caenorhabditis elegans fork head-related transcription factor AFF020343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="daf-16"
/gene="null phenotype is suppression of daf-2"
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Gaps: 0
Percent Identity: 100.000

    2565
/organism="Caenorhabditis elegans"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:6239"
/chromosome="1"
/map="1; between mgP45 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 2565)
Ogg,S., Paradis,S. and Ruvkun,G.
Direct Submission
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                                                                                                                                                       AF020343.1 GI:2618978
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US-08-653-294-7 x AF020343/rev
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Ratio: 4.833
Percent Similarity: 100.000
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      seq_documentation_block:
LOCUS AF020343
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE

JOURNAL MEDLINE REFERENCE

AUTHORS TITLE

JOURNAL

DEFINITION

ACCESSION

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caenorhabditis elegans.

Caenorhabditis elegans

Bukaryota, Metazoa, Nematoda; Secernentea; Rhabditia; Rhabditida;

Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 3035)

Lin,K., Dorman,J.B., Rodan,A and Kenyon,C.

daf-16; An HNF-3/forkhead family member that can function to double scene 278 (5341), 1319-1322 (1997)
                                                                                                                                                                                                                                                                                                                     Ludwig,W., Rossello-Mora,R., Aznar,R., Klugbauer,S., Spring,S., Reetz,K., Beimfohr,C., Brockmann,E., Kirchhof,G., Dorn,S., Bachleitner,M., Klugbauer,N., Springer,N., Lane,D., Nietupsky,R., Weizenegger,M. and Schleifer,K.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (18-MAY-1995) W. Ludwig, Lehrstuhl fuer Mikrobiologie, Submitted (18-MAY-1995) W. Ludwig, Lehrstuhl fuer Mikrobiologie, Technische Universitaet Muenchen, Muenchen, FRG (18-May 16-May 16-Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Comparative sequence analysis of 235 rRNA from proteobacteria Unpublished
                                                                                                                                                                                                          Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
Myxococcales; Sorangineae; Sorangiaceae; Nannocystis.
1 (bases 1 to 2955)
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Caenorhabditis elegans DAF-16 (daf-16) mRNA, complete cds.
AF032112
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Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="23s ribosomal RNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         545
X87286.1 GI:2244669
X87286.1 GI:2244669
Sas ribosomal RNA; 23S rRNA gene.
Nannocystis exedens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism-"Nannocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="DSM 71 T"
/db_xref="taxon:54"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ხ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="23S rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene-"23S rRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF032112.1 GI:2623942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 2955)
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US-08-653-294-7 x NE23S71TS/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    c 069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TyrArgleuAlaileArg 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio: 4.833
Percent Similarity: 100.000
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Ratio:
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AUTHORS
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FEATURES
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product-"fork head-related transcription factor DAF-16al"
//profusel_ad="AaAB4390.1"
//db_xref="f01:261897"
/translation="MMEMLVDQGTDASSSASTSTSSVSRFGADTFMNTPDDVMMNDDM
PERPRORENGYPEPPLNSSTIBO_PERDADLYSSREGGOLGGASSNGST
AMLHTPDGSNSHQTPSPSDFEMSESPDDTVSGKRTTRRNAMGNMSTAELITTAIMAS
PEKRLTLAQVYEWMVQNVPFFDXGDSNSSAGWKNSIRHNLSLHSRFWRIQNGGAGKS
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                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 2579)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ogg,S., Paradis,S., Gottlieb,S., Patterson,G.I., Lee,L.,
Tissenbaum,H.A. and Ruvkun,G.
The Fork head transcription factor DAF-16 transduces insulin-like metabolic and longevity signals in C. elegans
Nature 389 (6654), 994-999 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Codes 1 to 2579)
2 (bases 1 to 2579)
2 (og.S. Paradis,S. and Ruvkun,G. Direct Submission
Submitted (21-AUG-1997) Molecular Biology, MGH, 50 Blossom St., Boston, MA 02114, USA
                                                                                                           Caenorhabditis elegans fork head-related transcription factor
DAF-16a1 (daf-16) mRNA, complete cds.
AF020342.1 GI:2618976
                                                                                 13-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="daf-16" /
/note="null phenotype is suppression of daf-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: 2579
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Gaps: 0
Percent Identity: 100.000
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1. .2579
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/organism="Caenorhabditis
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                                                                                 mRNA
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/gene="daf-16"
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                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
Caenorhabditis elegans
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                                                                             2579 bp
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US-08-653-294-7 x AF020342/rev
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Percent Similarity: 100.000
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                                  seq_documentation_block:
LOCUS AF020342
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source

FEATURES

gene

CDS

(bases 1 to 3035)

MEDLINE REFERENCE

03-JUL-1997

BCT

seq_documentation_block: LOCUS NE23S71TS 2955 bp DEFINITION N.exedens 23S rRNA gene.

BASE COUNT

ORIGIN

JOURNAL

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/db_xref="taxon:9606"
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LOCUS PXVMENVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: gb_vi:PXVMENVA
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SOURCE
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ORIGIN
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MEDLINE
REFERENCE
AUTHORS
TITLE
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
                                                                                                                                                                          /note="defective dauer formation; suppresses Age phenotype of age-1, daf-2."
                                                                                                                                                                                                                                                                                                                                                                                                                                     HELNSVRGSCAQNPLLRNPIVPSTNFKPMPLPGAYGNYQNGGITPINWLSTSNSSPLP
GIQSCGIVAAQHTVASSSALPIDLENLTLPDQPLMDTMDVDALIRHELSQAGGQHIHF
                                                                                                                                                                                                                                                                                                                           /translation="MMEMLVDQGTDASSSASTSTSSVSRFGADTFMNTPDDVMMNDDM
                                                                                                                                                                                                                                                                                                                                                                                                                        DDLEFPSWVGESVPAIPSDIVDRTDOMRIDATTHIGGVQIKQESKPIKTEPIAPPSY
                                                                                                                                                                                                                                                                                                                                                                                           SWWVINPDAKPGRNPRRTRERSNTIETTTKAQLEKSRRGAKKRIKERALMGSLHSTLN
                                                                                                                                                                                                                                                                                                                                                EP I PRDRCNTWPMRRPQLEPPLNSSP I I HEQ I PEEDADLYGSNEQCGQLGGASSNGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stasiv, Y.Z.
Stasiv, Y.Z.
Direct Submission
Submitted (26-OCT-1994) Y.Z. Stasiv, Engelhardt Institute of
Submitted (26-OCT-1994) Y.Z. Stasiv, Engelhardt Institute of
Molecular Biol., Vavilov Str. 32, 117984, Moscow B-334, RUSSIA
Related sequence: X63417.
Location/Qualifiers
1. 3157
/organism="Homo saplens"
Homo sapiens
Eukaryota, Matazoa, Chordata, Vertebrata, Mammalia, Eutheria,
Eukaryota, Matazoa, Chordata, Vertebrata, Mammalia, Eutheria,
1 (bases 1 to 3157)
Stasiv,Y.Z. and Itkes,A.V.
(Upublished
2 (bases 1 to 3157)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 3035
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Percent Identity: 100.000
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                                                                                                                                                                                                                                                  note="HNF-3/forkhead homolog"
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                                                                                                                                                                                                                                                                                              /protein_id="AAC47803.1"
/db_xref="G1:2623943"
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                                                                                                                        /db_xref="taxon:6239"
/chromosome="I"
                                                                                                           'strain-"Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     511 g
                                                                                                                                                                                                                    334. ... 1866
/gene="daf-16"
                                                                                                                                                                        'qene="daf-16"
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US-08-653-294-7 x AF032112/rev
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Ratio: 4.833
Percent Similarity: 100.000
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LOCUS HSIRLB123
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SOURCE
ORGANISM
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                   TITLE
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AUTHORS
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VERSION
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    AUTHORS
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FEATURES
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2 (sites). Canwa,R., Yanagida,N. and Nazerian,K. Calvert,J.G., Ogawa,R., Yanagida,N. and Nazerian,K. Identification and functional analysis of the fowlpox virus homolog of the vaccinia virus p37K major envelope antigen gene Virology 191, 783-792 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION Pigeon pox virus major envelope antigen (p43K) gene, 3' end cds; envelope protein (p74K) gene, complete cds; ORF, 5' end cds. ACCESSION M88588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goebel, S. J., Johnson, G.P., Perkus, M.E., Davis, S.W., Winslow, J.P. and Paoletti, E. The complete DNA sequence of Vaccinia virus Virology 179, 247-266 (1990)
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                                                                                                                       /function="putative transcription factor"
/product="DNA-binding protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 others
                                                          /evidence-experimental
join(24. .166,2151. .2268,2891. .3054)
/gene-"irlb"
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Gaps: 0
Percent Identity: 100.000
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2269. .2890
/gene="irlB"
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2891. .3053
/gene="irlB"
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2151. . . 2268
/gene="irlB"
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579 c 583 g 1
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cell_line="Hela"
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/gene="irlB"
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Pigeon pox virus DNA.
Pigeonpox virus
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Ratio: 4.833
Percent Similarity: 100.000
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US-08-653-294-7 x HSIRLB123
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197

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LATVSLLPRKFRRDYSLYWPIIKDALIRAVLERGYKLRVLLGFWKRDVISKASIKSI
NELGVDHIDISTKVFRFPVNSKVDDINNSKMMIIDGRYAHVMTANLDGSHFNHHAFVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NFSGLLDILIFSIRYKNNNGNYYZPHISSAVNIALSSIYTDYYAIDDIDKDSKKLVFD
SIFPLIMBGYYPEGKPYYTTPKEGYLSICLCDVEISNDIKNPILYCKENKSARKFTG
YFFSVDIDTAWKLRGYKIKIEECIEWPNKIKLEDNICYLNKLFIEHQDYTHDEKSLOG
YLFSYLLKGNVTEDVLAMKSCRNNLSIISFIISYCRNYTYKLLECPVYESSNIVKCKY
NQVIK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
/codon_start=1
/function="involved in the release of progeny virions"
/function="id="aAA4/187.1"
/db_xref="GI:33524"
/translation="MALIEQLQSSEQSILSPFRYYGFKDFHNVIFTTIDDETLIVITV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNVPLVTRLITFEKITFFRŠFNSTCITTSNNNSDIDTDTYFIPNSLSLLDILKKRAYD
VELRDLSFAIMSEMNNDELRNSDIVSLNKWLHKHNLLDYKLVLISDIDRRYKLYNKKN
TIIDVISVNGRNYNIWVKDVIEYYSPEYLRWSIDIKRATESNNWLPYSQSINPLNENI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /trānslation-"MDTNRKRSLDEHDTGEESPGKLQIVEINDEEDITFTDNPYYKLV
KSRDNSINLVPLVGCVMIKINDIKGVTDKVNKLLPRTSSKTNSTSCINIPIDSIPLNF
LDDGNKYFNVSEVSILQVSHGNDMMNIDKYVDGSFDYIAVLCLKNSGRS"
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KHWTGKKLNFKNFFQKDSQLEKYINNNSVAERIYYLQSSLHKHISCLIEIFELNGFDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="disruption of this gene results in a small plaque
phenotype; homolog of vaccinia virus F12L; putative"
/citation=[1]
3 (bases 1 to 3178)
Ogawa,R., Yanagida,N., Nazerian,K. and Calvert,J.G.
Insertitional inactivation of a fowlpox virus homologue of the
vaccinia virus F12L gene inhibits release of enveloped virions
J. Gen. Virol. 74, 55-64 (1993)
                                                                                                                                                                                                                                                                                                                             /gene="p43K"
/note="homologue to vaccinia virus p37K (F13L) gene;
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/db_xref="G1:333523"
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                                                                                                                                                                                    /organism-"Pigeonpox virus"
/db_xref-"taxon:10264"
1. .756
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/db_xref="GI:333525"
                                                                                                                                                     Location/Qualifiers
1. .3178
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                                                                                                                                                                                                                                                                                                                                                                                                        /citation=[1]
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794. .2686
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/gene="p74K"
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US-08-653-294-7 x PXVMENVA/rev
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<1. .756
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Ratio: 4.833
Percent Similarity: 100.000
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/protein_id="AAA34314.1"
/protein_id="AAA34314.1"
/bc.xref="G1:170808"
/translation="Mimivolliverlocation to protein to a control to a 
                                                                                                                                                                                               seq_documentation_block:
LOCUS YS2BGLUA 3215 bp DNA PLN 27-APR-1993
DEFINITION S.fibuligera extracellular beta-glucosidase 1 (BGL1) gene, complete
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LYLKHPEDGKFETPIQLRGFEKVELSPGEKKTVDLRLLRRDLSVWDTTRQSWIVESGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Appl. Environ. Microbiol. 54, 3147-3155 (1988)
89133518
Draft entry and sequence for [1] kindly submitted by I.Yamashita,
                                                                                                                                                                                                                                                                                                                                                            M22475
M22475
M22475
M22475
M22475
M22475.1 GI:170807
M22475.1 GI:170807
M22475.2 GI:170807
M22475.2 GI:170807
M22475.3 GI:170807
M22475.1 GI:170807
M22475.2 GI:170807
M22464050918 fibuligera
M2247648.1 Fungi: Ascomycota; Saccharomycopsidaces; Saccharomycopsidaces; Saccharomycopsidaces; Saccharomycopsidaces; Saccharomycopsis.

1 (bases 1 to 3215)
M224464.M. Ohtsuki.; Fukui.S. and Yamashita.I.
Nucleotide sequences of Saccharomycopsis fibuligera genes for extracollular beta-glucosidases as expressed in Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualiflers
1. 3215
//organism="Saccharomycopsis fibuligera"
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//oce="beta-glucosidase 1 signal peptide"
//oce="beta-glucosidase 1 precursor"
//codon_start=1
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Percent Identity: 100.000
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328. .2904
/note="beta-glucosidase 1"
1 614 c 667 g 965 t
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Percent Similarity: 100.000
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US-08-653-294-7 x YS2BGLUA
                                                                                                                 seq_name: gb_pll:YS2BGLUA
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seq_name: gb_pr1:AB00189S11

1 TyrArgLeuAlalleArg

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YS2BGLUB 3371 bp DNA PLN 27-APR-1993
S.fibuligera extracellular beta-glucosidase 2 (BGL2) gene, complete
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GPDPKGYEGEDOGCVDGALFEGWGSGSVGYPKYQYDFFEEISANARKNKMOFDYIRES
FDLTQVSTVASDAHMSIVVAVSAVSGEGYLIIDGNRGDKNNVTLMHNSDNLIKAVAENC
ANTVVVTITSTGQVDVBSFADBPNYTALVWAGPLGDBGGTAIANLEGNANPSGRILPFT
VAKSNDDYIPIVTYNPPNGEPEDNTLAEHDLLVDYRYFEEKNIEPRYAFGYGLSYNEY
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DSNVTLKDGNYEYPDGYSTEORTTPIOPGGGLGGNDALWEVAYKVEVDVQNLGNSTDK
FVPQLYLKHPEDGKFETPVQLRGFEKVELSPGEKKTVEFELLRRDLSVWDTTRQSWIV
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PTPQGGRLQGWWQDAYTAKALJSQWTIVEKVNLTTGTGWQDGCBCVGNTGSVPRRGIP
NLCLQDGPLGVRLTDFSTGPSGWATGATFNKDLFLQRGQALGHEFNSKGVHIALGPA
VGPLGVKARGGRNFEAFGSDPYLQGIAAAATIKGLQENVWACVKHFIONEQDIRQP
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ENSYMINHLLKEELGFQGFVVSDWAAQMSGAYSAISGLDMSMPGELLGGWNTGKSYWG
ONLTRAVYNETVPIERLDDMATRILAALYATNSFPTKDRLPNFSSFTTKEYGNEFFVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Draft entry and sequence for [1] kindly submitted by I.Yamashita, 09-FEB-1989.
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M22476
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M2461. GI:170809
BGL2 protein; beta-glucosidase 2.
S.fibuligera (strain HUT7212) DNA, clones pSfbetaG[1,2,3,4].
Saccharomycopsis fibuligera
Eukaryota; Fungi; Ascomycota; Saccharomycopsis accharomycopsidaceae; Saccharomycopsis.

1 (bases 1 to 3371)
Machidam., Ohtsuki,I., Fukui,S. and Yamashita,I.
Nucleotide sequences of saccharomycopsis fibuligera genes for extracellular beta-glucosidases as expressed in Saccharomyces
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1. 3371
Aorganism="Saccharomycopsis fibuligera"
(Ab.zef="taxon:4944"
472. 477
Anote-"beta-glucosidase 2 signal peptide"
   11 others
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/note="beta-glucosidase 2 precursor"
/codon_start=1
                                                                                                                                                             Length: 6
Gaps: 0
Percent Identity: 100.000
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/db_xref="GI:170810"
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/note="beta-glucosidase
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US-08-653-294-7 x AB00189511/rev
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Percent Similarity: 100.000
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Protein_id-"BAA21622.1"
/db_xref="G1" BAA2173"
/translation-"MWYLHCGDKNSRCRSEMNVQAAWKRGYTGKNVVVTILDDGIERN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YGIKKGROGIGSIFVWASGNGGREGDYCSCDGYTNSIYTISVSSATENGYKPWYLEEC
ASTLATTYSSGAFYERKIVTTDLRORCTDGHTGTSVSAPMVAGIIALALEANSQLTWR
DVQHLLVKTSRPAHLKASDWKVNGAGHKVSHFYGFGLVDAEALVVEAKKWTAVPSQHM
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LVSPSGTKSQLLAKRLLDLSNEGFTNWEFMTVHCWGEKAEGQWTLEIQDLPSQVRNPE
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NAKIGGIRMLDGDVTDVVEAKSLGIRPNYIDIYSASWGPDDDGKTVDGPGRLAKQAFE
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/note="alternative splicing"
/note="alternative splicing"
/product="PACE4D"
/orduct="PACE4D"
/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (14-MAR-1997) to the DDBJ/EMBL/GenBank databases. Yos Matsuda, The University of Tokushima, Department of Biological Science and Technology; Minamijosanjima-cho 2-1, Tokushima, TOV. Japan (E-mail:matsuda@bio.tokushima-u.ac.jp, Tel:0886-56-7523, Fax:0886-55-3161)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tsuji,A., Hine,C., Tamai,Y., Yonemoto,K., Mori,K., Yoshida,S., Bando,M., Sakai,E., Mori,K., Akamatsu,T. and Matsuda,Y. Genomic organization and alternative splicing of human PACE4 (SPC4), Kexin-like processing endoprotease J. Blochem. 122 (2), 438-452 (1997)
                                                                                                                                                                                                                                                                 Homo sapiens DNA.
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
Matsuda,Y.
                                                                    13-FEB-1999
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/organism="Homo sapiens"

/db_xref="taxon:9606"

join(AB001899.1:1158. .1575,AB001900.1:906. .908,

AB001900.1:1005. .1010,AB001901.1:283. .2209,

AB001901.1:1434. .1577,AB001901.1:283. .2209,

AB001901.1:14912. .5000,AB001902.1:66. .238,

AB001903.1:1698. .1910,AB001904.1:292. .392,

AB001905.1:619. .922,AB001906.1:382. .499,

AB001907.1:7012. .7200,1154. .1290,2441. .2608)
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/note="alternative splicing; exon 15D"
/number=15
                                                                    PRI
                                                                                                      exon 14, 15
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                                                                                                                                                                                     PACE4; alternative splicing.
                                                                 AB00189S11 3227 bp D
Homo sapiens PACE4 gene,
AB001908
AB001908.1 GI:2281763
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                                  seq_documentation_block:
LOCUS AB00189S11
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alignment_scores:
Quality: 29.00 Length: 6
Ratio: 4.833 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

Align seg 1/1 to: YS2BGLUB from: 1 to: 3371 alignment_block: US-08-653-294-7 x YS2BGLUB

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Encodes a HeLa cell sialylt
Sialyltransferase. Proteins
H. pylori outer membrane pr
Australian banana cv. Willi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Purified RNA polymerase II holo:enzyme - comprises RNA polymerase II and one or more regulatory proteins, pref. suppressor of RNA polymerase B proteins or SNI/SNF proteins

The polymerase B proteins or SNI/SNF proteins
Claim 11; Fig 2C; 154pp; English.

Novel DNA aequences (T59904-11) code for yeast SRB (suppressor of NNA polymerase B) proteins SRB4, SRB5, SRB6, SRB9, SRB9, SRB9, SRB1 (W13821-28); respectively. SRBs are transcription regulatory factors that act as positive and negative regulators of RNA polymerase II activity. They are components of the RNA polymerase II activity. They are components of the RNA polymerase II activity. They are components of the RNA polymerase II c-terminal domain (CTD) function. A genomic clone polymerase II c-terminal domain (CTD) function. A genomic clone consuppress dominantly the cold-sensitive phenotype of a cell conty. SRB nucleic acids and RNA polymerase II holoenzymes can be used to treat diseases resulting from alteration or deletion of the genes can be used to detect SRB nucleic acids.

SRB genes can be used to detect SRB nucleic acids.

Sequence 1004 BP; 328 A; 193 C; 202 G; 281 T;
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Human gene fragment Q28B8 from chromosome 21q22.2 SEQ ID NO:22.
Human; chromosome 21; Down's syndrome; detection; isolation; carboxyreductase; ds.
                                                                                                                                                                                                                                                              74-070-1997 (first entry)
Yeast transcription regulatory factor SRB6 DNA.
Transcription regulatory factor; suppressor of RNA polymerase
SRB6; RNA polymerase II; holoenzyme; SWI/SNF; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps: 0
Percent Identity: 100.000
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28-AUG-1995; U44192.

31-AUG-1995; US-521872.

11-CT-1995; US-540804.

26-JAN-1996; US-590399.

(WHED ) WHITEHEAD INST BIOMEDICAL RES.

Chao DM, Koleske AJ, Thompson CM, Young RA;

WPI: 97-179258/16.
1.4e+03
1.4e+03
1.5e+03
1.5e+03
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286. .651
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ID T59906 standard; DNA; 1004
AC T59906;
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ID V15446 standard; DNA; 959
AC V15446;
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US-08-653-294-7 x T59906/rev
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                                                                                                                                      seq_name: N_Geneseq_36:T59906
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  N_Geneseq_36:Q31435
N_Geneseq_36:Q66890
N_Geneseq_36:X30558
N_Geneseq_36:X06864
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Alcohol-oxidase. New DNA seque

HSV-2 strain SB5 Contig ID 101

HSV-2 strain SB5 Contig ID 101

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BETA (1 -> 4
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DNA coding sequence for gentami
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Enterococcus faecalis genome c
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-Q=/cgn1_1/USPTO_spool/US08653294/runat_04022000_160701_15807/app_query.fasta.1
-Q=/cgn1_1/USPTO_spool/US08653294/runat_04022000_160701_15807/app_query.fasta.1
-Q=/cgn1_1/USPTO_spool/US08653294/runat_0402000_16000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPEXT=0.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPEXT=0.000
-GAPEXT=4.000 -GAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blocoun62
-TRANS=human40.cdi -LisT=45 -DOCALIGN=200 -TRR_SCORE-pct
-ALIGN=15 -MODE-LOCAL -OUTFWT=pfs -NORM=ext -MINLEN=0
-MAXLEN=1000000 -USER=US08653294 -NCPU=6 -ICPU=3 -NO_XLEXY -WAIT
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                                                                                                       About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
     out_format : pfs
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Database sequences: 311585
Database length: 125096042
Search time (sec): 590.520000
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Query: US-08-653-294-7
Query length: 6
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                                                     Date: Feb 8, 2000 1:27
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N_Geneseq_36:X36423
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N_Geneseq_36:N60174
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N_Geneseq_36:V62164
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N_Geneseq_36:Q68993
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N_Geneseq_36:T77493
N_Geneseq_36:Q97420
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detergent compsns.
See also Q11476 and Q11478-81.
Sequence 4775 BP; 1171 A;
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                                                                                                                                                                                                      seq_documentation_block:
ID Q11477 standard; DNA; 4775 BP.
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                                                                                                               1176 TATAGATTAGCTGTTAGG 1193
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                                                                                          1 TyrArgLeuAlaileArg 6
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US-08-653-294-7 x Q11477/rev
                                                                                                                                                                  seq_name: N_Geneseq_36:Q11477
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Percent Similarity: 100.000
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27-JUL-1984; EP-201114.
07-FEB-1985; GB-003160.
01-JAN-1990; EP-202731.
                                                      Align seg 1/1 to: X36423
alignment_block:
US-08-653-294-7 x X36423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alcohol-oxidase.
Alcohol-oxidase; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UNIL ) UNILEVER NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 91-119160/17.
P-PSDB; R11606.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hollenberg CP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JUL-1985; 27-JUL-1984; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP-173378-A
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                                                                                                                                                                                                                                                                                                                                                           24-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
                                                                                                                                                                                                                           Possible 1998.

F 16-AUG-1996; 216406.

A RIKAGARU KENKYUSHO.

A RIKAGARU KENKYUSHO.

R RIKA ) RIKAGARU KENKYUSHO.

R WPI: 98-254322/3.

Detection and isolation of active gene - by physically mapping a specific region on chromosome and detecting and isolating gene between sequence represents a base sequence from the human companies. The present sequence represents a base sequence from the human concomments of the present invention describes a method for detecting and isolating an active gene in which an uncommon restriction ensymetis prepared. The method comprises: (a) physically mapping a specified region of a chromosome and the base sequence upstream and downstream of the restriction ensyme site within the map, and (b) detecting and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated heregulin-like factor - used to develop products for the diagnosis and treatment of disorders involving regulation of cell growth, particularly cancers.

Claim 2: Page 86-87; 118pp; English.

This sequence encodes the human heregulin-like factor (HLF) of the linvention. The HLF is involved in the regulation of cell growth. Detection of different levels of expression of the HLF gene can be used for the diagnosis of disorders, e.g. in the neural system. In particular, detection of different levels of HLF gene can be used for the diagnosis of an individual can be used for diagnosing cancer. The products can also be used in the treatment of disorders involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-JUL-1999 (first entry)
Human heregulin-like factor coding sequence.
Human heregulin-like factor; HLF; cell growth regulator; diagnosis; neural system disorder; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   603 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps: 6 Gaps: Percent Identity: 83.333
                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity: 100.000 Percent Identity: 83.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   462 G;
                                                                                                                                                                                                                                                                                                                    289 G;
                                                                                                                                                                                                                                                                                                                                                                                            Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   445 C;
                                                                                                                                                                                                                                                                                                                    240 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hijazi MM, King CR, Ruben SM, Young P;
WPI; 99-095327/08.
P-PSDB; Y05451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ដូ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               abnormal levels of HLF activity.
Sequence 2199 BP; 689 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: V15446 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-JUN-1998; U12403.
17-JUN-1997; US-049942.
(HUMA-) HUMAN GENOME SCI INC.
(GEOU) UNIV GEORGETOWN.
                                                                                                                                                                                                                                                                                                                      247 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              594 TACAGGTTGGCGGTCAGA 611
                                                                                                                                                                                                                                                                                               isolating the active gene. Sequence 959 BP; 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TyrArgLeuAlaIleArg 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio: 4.667
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: N_Geneseq_36:X36423
                                                                                                                                                                                                                                                                                                                                                                                            28.00
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                                                                                                                                                                                                                                                                                                                                                                                                               4.667
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US-08-653-294-7 x V15446
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
J10057062-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X36423;
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HD DACKER KKE BACKER BA

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20-JUN-1991 (first entry)
Sequence of clone encoding alcohol oxidase, MOX enzyme.
Oxidoreductase; bleaching; detergents; dihydroxyacetone synthase;
alcohol axidase; MOX; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       composes. by recombinant DNA technology
Disclosure; fig 11; 54pp; English.
This sequence is contained in a plasmid along with regulatory
DNA, e.g. a sequence allowing autonomous replication in host
cells, for recombinant prodn. of MOX in high yields. MOX catal-
yses the oxidation of methanol to formaldehyde and hydrogen
peroxide in the bleaching process and is useful in bleach and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1069 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oxido-reductase prepn. - for use in bleaching and/or detergent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1286 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ledeboer AM, Maat J, Verrips CT, Visser C, Janowicz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps: 0
Percent Identity: 83.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to reverse of: 011477 from: 1 to: 4775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a
/label= alcohol-oxidase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1249 C;
to: 2199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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mammal
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 . 4.
                                      New DNA sequences coding for oxido:reductase(s) and other enzyme(s) - useful for expression in microorganisms to give high yields for bleaches and detergents.

The sequence encodes the alcohol-oxidase gene, which is used (in combination with its regulatory sequences and/or those of microorganisms that produce oxidases or other enzymes in yields that allow industrial application on a large scale. The engineered allow industrial application on a large scale. The engineered to their application in oxidation reactions and/or in bleaching and
(UNIL ) UNILEVER NV.
Ledeboer AM, Verrips CT, Visser CT, Janowicz ZA, Hollenberg CP;
WPI; 86-063249/10.
                                                                                                                                                                                                                                                                                                                                                                                                   07-DEC-1998 (first entry)
HSV-2 strain SB5 Contig ID 101 DNA sequence.
HSV-2 strain SB5; immunological response induction; therapy;
HSV-2 strain SB5; immunological response induction; therapy;
Harpes simplex virus type 2.

Key
Coation/Qualifiers
CDS
345. 1253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "encoded protein shown in W72013" complement (7434. .7547)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "encoded protein shown in W72007"
complement (1865. .2134)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "ORF#2 protein"
/note= "encoded protein shown in W72008"
complement (2234. .2371)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "ORF#3 protein"
/note= "encoded protein shown in W72009"
complement (2523. .3566)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "encoded protein shown in W72010"
complement (3454. .4170)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note- "encoded protein shown in W72011"
complement (4489. .5790)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "encoded protein shown in W72012"
complement (5809. .7011)
                                                                                                                                                                     1258 G;
                                                                                                                                                                                                                                                                                     Align seg 1/1 to reverse of: N60174 from: 1 to: 4775
                                                                                                                                                                                                             Length: 6
Gaps: 0
Percent Identity: 83.333
                                                                                                                                                                     1277 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/product= "ORF#1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= g
/product= "ORF#7 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'product- "ORF#5 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product- "ORF#6 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "ORF#4 protein"
                                                                                                                                                                    1170 A;
                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
ID V62131 standard; DNA; 9217 BP.
                                                                                                                                                                                                                                                                                                        alignment_block:
US-08-653-294-7 x N60174/rev
                                                                                                                                                                                                                                                                                                                                                  seq_name: N_Geneseq_36:V62131
                                                                                                                                                                                              alignment_scores:
Quality: 28.00
Ratio: 4.667
                                                                                                                                                                                                                         Ratio: 4.667
Percent Similarity: 100.000
                                                                                                                                                          surfactant products.
Sequence 4775 BP;
                               P-PSDB: P60229
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Claim 1; Page 175-179; 748pp; English.

This sequence represents a Herpes simplex virus type-2 (HSV-2) DNA sequence of the invention. This sequence was isolated from HSV-2 strain SB5 (deposited as APCC VR-2546), is designated Contig ID 101, and encodes 8 HSV-2 proteins. The proteins can be used for the treatment or prevention of disease, to induce an immunological response in a mammal or to identify inhibitors, activators or novel antivirals. Antagonists of the proteins can be used to inhibit a viral polypeptide. The DNA sequence or a vector containing it can also be used to induce an immunological
                                                                                                    14-MAY-1998.
31-027-1997; US-049018.
09-UTN-1995; US-049018.
04-NOV-1996; US-030279.
(SMIK ) SMITHKINE BEECHAM CORP.
(SMIK ) Leary JJ;
WPI: 98-286847/25.
WPI: 98-286847/25.
Herpes simplex virus type-2 sequences - useful in, e.g. prevention and treatment of infection or inducing immunological response in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-DEC-1998 (first entry)
HSV-2 strain SB5 Contig ID 3 DNA sequence.
HSV-2 strain SB5: immunological response induction; therapy;
antiviral identification; viral protein inhibitor; ss.
Herpes simplex virus type 2.
/*tag= h
/product= "ORF#8 protein"
/note= "encoded protein shown in W72014"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in W72142"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W72140'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 9217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 6
Gaps: 0
Percent Identity: 83.333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                디
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hote= "encoded protein shown
3239. .8352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product- "ORF#4 protein"
/note- "encoded protein shown
8775. .9977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "ORF#2 protein"
/note= "encoded protein shown
4028. .5563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to reverse of: V62131 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2837 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'product- "ORF#1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1531. .2775
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1594 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               V62164 standard; DNA; 15899 BP. V62164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3266 TACCGCCTGGCGGTCCGC 3249
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Ratio: 4.667
Percent Similarity: 100.000
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US-08-653-294-7 x V62131/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          response in a mammal.
Sequence 9217 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
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/product- "ORF#5 protein"

CDS

CDS

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CDS

CDS

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Claiming the control of control co
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Herpes simplex virus type-2 sequences - useful in, e.g. prevention and treatment of infection or inducing immunological response in
                                                                                                                                                                                                                                                                                                                                                                                                      /product "ORF#5 protein"
hote "encoded protein shown in W72163"
8775. 9893
/*tag f
                                                                                                                                                                                                                                                                                                                                      /product= "ORF#4 protein"
/hote= "encoded protein shown in W72162"
7392. :8573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="ORF#8 protein"
/note="encoded protein shown in W72166"
12247. .12516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note- "encoded protein shown in W72169"
                                                                                                                                                                                                                         /product= "ORF#3 protein"
/note= "encoded protein shown in W72161'
6835. .6948
/*tag= d
                                                                                                                                                                    in W72160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note- "encoded protein shown in W72164' 0212. .11858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in W72167'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-MAY-1998.
131-0CT-1997; U20016.
09-JUN-1997; US-049018.
04-NOV-1996; US-032079.
(SMIK) SMITHKLINE BEECHAM CORP.
Chan JY, Dabrowski-Amaral CE, Delvecchio AM, Dillon SB, Esser RM, Leary JJ;
WPI; 98-286847y JJ;
WPI; 98-286847y Z5.
                                                                    in W72159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in W72165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= g
/product= "ORF#7 protein"
/note= "encoded protein shown
121010. .12147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= 1
/product= "ORF#9 protein"
/note= "encoded protein shown
complement (13004. .13912)
                                           /product- "ORF#1 protein"
/note- "encoded protein shown
complement (1553, .2428)
                                                                                                                                        /product "ORF#2 protein"
/note "encoded protein shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'product- "ORF#6 protein"
                                                                                                                                                                                        2714. .4159
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.00
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Quality:
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                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Continued to the control of the control of the control of the control of the invention. This sequence was isolated from HSV-2) DNA sequence of the invention. This sequence was isolated from HSV-2 strain september of the invention. This sequence was isolated from HSV-2 strain SBS (deposited as ATCC VR-2546), is designated Contig ID 2, and encodes ID HSV-2 proteins. The proteins can be used for the treatment or to dentify inhibitors, activators or nowel antivirals. Antagonists of the proteins can be used to inhibit a viral polypeptide. The DNA sequence or a vector contraining it can also be used to induce an immunological response in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-JAN-1999 (first entry)
HSV-2 strain SB5 Contig ID 12 DNA sequence.
HSV-2 strain SB5; immunological response induction; therapy; antiviral identification; viral protein inhibitor; ss.
Herpes simplex virus type 2.
Key
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= j
/product= "ORF#10 protein"
/note= "encoded protein shown in W72148"
                                                                    product= "ORF#6 protein"
note= "encoded protein shown in W72144"
                                                                                                                                                                                                                                                                                                                                                                                         /note= "encoded protein shown in W72147" complement (14409. 15317)
"encoded protein shown in W72143"
                                                                                                                                                                                        /note- "encoded protein shown in W72145" 13415. 13552
                                                                                                                                                                                                                                                                                              /note= "encoded protein shown in W72146"
13652. .13921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 6
Gaps: 0
Percent Identity: 83.333
                                                                                                                                                                                                                                                                                                                                              /*tag= i
/product= "ORF#9 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: 15899
                                                                                                                                                  /*tag= g
/product= "ORF#7 protein"
                                                                                                                                                                                                                                                                    /product- "ORF#8 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
ID V62175 standard; DNA; 16812 BP.
AC V62175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: V62164 from: 1
                                                                                                                         11616. .12968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .11297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: N_Geneseq_36:V62175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.00
                                                                                                                                                                                                                                                     /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-08-653-294-7 x V62164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
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14-SEP-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       activity
 Human secreted protein 5' EST EEQ ID NO: 109.

Human secreted protein, EST: expressed sequence tag; diagnosis;

Human; secreted protein, EST: expressed sequence tag; diagnosis;

forensic; gene therapy: chromosome mapping; signal peptide;

upstream regulatory sequence; cytokine activity; cell proliferation;

differentiation; haematopoiesis regulation; tissue growth regulation;

reproductive hormone regulation; chemocactic; chemokinetic; haemostatic;

thrombolytic; anti-inflammatory; tumour inhibition; ds.
                                                                                                                                                                                                                                                                                                                                                sequences exhibit no more than 90% homology to a human
                                                                                                                                                                                                                                              23-SEP-1994 (first entry)
Human genome fragment (Preferred).
Brain: placenta: bone marrow; genetic analysis; gene mapping;
detection; homology; human; adrenal tissue; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio: 4.500 Gaps: 6
Percent Similarity: 100.000 Percent Identity: 83.333
Gaps: 0
Percent Identity: 83.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 G;
                                                                                     to: 16812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36 C;
                                                                                Align seg 1/1 to: V62175 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: Q77254 from: 1
                                                                                                                                                                                                                    077254 standard; DNA; 186 BP.
                                                                                                                             11115 TACCGCCTGGCGGTCCGC 11132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X51895 standard; DNA; 278 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TyrArgLeuAlalleArg 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TyrArgLeuAlaileArg 6
Ratio: 4.667
Percent Similarity: 100.000
                                                                                                                                                                         seq_name: N_Geneseq_36:Q77254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence known per se.
Sequence 186 BP;
                                          alignment_block:
US-08-653-294-7 x V62175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-08-653-294-7 x Q77254
                                                                                                                                                                                                      seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                           Homo sapiens.
WO9401548-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9906552-A2
                                                                                                                                                                                                                                                                                                                                        20-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to (A) or
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NAME OF THE PART O

11-FEB-1999

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X1787 to X52019 represent 5 secreted broteins given in Y12987 to Y1319, secreted proteins, and encode the proteins given in Y12987 to Y1319, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation/differentiation activity, haematopolesis regulating activity, tissue growth regulating activity, chemotractic/chemokinetic activity haemostatic and thrombolytic activity. receptor/ligand activity, anti-inflammatory activity, tumour inhibition activity or other activities. The products can be used in forensic, gene therapy or other activities. The products can be used in forensic, gene therapy the signal peptide can be used for directing extracellular secretion of the signal peptide can be used for directing extracellular secretion of a polypeptide into a membrane, or importing a polypeptide into a cell.

Sequence 278 BP; 95 A; 56 C; 58 G; 67 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence encoding new physiologically active polypeptide with antitumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; P81068.

New physiologically active polypeptide used as antitumour agent -
obtd. by culturing recombinant Escherichia coli cell transformed by
plasmid contg. DNA region coding the polypeptide
Claim 2 (4); Page 670; 20pp; Japanese.
A recombinant microorganism cell transformed by recombinant plasmid
contg. the DNA region coding for the polypeptide is cultured. The
polypeptide is isolated from the resulting culture. The microorganism
                                                                                                                                                            products
                                                                                                                                                    New isolated brain-derived nucleic acids - used to develop in which may have cytokine, immune, regulatory, haematopoiesis regulating, anti-inflammatory or tumour inhibition activity claim i; Page 255; 577pp; English.

X51787 to X52019 represent 5' expressed sequence tags (ESTS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps: 6 Gaps: 0 Percent Identity: 83.333
31-JUL-1998; IB1236.
01-AUG-1997; US-905223.
(GEST ) GENSET.
WPI; 99-LA; Dumas Milne Edwards J, Lacroix B;
WPI; 99-L3782/13.
P-PSDB; Y13095.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>:</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antitumour; Escherichia coli; ss.
Key
Location/Qualifiers
mat_peptide 1. .450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
ID N81494 standard; DNA; 450 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 TACAGACTAGCTCTGCGC 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is pref. Escherichia coli.
Sequence 450 BP; 95 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality: 27.00
Ratio: 4.500
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TyrArgLeuAlaileArg 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: N_Geneseq_36:N81494
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16-MAR-1987; 059007.
16-MAR-1987; JP-059007.
(TEIJ) Teijin Kk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: X51895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-08-653-294-7 x X51895
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WPI; 99-081273/07.

New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis claim 1; Page 840-841; 1150pp; English.

X20500-21243 represent polynucleotide sequences from the genome of Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detecting diseases related to Borrelia infections in animals, and for the production of biosynthetic products such as enzymes.

Sequence 2535 BP; 651 A; 831 C; 597 G; 455 T;
               05-WAY-1999 (first entry)
Polynuclectide sequence from the genome of Treponema pallidum.
Treponema pallidum infection; syphilis; Borrelia infection; animal; enzyme production; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This polynuclectide encodes a thermostable phosphatase, designated 31phl, of Thermococcus 9N-2. The invention relates to claimed 31phl, of Thermococcus 9N-2. The invention relates to claimed 31phl, of Thermococcus 9N-2. The invention relates to claimed belonged clotdes (see V03301-20) coding for novel thermostable phosphatases (see W42380-95). Claimed vector and host cells are used to produce the enzymes, which can be used in a claimed method to hydrolyse phosphate bonds. They can also be used in enzyme labelling processes, in certain recombinant DNA techniques, in ELISA immunoassays, in enzyme linked gene probes, in research applications for removing 5' phosphates in polynucleotides prior to baking industries. Polynucleotides can also be used as probes. Sequence 5520 Bp; 1297 A; 1491 C; 1587 G; 1145 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-50N-1998 (first entry)
Thermococcus 3N-2 phosphatase (21phl) gene.
Alkaline phosphatase; thermostable enzyme; thermophilic bacterium; food; detergent; baking; ss.
Thermococcus sp. strain 9N-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermostable phosphatase(s) - useful in pharmaceutical, food, detergent, and baking industries
Claim 12; Page 77-81; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 6
Gaps: 0
Percent Identity: 83,333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JUN-1997; U10784.

19-JUN-1996; US-033752.

(RECO-) RECOMBINANT BIOCATALYSIS INC.

MATHUR E. Lee E. Mathur EJ;

WPI; 98-062851/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to reverse of: X20674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
ID V03311 standard; DNA; 5520 BP.
                                                                                                                                                                                                                                 23-JUN-1998; U13041.
24-JUN-1997; US-050667.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                327 TACCGGCTTGCGCTGCGG 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-08-653-294-7 x X20674/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: N_Geneseq_36:V03311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality: 27.00
Ratio: 4.500
Percent Similarity: 100.000
                                                                                                                                             Treponema pallidum WO9859034-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                           30-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 - DEC - 1997
                                                                                                                                                                                                                                                                                                                             Fraser CM;
New polynucleotides encoding human secreted proteins - derived from
e.g. human blood, kidney, foetal lung, placenta, testes, brain,
e.g. human blood, kidney, foetal lung, placenta, testes, brain,
ovary, pituitary, retina and colon cDNA libraries.
Claim 1; Page 151; 618pp; English.
The present sequence represents a human expressed sequence tag (EST).
The present sequence represents a human expressed sequence tag (EST).
The polynucleotide, which is a secreted EST, and the encoded protein
are predicted to have useful biological activities which would make
them suitable for treating, preventing or ameliorating medical
conditions in humans and animals, although no supporting data is
given. Suggested activities include nutritional activity, immune
stimulating or suppressing activity, haematopolesis regulating
activity, tissue growth activity, haematopolesis regulating
activity, receptor/ligand activity, activin/inhibin activity,
cadherin/rumour invasion suppressor activity, unmour inhibition
cativity. The polynucleotide may also be useful for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST clone CH421.
Human; secreted protein; expressed sequence tag; EST; haematopolesis; tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic; receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GEMY ) GENETICS INST INC.
Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D,
Racie LA, Spaulding V, Treacy M;
WPI; 99-07007/706.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
Gaps:
Percent Identity: 83.333
                                                                                   Length: 6
Gaps: 0
Percent Identity: 83.333
                                                                                                                                                                                                                                                                                        Align seg 1/1 to reverse of: N81494 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: V89229 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
ID V89229 standard; cDNA; 462 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: 27.00
Ratio: 4.500
Percent Similarity: 100.000
                                                                                                              Ratio: 4.500
Percent Similarity: 100.000
                                                                                                                                                                                                     alignment_block:
US-08-653-294-7 x N81494/rev
                                                                                                                                                                                                                                                                                                                                                      1 TyrArgLeuAlaileArg 6
                                                                                                                                                                                                                                                                                                                                                                                    seq_name: N_Geneseq_36:V89229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-APR-1998; U06955.
10-APR-1997; US-838821.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-653-294-7 x V89229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
WO9845436-A2.
                                                          alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
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seq_documentation_block: ID X20674 standard; DNA; 2535 BP.

seg_name: N_Geneseg_36:X20674

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The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (752134 to V52524) recorded on it, or a representative fragment or a sequence at least 95% identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 to 391 (V52134 to V52524) are genomic fragments from Streptococcus monemonate. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         by a process comprising: (a) acreening agenomic DNA library using as probes a target sequence defined by any of the sequences in SEQ ID NO:1 to 31, identifying members of the library which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating mRNA, DNA or cDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from the fragment of the S. pneumoniae genome to prime the amplification and isolating the amplified sequences. The computer readable medium can be used in a computer-based system for identifying fragments of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5. pneumoniae genome of commercial importance, or expression modulating fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, and pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-CT-1997; U19588.
31-CT-1996; U5-029960.
(HUMA-) HUMAN GENOME SCI INC.
Barash SC, Choi GH, Dillon PJ, Dougherty BA, Fannon M,
Kunsch CA, Rosen CA;
WPI: 98-27225/24.
Computer-readable medium with recorded Streptococcus pneumoniae
Polynucleotide sequences - useful in diagnostic kits and assays, and
pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pneumoniae genome fragment SEQ ID NO:10.
Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay; computer readable medium, vaccine; pharmaceutical composition; ds. Streptococcus pneumoniae.
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                           Quality: 27.00 Length: 6
Ratio: 4.500 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 83.333
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Sequence 9897 BP; 3110 A; 1980 C;
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ID V52143 standard; DNA; 9897 BP.
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                                                                                                                             alignment_block:
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Align seg 1/1 to reverse of: V52143 from: 1 to: 9897

Gaps: 0 Percent Identity: 83.333

alignment_scores:
Quality: 27.00
Ratio: 4.500
Percent Similarity: 100.000

alignment_block: US-08-653-294-7 x V52143/rev

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1 TyrArgLeuAlaIleArg
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W83178 mf27g02.rl Soares mou
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 205)

Evkuda; S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Radora, K., Ragawa, I., Kadi, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Shipata, Y., Shigemoto, Y., Shiraki, T., Sato, K., Shibata, K., Shigemoto, Y., Shiraki, T., Sato, K., Shibata, Y., Sugahara, Y., Suzuki, H., Takahshi, F., Tateno, M., Tominaga, N., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yoshiki, M., Watanabe, S., Yamamura, T., Yasunishi, A., Yoshiki, M., Batanabe, S., Yamamura, T., Yasunishi, A., Yoshiki, M., H. 1999)

In Oppublished (1999)

On May 18, 1998 this sequence version replaced gi:3137512.
Contact: Yoshikide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center, Genome Calboratory
The Institute of Physical and Chemical Research (RIKEN), Genomic
                                                                                                                                                                                                                       AV344569 205 bp mRNA EST 12-NOV-1999 AV344569 RIKEN full-length enriched, adult male olfactory brain Mus musculus cDNA clone 6430545L17 3', mRNA sequence.
AV344569.1 GI:6385628
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Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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Hea: +81-2288-5-9013

Fax: +81-298-36-9098

Email: genome-res@rtc.riken.go.jp,

Suklihttp://genome.rtc.riken.go.jp,

Saski,N., Izawa,M., watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,

Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
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Please visit our web site (http://genome.rtc.riken.go.jp)
further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gb_gss11:AQ327017
gb_gss8:AQ051483
gb_est44:AF122505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gb_est11:AA216201
gb_est33:AV097218
gb_est29:AI556167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gb_est12:AA305015
gb_est9:AA111469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence
gb_est43:AV344569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gb_gss11:AQ303382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1:AQ327017
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gb_est23:A1098478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_gss9:AQ095977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gb_est40:AW1472
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70
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VERSION
KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
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JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                           ORIGIN
              1 (bases 1 to 235)
Johnson, S.L., Blumberg, B., Song, J., Clifton, S., Hillier, L.,
Johnson, Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y.,
Person, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R.,
Waterston, R., and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: estewaton.wustl.edu
Library constructed by Bruce Blumberg
Library normalized by Jihwan Song
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clone distribution information for
this library can be found through Research Genetics, visit their
web page at: http://www.resgen.com/
Seq primer: -400P from Gibco.
contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dal6c03.x1 normalized Xenopus laevis gastrula Xenopus laevis cDNA clone xENOPUS_SOURCE_ID:xInga001n05 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WashU Xenopus EST project, 1999
Unpublished (1999)
On Dec 20, 1995 this sequence version replaced gi:1135577.
On Dec 20, 1995 this sequence version replaced gi:1135577.
Octact: Stephen L. Johnson/WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="xENOPUS_SOURCE_ID:x1nga001n05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 205
                                                                                                                                                                                                                                                                                                                                                    Gaps: 6
Gaps: 0
Percent Identity: 100.000
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Xenopus laevis
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US-08-653-294-7 x AV344569/rev
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Percent Similarity: 100.000
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LOCUS AW147227
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ORGANISM
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ORIGIN
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VERSION
KEYWORDS
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JOURNAL
COMMENT
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/clone_lib="normalized Xenopus laevis gastrula"
/tissue_type="gastrula (stages 10.5, 11.5 mixed)"
/lab_lost="Yop:10 F."
/note="Wettor: pBluescript SK-; Site_1: ECORI; Site_2:
XhOI; CDNA was prepared from 2ug of poly A+ RNA (equal parts from stage 10.5 and stage 11.5 gastrulae).
ECORI.XhOI cut CDNA was then ligated into UniZap-xR (Stratagene) with ECORI at the 5' end and XhOI at the 3' end. SS-library phagemids were prepared by mass excision from the original library and normalized by hybridization to blotinylated driver (prepared from the same library by PCR) to Cot-omega of 11. After removal of hybrids and excess driver by streptavidin sepharose chromatography, the ss-phagemids were made double stranded and electroporated into Top-10 F'. Original library contruction by Bruce Blumberg (Cho et al. 1991 Cell 67, 111-1120). Normalized by Jihwan Song (Song, Cho and Blumberg, unpublished)."
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S Johnson, S.L., Blumberg, B., Song, J., Clifton, S., Hillier, L.,
Johnson, S.L., Blumberg, B., Song, J., Clifton, S., Hillier, L.,
Pape, D., Marthn, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y.,
Parson, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R.,
Wash Yacopus EST project, 1999

Unpublished (1999)

On May 1, 1997 this sequence version replaced gi:2059622.

Other_ESTs dalfc03.x1

Contact: Stephen L. Johnson/WashU Xenopus EST project, 1999
WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, Mo 63108, USA

Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Library constructed by Bruce Blumberg
Library normalized by Jihwan Song
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Kenopus clone distribution information for
this library can be found through Research Genetics, visit their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AW147713 246 bp mRNA EST 30-NOV-1999 da16c03.yl normalized Xenopus laevis gastrula Xenopus laevis cDNA clone XENOPUS_SOURCE_ID:xlnga001n05 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 235
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Ratio: 4.833 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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Seg primer: -40RP from Gibco.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AW147713
AW147713.1 GI:6195609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-08-653-294-7 x AW147227/rev
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LOCUS AW147713
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UJ5336 360 bp mRNA EST 08-AUG-1994 CELKO31FXF Yuji Kohara unpublished cDNA Caenorhabditis elegans CDNA Calone yk31f10 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_llb="Oncorhynchus mykiss Kidney infected by Infectious hematopoletic necrosis virus"
//tissue_type="Kidney infected by infectious hematopoletic necrosis virus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/db_xxef="taxon:6239"
/clone="yk31f10"
/clone="jk31f10"
/clone="jk31f10"
/sex="hermaphrodite, male"
/tissue_type="whole animal"
/do_stage="whole animal"
/do_stage="whole animal"
/do_stage="whole animal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Toward an expression map of the C.elegans genome Unpublished (1994)
Contact: Yuli Kohara
Gene Library Lab
National Institute of Genetics
Yata 1111, Mishlam, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                       to: 305
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Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                 Quality: 29.00 Length: 6
Ratio: 4.833 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
1. .360
                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to reverse of: AU081183
                                                                                         g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to reverse of: D36336
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                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-7 x AU081183/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                             257 TACCGTTTGGCAATCCGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D36336.1 GI:528262
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C
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US-08-653-294-7 x D36336/rev
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Ratio: 4.833
Percent Similarity: 100.000
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LOCUS D36336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seg_name: gb_est1:D36336
                                                                                       67
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JOURNAL
COMMENT
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AUTHORS
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             1...246
//organism="Xenopus laevis"
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//do_xref="taxon:8355=evis"
//do_xref="taxon:8355=evis"
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//clone="XENOPUS_GOURCE_ID:xinga001n05"
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//lab_bost="Top-10.F"
//note="Vector: pBluescript SK-: Site_1: EcoRI; Site_2:
XhOi; cDNA was prepared from Cop poly A+ RNA (equal parts from stage 10.5 and stage 11.5 gastrulae).
ECORI.xhOi cut cDNA was then ligated into Unlap.xR
(Stratagene) with EcoRI at the 5' end and XhOI at the 3' end. SS-library phagemids were prepared by mass excision from the original library and normalized by hybridization to biotinylated diver (prepared from the same library pCR) to Cot-omega of 11. After removal of hybrids and excess driver by streptavidin sephancose chromatography, the ss-phagemids were made doluble stranded and electroporated into Top-10 F'. Original library contruction by Bruce Blumberg (Cho et al. 1991 Cell 67, 1111-1120). Normalized by Jihwan Song (Song, Cho and Blumberg, unpublished)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygil;
Meopterygil; Teleostel; Euteleostel; Protacanthopterygil;
Salmoniformes; Salmonidae; Oncorhynchus.

1 (bases 1 to 305)
Sakai,M and Kono,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
LOCUS AU081183 305 bp mRNA EST 15-NOV-1999
DEFINITION AU081183 Oncorhynchus mykiss Kidney infected by infectious hematopoietic necrosis virus Oncorhynchus mykiss cDNA clone KN4, mRNA sequence.
ACCESSION AU081183. GI:6431531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mayazaki University
1-1 nishi gakuenkibanadai, Miyazaki, Miyazaki 889-2192, Japan
Email: a0b208u@cc.miyazakiu.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The EST analysis of kidney and gill cells rainbow trout, Oncorhynchus mykiss, infected with infectious hematopoletic necrosis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
On Jun 5, 1998 this sequence version replaced gi:3189172.
Contact: Masahiro Sakai
Faculty of Agriculture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps: 0 0 0000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: AW147713 from: 1 to: 246
    Location/Qualifiers
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Ratio: 4.833
Percent Similarity: 100.000
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US-08-653-294-7 x AW147713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63
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                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
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Wed Feb

176 TATCGTCTGGCGATTCGG 159

seq_name: gb_est24:AI165099 seq_documentation_block: LOCUS A1165099 A1165099 A1165099.1 GI:3856384

ACCESSION VERSION KEYWORDS

ORGANISM

AUTHORS REFERENCE

JOURNAL MEDLINE COMMENT

TITLE

DEFINITION

```
Homo saplens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
Eutheria; Primates; Catarrhini; Hominidae; Homo.
Eutheria; Primates; Catarrhini; Hominidae; Homo.
E (10 Septembras; C.G., Zackrone, K.D., Smith, T., Tipton, S., Schmidt, S.,
Traicoff, R., Abajian, C., Blanchard, A., West, A. and Hood, L.E.
Construction of a Characterized Clone Resource for Genomic
Sequencing: Generation and Preliminary Analysis of 20,000 Sequence
I agged Connectors
Unpublished (1997)
Contact: Mahairas GG, Zackrone KD, Hood L
University of Washington
Seattle, WA 99195, USA
Tel: (206) 685-7301
Email: kzackron@u washington.edu
Sequence Tagged Connector
Plate: CT 328 row: O column: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditina; Rhabditina; Rhabditioidea; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 376)
Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A.,
Sano,M., Miyata,A. and Nishigaki,A.
Expression map of the C.elegans genome
                          B31284 367 bp DNA GSS 17-0CT-1997 HS-1007-A2-H08-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 328 Col=16 Row-O, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note"Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH108" 54 c 89 g 137 t
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LOCUS C64475 Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA CLOSSION C64475 YX359C8 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .367
/organism-"Homo sapiens"
/db_xref="taxon:9606"
/db_vred="plate=CT 328 Col=16 Row=O"
/clone_lib="CIT Human Genomic Sperm Library C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality: 29.00 Length: 6
Ratio: 4.833 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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Location/Qualifiers
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                                                                                                                                            B31284.1 GI:2530653
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US-08-653-294-7 x B31284
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seq_documentation_block:
LOCUS B31284
                                                                                                                     edneuce.
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                                                                                                                                       ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pBluescript SK; Site_1: SalI; Site_2: NotI; Cambial region tissues, including developing xylem, the meristematic cambial zone and the developing and mature philoem, was harvested from 1.5 m actively growing trees. CDNA was prepared and cloned into lambda gt22a. DNA was isolated and subcloned into pBluescript SK using SalI and NotI restriction enzymes."

3 others
                                                                                                                                                                                                                                                                                                        Populus tremula x Populus tremuloides.
Populus tremula x Populus tremuloides
Populus tremula x Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Spermatophyta; Magnoliophyta; eudicotyledons; core-
eudicots; Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.
I (bases I to 366)
Sterky,F., Regan,S., Karlsson,J., Hertzberg,M., Rohde,A.,
Holmberg,A., Amini,B., Bhalerao,R., Larsson,M., Villarroel,R., Van
Gustafsson,P., Uhlen,M., Sundberg,B. and Lundeberg,J.
Gene discovery in the wood forming tissues of poplar: Analysis of
5,692 expressed sequence tags
                                                                                                                                            AI165099 366 bp mRNA EST 03-DEC-1998 A075p18u Hybrid aspen plasmid library Populus tremula x Populus tremuloides cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            On Jan 17, 1998 this sequence version replaced gi:1900778. Contact: Sterky F
Contact: Of Biotechnology
Royal Institute of Technology (KTH)
Technikringen 34, S-100 44 STOCKHOLM, Sweden
Tel: +46 8 790 8287
Fax: +46 8 24 54 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Populus tremula x Populus tremuloides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 95 (22), 13330-13335 (1998)
99007314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:47664"
/clone_lib="Hybrid aspen plasmid library"
/fssue_type="cambial region"
/dev_stage="l.5 m actively growing tree"
/lab_host="E.coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: 366
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Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BACKWARD: GCTTCCGCTCGTATGTGTGTG
Seq primer: CGTTCTAAAACAGCGCCAG
High quality sequence stop: 366.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: fredrik@biochem.kth.se
PCR PRimers
FORWARD: AAAGGGGGATGTGCTGCAAGGCG
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source

FEATURES

Align seg 1/1 to reverse of: AI165099

188 TATCGCCTTGCTATCCGA 171

seq_name: gb_gss3:B31284

l TyrArgLeuAlaIleArg 6

alignment_block: US-08-653-294-7 x AI165099/rev

Ratio: 4.833 Percent Similarity: 100.000

29.00

Quality:

alignment_scores:

107

BASE COUNT

ORIGIN

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Contact: Soares, MB Program for Rat Gene Discovery and Mapping University of Iowa Fat Gene Discovery and Mapping University of Iowa Fat: 319 335 9565
Fax: 3
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//dev_stage="Adult"
//lab_host="DH10B (Life Technologies)"
//note="Vector: pT773D-Pac (Pharmacia) with a modified
polyllnker; Site_1: Not 1; Site_2: Eco Ri; The UI-R-C1
library is a subtracted library derived from the UI-R-C0
library, which is a subtracted library derived from the UI-R-A1 and UI-R-E1 libraries; The UI-R-A1 library
consisted of a mixture of individually tagged normalized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Norway rat.

Stattus norvegicus

Eukaryota; Marmalia; Craniata; Vertebrata; Mammalia;

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

I (bases 1 to 394)

Bonaldo, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene
1. .391
/organism-"Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=2263 Col=21 Row=J"
/clone=lib="CIT Approved Human Genomic Sperm Library D"
                                                                                                                                                                                                         /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
73 c 65 g 148 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS AI044481 394 bp mRNA EST 11 LOCUS
DEFINITION UI-R-C1-jw-d-09-0-UI.S1 UI-R-C1 Rattus norvegicus CDNA Clone
UI-R-C1-jw-d-09-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On Jan 19, 1998 this sequence version replaced gi:2287562
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps: 0
Percent Identity: 100.000
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1. 394
/organiam="Rattus norvegicus"
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/db_xref="taxon:10116"
/clone="UI-R-C1-jw-d-09-0-UI"
/clone_11b="UI-R-C1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: AQ804632 from: 1
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Percent Similarity: 100.000
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US-08-653-294-7 x AQ804632
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Ratio:
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 391)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQ804632 391 bp DNA GSS 09-AUG-1999 HS_2263_B1_E11_T7C CIT Approved Human Genomic Sperm Library D Homo saplens genomic clone Plate=2263 Col=21 Row=J, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).

BAC end Web Server: http://www.htsc.washington.edu
Plate: 2263 row: J column: 21
Seg primer: T7
Class: BAC ends
High quality sequence stop: 391.
Location/Qualifiers
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             Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1288442.
Contact: Yuji Kohara
Gene Library Lab
National Institute of Genetics
Yata 111, Mishima, Shizuoka 411, Japan
Fax: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
                                                                                                                                                                                                                                                                                                                                   1. 376
/organism="Caenorhabditis elegans"
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/strain="CB1489 him=8(e1489)"
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/gereref="waried"
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High Throughput Sequencing Center
University of Washington
VGO Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 6
Gaps: 0
Percent Identity: 100.000
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AQ804632.1 GI:5721964
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US-08-653-294-7 x C64475/rev
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Percent Similarity: 100.000
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LOCUS AQ804632
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AUTHORS
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Wed Feb

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/sex="remale"
/tissue_type="normal surface epithelium"
/tab_host="normal surface epithelium"
/lab_host="normal surface epithelium"
/note="Organ: ovary: Vector: pAMP10; mRNA made from normal
ovarian epithelium, cDNA made by oligo-dT priming.
Non-directionally cloned. Size-selected on agarose gel,
average insert size 600 bp. Reference: Krizman et al.
(1996) Cancer Research 56:3380-5383."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 401)
Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
Use of BAC End Sequences for Sequence-Ready Map Building (1998)
Other GSSS: RPCIII-3505.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Research Genetics (info@resgen.com), BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
LOCUS AQ046586 401 bp DNA GSS 14-APR-1999
DEFINITION RPCII1-3505.TK RPCI-11 Homo sapiens genomic clone RPCI-11-3505,
genomic_survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 6
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from: 1
                                                                     /clone="IMAGE:1192220"
/clone_lib="NCI_CGAP_Ov5"
               /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .401
/organism="Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="GDB:7513396"
/db_xref="taxon:9606"
                                             /db_xref="taxon:9606"
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US-08-653-294-7 x AA653822/rev
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Percent Similarity: 100.000
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Ratio:
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KEYWORDS
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libraries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, and muscle. The UI-R-EI library consisted of a mixture of individually tagged normalized libraries constructed from 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted ilbrary (UI-R-CI) was constructed as follows: PCR amplified colon miserts from UI-R-CO clones from which 3' ESTs had been derived was used as driver in a hybridization with the UI-R-CO library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated the UI-R-CI library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   on Sep 12, 1996 this sequence version replaced gi:1392727.

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1552.

Tel: (401) 496-1552.

Tel: (All 496-1552)

Tissue Procurement: Andrew Berchuck, M.D., Elise Kohn, M.D., Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D., CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NI-CGAP clone distribution information can be found through the I.M.A.G.E., Consortium/Link at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA653822 399 bp mRNA EST 04-NOV-1997 nt05all.sl NCI_CGAP_Ov5 Homo sapiens cDNA clone IMAGE:1192220, mRNA sequence.
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1 (bases 1 to 399)

NGI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
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Gaps: 0
Percent Identity: 100.000
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High quality sequence stop: 398.
Location/Qualifiers
1. .399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 c
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Percent Similarity: 100.000
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US-08-653-294-7 x AI044481
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LOCUS AA653822
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DEFINITION

ACCESSION VERSION KEYWORDS ORGANISM

AUTHORS TITLE

REFERENCE

JOURNAL

COMMENT

FEATURES

alignment_scores:

BASE COUNT

ORIGIN

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Length: 6
Gaps: 0
Percent Identity: 100.000
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The Crop Biotechnology Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to reverse of: AW202244
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AQ629040.1 GI:5091432
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US-08-653-294-7 x AW202244/rev
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Ratio: 4.833
Percent Similarity: 100.000
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ORGANISM
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COMMENT
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KEYWORDS
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Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Shoemaker, R., Marra, M., Hiller, L., Kucaba, T., Martin, J.,
Rhanna, A., Bolla, B., Marra, M., Hiller, L., Kucaba, T., Martin, J.,
Bock, C., Wylle, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Hitter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; This cDNA library was constructed from mRNA isolated from cotyledons of 3- and 7-day-old Williams seedlings which were propagated on paper towels with distilled water. The cotyledons were flash-frozen in liquid nitrogen, then lyophilized for 72 hours. Unequal amounts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW202244 424 bp mRNA EST 30-NOV-1999 sf12g06.yl Gm-c1027 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1027-2099 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Our Jul 7, 1999 this sequence version replaced gi:5866118.

Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
Call: (800) 430-0030 or (314) 427-3322 FAX:(888) 919-3324 or (314)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; coreeudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae;
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"

87 c 59 g 144 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1027-2099"
/clone_lib="Gm-c1027"
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High quality sequence stop: 423.
                                                                                                                                                                                                                                                                                                                                                 to: 401
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Ratio: 4.833 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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US-08-653-294-7 x AQ046586/rev
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LOCUS AW202244
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                                                                        ORIGIN
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of mRNA was used for cDNA synthesis. Stratagene's cDNA synthexix Kit (catalog number 200401) was used to synthesiz kit (catalog number 200401) was used to synthesiz the cDNA. First- stranded synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An anchor nucleotide (V-A, C, or G) was added to the 3' end of the primer ight of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Fu DNA, ligated to ECORI adapters and subsequently phosphorylated. The XNOI site within the first-strand synthesis primer was then restricted by digestion with XNOI; all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with 500 bp cutoff, using GibcoBRL Life Teachhologies' CDNA Size Fractionation Stratagene's spaluescript(tm) II XR Predigested vector (PBluescript II SK(+) that has been digested with EcoNI and XhoI, and phosphorylated by Stratagene's 97% of the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n-30). This library was constructed by DI. Paul Keim and DI. Virginia Coryell."
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
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Other name: 3N177; date: 05/28/99; Submitted to the Database of
Genome Survey Sequences (GSS) on 06/15/99; More information is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQ629040 439 bp DNA GSS 27-SEP-1999 T120064b Medicago truncatula BAC library Medicago truncatula genomic clone 03N17, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Frugoli,J., Peng,H., Ellis,L. and Cook,D.R.
Medicago truncatula genome project
Unpublished (1999)
On Mar 23, 1999 this sequence version replaced gi:3323787.
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available at 'http://chrysie.tamu.edu/medicago'; Cultivar: Medicago truncatula genotype A-17; Note: BAC end.
Seg primer: T7
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
LOCUS A0913824 486 bp DNA GSS 02-DEC-1999
DEFINITION nbeb0045M01r CUGI Rice BAC Library (EcoRI) Oryza sativa genomic clone nbeb0045M01r, genomic survey sequence.
ACCESSION A0913824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 486)
Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Identity: 100.000
                                                                                                               /organism="Medicago truncatula"
/cultivar="genotype_A17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clemson University Genomics Institute Clemson University 100 Uradan Hall, Clemson, SC 29634, USA Tel: 864 656 7288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: rwing@clemson.edu
Seq primer: GGAAACAGCTATGACCATG
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High quality sequence stop: 403
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Percent Similarity: 100.000
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                                                                                                    .439
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US-08-653-294-7 x AQ629040
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Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
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AUTHORS
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/lab_host="E. coli DH10B"

/note="Vector: padcindigo; Site_1: EcoRI; Site_2: EcoRI;
Rice is the most important food crop in the world. Half of
Rice is the most important food crop in the world. Half of
the world population, especially those inhabiting highly
populated areas of the humid tropics and subtropics, rely
on rice as their primary source of carbohydrate.

Monocotyledonous rice is a diploid plant (2n=24) with a
haploid genome equivalent of 431 Mbp (Arumqanathan and
Earle, 1991). The relatively small genome of rice, three
times larger than that of Arabidopsis, makes it suitable
for genomic studies. In order to facilitate positional
cloning, physical mapping and genome sequencing of rice,
we have constructed a BAC library from Oryza sativa,
Nipponbare variety using EcoRI as the cloning enzyme. The
library contains 55,296 clones with an average insert size
of 121 Kb providing approximatley 15 haploid genome
equivalents. The deep coverage allows the isolation a
particular sequence with a probability of 99.9 %. Three
high density filters, each containing 18,432 clones
(doubly spotted), represent the whole library for colony
screening and can be requested from the Clemson University
BAC/EST Resource Center (www.genome.clemson.edu)."

184 a 78 c 69 g 147 t
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alignment_scores:

BASE COUNT ORIGIN Quality: 29.00 Length: 6
Ratio: 4.833 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block: US-08-653-294-7 x AQ913824/rev Align seg 1/1 to reverse of: AQ913824 from: 1 to:

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

February 8, 2000, 01:29:37; Search time 122.56 Seconds (without alignments) 1.933 Million cell updates/sec Run on:

US-08-653-294-8 49 1 RENLRIALRY 10 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

188963 seqs, 23686106 residues Searched:

188963 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

A_Geneseq_36:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Peptide fragment o	702 CTL mo	•	T-cell modulating	Immunomodulatory p	2702.	밁	0	HLA-B2702 CTL modu	TL mod	HLA-B2702 84-75-84	Immunomodulating d	B2702.84-	agment	44	HLA-B2702 CTL modu	HLAB38 CTL modulat	HLA-B2702.60-84. C	HLAB38.6084. Comps	Peptide B2702.60-8	Seq	e of	ance	3 exc	32702 CTL	32702 CTL	32702	HLA-B2702.75-84(D)	HLA-B2702.75-84(T)	T-cell modulating	Immunomodulatory p	dulatory	Peptide B2702.75-8	B2702.75-
SUMMARIES	а	R41208	9	7,	751	W47265	W33784	R92912	W33795	R92907	R92908	R95428	W33778	W33791	R41205	R48286	R83090	R83093	R95416	R95422	W33794	X06801	R03142	R03144	R12463	R83094	R83095	R83096	R95425	R95426	W07513	W47267	W47269	W33788	78
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Peptide B2702.75-8 HLA-B2702 CTL modu HLA-B2702 CTL modu Peptide B2702.84-7 HLA-B2702.84-7 HLA-B2702.75-84(L) T-Cell modulating Immunomodulatory p T-Cell modulating P-Cell modulating	ALIGNMENTS	TATION TO THE STANDARD STANDAR	commonly found within larger peptide amino acids in length.  Score 49; DB 1; Length 10;  Pred. No. 0.00034;  Mismatches 0; Indels 0; Gaps 0		entry) ting peptide (B2702.75-84). tring pept
W33789 R929109 R329109 W33792 W33792 R95427 W07514 W47271 R41212	ALIG	HIA PEF HIA PEF A, PEPTI T LYME D JUNION SS I HIA SS I HIA 1115h. a 1115h. a 1115h. a 1115h. a 1115h. a 1115h. a 1115h. a	Score Score Pred.		AA.  1de ( major us ho JUNIC arham
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44444MMMMM		R41208 standard; peptide; R41208; 15.00 (first entry) Peptide fragment of Class Human leukocyte antigen; Human leukocyte antigen; Human leukocyte antigen; Howstetic disease; cytotox Synthetic disease; cytotox 3317699-A.  16-SEB-1993; U01758.  16-SEB-1993; U01758.  16-SEB-1993; U01758.  17-REB-1993; U01758.  18-REB-1993; U01758.  19-PEPTIGE CA, Krensky AM WPI; 93-03134,38.  Clayberger CA, Krensky AM WPI; 93-03134,38.  Clayberger CA, krensky AM WPI; 93-03134,38.  Claim 11; Page 54; 61pp; ETH PEPTIGE SY 10hibitide is used to mod activity, either by inhibiting CTL toxicit activity; either by inhibiting cTL toxicit activity; in parasitic dise activity in parasitic dise infection. The peptide cabind removing such and removing such and removing such activity.	his peptide sequence compounds of not more equence 10 AA; y Match Local Similarity hes 10; Conservat.	1 RENLRIALRY 	2 3062; 3062; -MAYMAY Cotox nunos nunos nunos nunos nunos -APR APR APR APR APR APR IRD )
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Compans. comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLs.

Example: Page 11: 29pp: English.

This sequence represents the alphal-helix of the human-leucocyte-associated antigen B2702 (HIA-B2702). This sequence, epitopes, and palindromes of it (such as R95428) can be used to isolate the protein p74 from a T-cell yaste. p74 is a T-cell surface membrane protein p74 from a T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein HSC70. p74 is found in a limited number of cell types, but is particularly expressed on B and T cells. p74 can be isolated by lysis of a suitable cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HIA-B2702 palindromic peptide.

Compositions comprising the extracellular fragment of p74 combined with the extracellular portion of p74 and determining the amount of binding between the candidate compound and p74. Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCS). by adding to the mix the extracellular portion of p74, in a manount sufficient to compete containing the binding of the p74 in a mount sufficient to compete containing the binding of the p74 in a manount sufficient to compete containing the binding of the p74 in a manount sufficient to compete containing the mix he extracellular portion of p74, in a manount sufficient to compete containing the binding of the p74 in an amount sufficient to compete containing the binding of the p74 in an amount sufficient to compete containing the binding of the p74 in an amount sufficient to compete containing the mix he extracellular portion of p74.
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                                 Claim 15; Page 9; 80pp; English.
R83061-R83085, R83096, and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 75-84 of the alpha-1 domain of the class I MHC HLA-B2702. These sequences can be used to extend the period of The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLs) of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIA: p74; alphal-helix; human-leucocyte-associated antigen; inhibitor; recal lysate; membrane protein; mammal; heat shock protein; Hsc70; APC; B cell; calcium influx; cytotoxic I lymphocyte; CTL; differentiation; cytolysis; antigen presenting cell.
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
donor hosts - using Class I B75-84 MHC antigen of the recipient
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 49; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 0.00034; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                               100.0%; Score 49; DB 1; Length 10; 100.0%; Pred. No. 0.00034; Live 0; Mismatches 0; Indels
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10-NOV-1993; US-150493.
(STRD) UNIV LELAND STANFORD JUNIOR.
CLayberger C, Krensky AM;
WPI; 95-194027/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R95413 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-NOV-1996 (first entry) Alphal-helix of HLA-B2702.
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Best Local Similarity 100.

Matches 10; Conservative
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R95413
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Gaps

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Treatment of auto-immune disease by admin. of peptide(s) corresp. to major histocompatibility complex antigens - esp. for delaying onset of clinical symptoms of insulin dependent diabetes by modulating T cell mediated attack on target cells

Claim 7: Page 20: 24pp: English.

WO7512-W07518 represent T-cell modulating peptides that can be used in the method of the invention. These sequences are based on a portion of the method of the invention. These sequences are based on a portion of the method of the invention. These sequences are based on a portion of the method of the invention. These sequences are based on a portion of the method of the invention of tissue in mammals. These involving T-cell mediated destruction of tissue in mammals. These peptides are used especially to treat insulin-dependent diabetes mellitus, preferably being administered during the pre-clinical stage to delay onset of the disease. Other diseases that can be treated are militus, preferably being administered during the pre-clinical stage to delay onset of the disease, Other diseases that can be treated are multius, etc. The peptides modulate T-cell mediated attack on autologous gravis, etc. The peptides modulate T-cell mediated attack on autologous cavics, performs, performins, granzymes etc. associated with T cell activation. Sequence 10 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T-cell modulating peptide #1.

T-cell modulator; autoimmune disease; tissue destruction; alphal-domain;

T-cell modulator; autoimmune disease; tissue destruction; alphal-domain;

mammal; major histocompatability complex; MHC class I; antigen; perforin;

insulin-dependent diabetes mellitus; multiple sclerosis; inflammation;

rheumatoid arthritis; psoriasis; pemphigus vulgaris; Sjogren's disease;

thyroid disease; Hashimoto's thyroiditis; myasthenia gravis; granzyme;

autologous target cell; cytokine release; r cell activation; therapy.
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Immunomodulatory peptide.
Immunomodulator; Class I HLA-B alpha-1 domain; inhibition;
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05-ARR-1996; U04710.
12-MAY-1995; US-440504.
(SANG-) SANGSTAT MEDICAL CORP.
Buelow R;
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Best Local Similarity 100.
Matches 10; Conservative
1 RENLRIALRY 10
                                                           1 RENLRIALRY 10
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Synthetic.
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27-NOV-1997.
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Conservative
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                                  1 RENLRIALRY
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WO9744351-A1.
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19-JUN-1998
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Synthetic.
 Query Match
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          Best Loca
Matches
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R92912
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Novel immunomodulatory peptide-type compound - useful for inhibiting
                                                                   The present sequence is an immunomodulatory peptide, which comprises a Class I HLA-B alpha-1 domain sequence. It can be used in a pharmaceutical composition together with a subtherapeutic dose of an immunosuppressant, to extend the period of acceptance of a transplant from a major histocompatibility complex (MHC) unmatched donor, i.e. to inhibit transplant rejection. It can also be used in
                                                                                                                                                                                                                                                                                          19-JUN-1998 (first entry)
Peptide B2702.75-84 tested for immunomodulating activity.
Immunomodulating dimer. Immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I MLA-B alpha-1 domain;
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                                                                                                                                                                           100.0%; Score 49; DB 1; Length 10; 100.0%; Pred. No. 0.00034;
                                                                                                                      the treatment of autoimmune diseases.
Peptides using the D-form amino acids are more effective
immunomodulators than their diastereomers or enantiomers.
                                                                                                                                                                                            0; Indels
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23-APR-1997; U06705.
22-MAY-1996; US-651650.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                               24-MAY-1996; US-653294,
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                           Claim 10; Page 36; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 used for detection and diagnosis
                                                                                                                                                                                                                                                                          W33784 standard; peptide; 10 AA.
                         Clayberger C, Krensky AM;
                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                    transplant rejection
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WO9744351-A1.
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                                                                                                                                                                                                                                                                                                                               rejection.
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Yothotoxic T jumphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HIA-B2702.
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R8306-R83085, R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 70-84 of the alpha-1 domain of the class I MHC HIA-B3702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLS)
                                                                                                          Gaps
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12-OCT-1995.
05-APR-1995; U04349.
05-APR-1994; US-222851.
(GTRD ) UNIV LELAND STANFORD JUNIOR.
(GTRD ) UNIV LELAND STANFORD JUNIOR.
(GTRD ) GENERAL C, KENESKY AM, Parham P;
WPI: 95-358582/46.
Extension of acceptance period of transplants from MHC unmatched Extension of acceptance period of transplants from MHC unmatched Extension of acceptance period of transplants from MHC unmatched Extension of acceptance period of transplants from MHC unmatched Extension of acceptance period of transplants from MHC unmatched Extension of acceptance period of transplants from MHC unmatched Extension of acceptance period of transplants from MHC unmatched Extension of acceptance period of transplants from MHC unmatched Extension of acceptance period of transplants from MHC unmatched Extension of acceptance period of transplants from MHC unmatched Extension of acceptance period of transplants from MHC unmatched Extension of acceptance period of transplants from MHC unmatched Extension of acceptance period of transplants from MHC unmatched Extension of acceptance period of transplants from MHC unmatched Extension of acceptance period of transplants from MHC unmatched Extension of acceptance period of transplants from MHC unmatched Extension of acceptance period of transplants from MHC unmatched Extension of acceptance period of transplants from MHC unmatched Extension of 
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Peptide BS702.70-84 tested for immunomodulating activity.
Immunomodulating dimer: immunosuppressant drug; CTL activation; transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
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100.0%; Score 49; DB 1; Length 10; 100.0%; Pred. No. 0.00034;
                                                                                                     0; Indels
                                                                                                          Mismatches
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22-MAY-1995, U08689.
24-MAY-1996, US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Beulow R, Clayberger C, Krensky AM;
WPI; 98-086530/08.
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R83061-R83085, R83090-R83096 and R92207-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702.

These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (comparate to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CILS)
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Cytotoxic I lymphocyte; CTL; major histocompatibility complex; MHC;
cytotoxic I lymphocyte; CTL; major histocompatibility complex; MHC;
ilmunosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HLA-B2702.
Synthetic:
W09526979-A1.
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100.0%; Pred. No. 0.00053;
.ive 0; Mismatches 0;
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05-APR-1994; US-222851.
(STRD) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM, Parham P;
WPI; 95-358582/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          used for detection and diagnosis.
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Best Local Similarity
Matches 10; Conserv
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Example 15; Page 36; 80pp; English.

R83061-R83085, R8309-R83096 and R92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of The peptides are administered to a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to administration for a limited period of time (compared to the lifetime modulate for a limited period of time (compared to the lifetime modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CILS) of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84). 
Yytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Compsons. comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLs.
Example: Page 12: 29pp; English.
Example: Page 18: 29pp; English.
Example: Page 28: 29pp; English.
Example: Page 20pp; English.
Example: Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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100.0%; Pred. No. 0.00073;
iive 0; Mismatches 0;
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WPI; 95-358582/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-OCT-1995.
05-APR-1995.
05-APR-1994; UGS-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                     R92908 standard; peptide; 20 AA.
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WO9513288-A1.
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Query Match 100. Best Local Similarity 100. Matches 10; Conservative

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Gaps

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Length 20;

100.0%; Score 49; DB 1; Length 20 100.0%; Pred. No. 0.00073; ive 0; Mismatches 0; Indels

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protein associated with T-cell activation in mammalian T-cells, and is
also immunologically cross reactive with the heat shock protein Hsc70.

p74 is found in a limited number of cell types, but is particularly expressed on B and T cells. p74 can be isolated by lysis of a suitable cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HLA-B2702 palindromic peptide.

Compositions comprising the extracellular fragment of p74 combined with HLA-B2702.66-84 (see R95416), induces calcium influx, and inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate compounds can be screened for their effect on the cytolysis cativity of T-cells, by combining them with the extracellular portion of p74 and determining the amount of binding between the candidate compound and p74.

Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCs), by adding to the with p74 for the binding of the p74, in an amount sufficient to compete with p74 for the binding of the p74 ilgand.
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ö Gaps ö 100.0%; Score 49; DB 1; Length 20; 100.0%; Pred. No. 0.00073; Live 0; Mismatches 0; Indels 10; Conservative Query Match Best Local Similarity Matches 10; Conserv

1 RENLRIALRY 10 11 RENLRIALRY 20 g ò

RESULT

Immunomodulating dimer peptide #1.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain; W33778 standard; peptide; 20 AA. (first entry) Homo sapiens. WO9744351-A1. 19-JUN-1998 rejection 

24-MAY-1996; US-653294. (STRD ) UNIV LELAND STANFORD JUNIOR. Beulow R, Clayberger C, Krensky AM; 27-NOV-1997. 22-MAY-1997; U08689. WPI; 98-086530/08

Will be understand the peptide(s) - based on a class I HLA-B alpha-1 domain, used for preventing rejection of transplants or treating autoimmune diseases.

Titable-1 domain, used for preventing rejection of transplants or treating autoimmune diseases.

Claim 16; Page 35: 41pp; English.

Claim 16; Page 35: 41pp; English.

This sequence represents a specifically claimed immunomodulating dimer peptide of the invention. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or C-terminal and dated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B = (R aa76-77L) (aa39-84) or (aa84-7) (laa81-a884-a hydrophobic or small amino acid; aa82 - R or L; aa83 - G or R; and as represents annion acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a class I HLA-B absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a class I HLA-B absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a class I HLA-B absent or truncated of a lass of a lass of a lass of a lass of linerast to activate CTLs. They can also inhibit the proteins of interest to activate CTLs. They can also inhibit the used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosis.

The products can also be used for detection and diagnosis.

Willy 99 '080230/08'.

New immunomodulating dimer peptide(s) - based on a class I HiA-B alpha-1 domain, used for preventing rejection of transplants or treating autoimmune diseases.

Example 1; Page 19; 41pp; English.

Peptides Wi3784-98 and Wi3778-9 were assayed for their immunomodulating activity. A peptide-type compound or variant is claimed which has activity. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acjated and/or c-terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B = the peptide-type compound comprises the formula; A-B, where A, B = the peptide-type compound comprises the formula; A-B, where A, B = the peptide-type compound comprises the formula; A-B, where A, B = the peptide-type compound comprises the formula; A-B, where A, B = the peptide type bond within the brackets. The compounds comprise amino acid sequences related to a Class I HiA-B alphal domain (positions of at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a Class I HiA-B alphal domain (positions 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CIL) from undealination with antigent peptides or proteins of interest to activate CILs. They can also inhibit the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes. The compounds arthritis and lupus enticimmune diseases, e.g. diabetes. The compounds of the control of t ö Gaps Immunomodulating dimer; immunosuppressant drug; CTL activation; transplantation; autoimmune disease; Class I HLA-B alpha-1 domain; 19-JUN-1998 (first entry)
Peptide B2702.84-75r/75-84 tested for immunomodulating activity. ö Indels Pred. No. 0.00073; Mismatches 0; Homo sapiens. WO9744351-Al. 27-NOV-1997. 22-MAY-1995; US-653294. 6STRD ) UNIV LELAND STANFORD JUNIOR. Beulow R. Clayberger C, Krensky AM; WPI; 98-086530/08. 100.0%; Pre-W33791 standard; peptide; 20 AA. Best Local Similarity 100. Matches 10; Conservative 1 RENLRIALRY 10 11 RENLRIALRY 20 rejection. Synthetic Sequence ò 윱 

Gaps ö 100.0%; Score 49; DB 1; Length 20; 100.0%; Pred. No. 0.00073; 1ve 0; Mismatches 0; Indels 100.08; Query Match
Best Local Similarity 100.
Matches 10; Conservative

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1 RENLRIALRY 10 20 ö 셤 R41205 standard; peptide; 25 AA.

R41205;
15-MAR-1994 (first entry)
Peptide fragment of Class I HLA peptide.
Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
Byarasitic disease; cytotoxic T lymphocyte; modulation.
Synthetic.
W09317699-A. RESULT 14
R41205
AC R41205
DT 15-MAR
DE PEPTIG
KW Human
KW Parazi
OS Synthe
PN W9317
PD 16-9EP
PF 25-FEB

16-SEP-1993, 25-FEB-1993; U01758.

Query Match

Sequence

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                                                              New peptide(s) based on Class I HLA antigen domains - used for modulating cytotoxic T-lymphocyte activity towards targets Claim 8; Page 53; 61pp; English.
The peptide (or a fragment of at least 10 amino acids, joined at at least one terminus to a sequence other than that of wild type HLA antigen) is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL activity in parasitic diseases and neoplasia and in studies on viral infection. The peptide can also be used for identifying CTLs which beind to it and removing subsets of CTLs from a T-cell composition.
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Example 13; Page 39; 61pp; English.

The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL infection. The peptide can also be used for identifying CTLs which bind to it and removing subsets of CTLs from a T-cell composition. This peptide is derived from the HLA-B38 antigen and corresponds Sequence 25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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Peptide fragment of HLA-1838 antigen.
Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
parasitic disease; cytotoxic T lymphocyte; modulation.
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02-MAR-1992; US-844716.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R48286 standard; peptide; 25 AA.
                                      Krensky AM;
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WPI; 93-303134/38.
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25-FEB-1993; U01758
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                                    layberger CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
409317699-A.
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R48286
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February 7, 2000, 11:54:20; Search time 117.7 Seconds (without alignments) 4.008 Million cell updates/sec Run on:

US-08-653-294-8 49 1 RENLRIALRY 10 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

142080 seqs, 47169319 residues Searched:

142080 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:* PIR_62:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	MHC class I histoc	MHC HLA-B38 chain	class I histocompa	H	н	н	class I histocompa	class I	class I	MHC class I histoc	н	н	class I histocompa	MHC class I histoc	transmembrane glyc	gene HLA B-1517 pr	lymphocyte antigen	ದ	class I	LA-B tr	ss I hist	MHC class I histoc	н	class I histocompa	MHC class I histoc	MHC class I histoc	-AW24 pro	class I	class I his	HLA-B alpha-chain
			_	<b>.</b>	m	_	<b>.</b>	_	~	m		1	6	_			10	_	_	٠,	_		_	m	7	_	<u></u>		8	7	
	Q	13850	I5446	I2930	I80168	18016	I8016	I8017	HLHU12	HLHUB8	B30345	JH0541	JH053	JH0540	A45834	I84486	16204	I8449(	13752	A3034	I59633	S2443	13712	S0711	S0353	D35997	877963	I5441	•	HO3	13751(
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	ch	0.00	0.00	0.	0.	0.	0.	0.	0.	0.	0.	0.	0	0.	<u>.</u>	0.		0.		0.			0.		0.	0.	0.	0.			
æ (	Match	100	100	100	100	100	100	100.0	100	100	100	100	100.	100	100.0	100	100	100	100	100	100	100	100	100	100	100	100	100	100	8	8
	Score	49	49	49	49	49	49	49	49	49	49	49	49	49	49	49	49	49	49	49	49	49	49	49	49	49	49	49	49	44	44
	No.		7	m	4	'n	Q	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59	30

T)	MHC class I histoc	MHC HLA-B44.2 chai	MHC class I histoc	MHC class I histoc	class I histocompa	MHC class I histoc	MHC class I lympho	class I histocompa	MHC H-2K-kml mRNA	class I histocompa	MHC class I histoc	H-2K-s - mouse	H-2K-sml - mouse	MHC class I histoc	
S25415	A45850	161861	I54442	A35997	I80174	HLHUB4	I54457	JH0537	157806	B45876	A60854	149712	149713	HLMSKK	
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362	362	362	362	364	137	359	362	365	292	362	368	368	368	369	
83.8	8.8	8.88	89.8	86.8	79.6	9.6	9.6	79.6	75.5	75.5	75.5	75.5	75.5	75.5	
44	44	44	44	44	39	39	39	36	37	37	37	37	37	37	
31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

# ALIGNMENTS

-	509	
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MFG class I histocompatibility antigen - human (fragment)
C; Species: Homo sapiens (man)
C; Accession: 138509
R; Cereb, N.; Choi, J.W.; Riu, K.Z.; Yang, S.Y.
Tissue Antigens 44, 271-273, 1994
A; Title: HiA-B*5105, a newly identified B51 IEF variant.
A; Reference number: 138509; MUID: 95176331
A; Accession: 138509
A; Accession: 138509
A; Accession: 138509
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-273 <RES>
A; Residues: 1-273 <RES>
A; Residues: GBS: 120048; OMIN: 142830
A; Genetics:
A; Genetics: A; A; Coros-references: GDB: 120048; OMIN: 142830
A; Cross-references: GDB: 120048; OMIN: 142830
A; Map position: 6p21.3 6p21.3
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology

Gaps ö Length 273; 0; Indels Query Match 100.0%; Score 49; DB 2; Best Local Similarity 100.0%; Pred. No. 0.0076; Matches 10; Conservative 0; Mismatches 0;

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1 RENLRIALRY 10 à g

74 RENLRIALRY 83

RESULT 2 I54463 MHC HLA-B38 chain - human (fragment)

C; Species: Homo saplens (man)
C; Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
C; Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
C; Accession: 154663
B; Mueller, C.A.; Engler-Blum, G.; Gekeler, V.; Steiert, I.; Weiss, E.; Schmidt, H.
Immunogenetics 30, 200-207, 1989
A; Title: Genetic and serological heterogeneity of the supertypic HLA-B locus specific
A; Title: Genetic and serological heterogeneity of the supertypic HLA-B locus specific
A; Treference number: 15463; MUID:89379286
A; Reference number: 15463
A; Reference number: 15463; MUID:89379286
A; Residues: 1-274 < RES>
A; Cross-references: GB:M29864; NID:g187674; PIDN:AAA36222.1; PID:g187675
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology

ö Gaps ö Query Match 100.0%; Score 49; DB 2; Length 274; Best Local Similarity 100.0%; Pred. No. 0.0077; Matches 10; Conservative 0; Mismatches 0; Indels ö

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R;McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Wat Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A;Title: A uniquely high level of recombination at the HLA-B locus.
A;Reference number: 159308; WUID:94286544
A;Accession: 180169
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A;Title: A uniquely high level of recombination at the HLA-B locus.
A;Reference number: 159308; WUID:94286544
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                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Pan troglodytes (chimpanzee)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999
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C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999
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C;Date: 05-Apr-1983 #sequence_revision 05-Apr-1983 #text_change 22-Jun-1999
C;Accession: A02189
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Rosidues 1.352 CRES.
A:Gross-references: EMB:U05580; NID:q454777; PIDN:AAA50183.1; PID:q454778
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
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A;Residues: 1.352 CRES.
A;Cross-references: EMBL:U05582; NID:q454781; PIDN:AAA50185.1; PID:q454782
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
A;Cross-references: EMBL:U05578; NID:q454773; PIDN:AAA50181.1; PID:g454774 C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
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C;Species: Pan troglodytes (chimpanzee)
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C;Species: Pan troglodytes (chimpanzee)
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A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                          Score 49; DB 2. Pred. No. 0.01;
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                                                                                                                                                                                   Class I histocompatibility antigen - pygmy chimpanzee (fragment)
C;Species: Pan paniscus (pygmy chimpanzee, bonobo)
C;Dacte: 31-May-1996 #sequence_revision 31-May-1996 #text_change 23-Jul-1999
C;Accession: I59308
R;McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A;Reference number: I59308; MUID: 94286544
A;Reference number: I59308; MUID: 94286544
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1354 *REES>
A;Cross-references: EMBL: U05575; NID: 9454767; PIDN: AAA50178.1; PID: 9454768
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
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class I histocompatibility antigen - chimpanzee)
class I histocompatibility antigen - chimpanzee)
claste: 24-May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999
clacession: 180168
clacession: 180168
A.Title: A uniquely high level of recombination at the HLA-B locus.
A.Reference number: 159308; MUID: 94286544
A.Title: A uniquely high level of recombination at the HLA-B locus.
A.Accession: 180168
A.Accession: 180168
A.Accession: 180168
A.Accession: 180168
A.Residues: 1-354
A.Residues: 1-354
A.Residues: Last A.Rebi: U05579; NID:q454775; PIDN:AAA50182.1; PID:g454776
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
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class I histocompatibility antigen - pygmy chimpanzee (fragment)
class I histocompatibility antigen - pygmy chimpanzee, bonobo)
C;Species: Pan paniscus (pygmy chimpanzee, bonobo)
C;Date: 24-May.1996 #sequence_revision 24-May.1996 #text_change 23-Jul-1999
C;Accession: 180167
Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A;Title: A uniqueby high level of recombination at the HIA-B locus.
A;Reference number: 159308 MuID:94286544
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A:Molecule type: mRNA
A:Residues: 1-354 <RES>
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B30345
MHC class I histocompatibility antigen HLA-Bw52 precursor - human
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RENLRIALRY
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A;Map position: 6p21.3-6p21.3
A;Map position: 6p21.3-6p21.3
A;Introns: 25/1, 115/1, 207/1, 299/1; 349/1
A;Introns: 25/1, 115/1, 207/1, 299/1; 338/1; 349/1
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Reywords: duplication; glycoprotein; heterodimer; transmembrane protein; transplantati
F;1-24/Domain: signal sequence #status predicted <SIG>
F;2-5-367/Product: class I histocompatibility antigen HLA-Bw58 alpha chain #status predicted <EXT>
F;25-114/Domain: alpha-1 <EXI>
F;15-206/Domain: alpha-2 <EX2>
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C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
C; Keywords: duplication; glycoprotein; heterodimer; transmembrane protein; transplantati
F; 1-21/Domain: signal sequence #status predicted <SIG>
F; 22-359/Product: class I histocompatibility antigen HLA alpha chain #status predicted <F; 22-304/Domain: extracellular #status predicted <EXT>
                                                                                                                                                                                                   PIDN:AAA36218.1; PID:g386873
the domain structure of this
                                                                 gene.
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                                                              an HLA
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C;Date: 31-Dec-1988 *sequence_revision 31-Dec-1988 *text_change 05-Sep-1997
C;Accession: A23895
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R;Malissen, M.; Malissen, B.; Jordan, B.R.
Proc. Natl. Acad. Sci. U.S.A. 79, 893-897, 1982
A;Title: Exon/intron organization and complete nucleotide sequence of A;Reference number: A02189; MUID:82151002
A;Accession: A02189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MHC class I histocompatibility antigen HLA-Bw58 alpha chain precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;12-203/Domain: alpha-1, 20025
F;112-203/Domain: alpha-2, 20025
F;217-282/Domain: immunoglobulin homology <IMM>
F;305-329/Domain: intracellular #status predicted <IMM>
F;305-359/Domain: intracellular #status predicted <INT>
F;107/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;224-280/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 49; DB 1; Length 359; 100.0%; Pred. No. 0.01; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-362 <WAY>
A;Note: the authors translated the codon GCC for residue 349 as
C;Comment: This protein is a subtype of the HLA-B17 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 49; DB 1; Length 362; 100.0%; Pred. No. 0.01; 1.ve 0; Mismatches 0; Indels
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                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-359 <MAL>
A;Cross-references: GB:J00191; GB:V00526; NID:g187600;
C;Comment: The seven exons correspond approximately to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;308-331/Domain: transmembrane #status predicted <TMM>F;332-362/Domain: intracellular #status predicted <INT>
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J. Biol. Chem. 260, 11924-11933, 1985
A;Title: The complete primary structure of HLA-Bw58.
A;Reference number: A23895; WUID:86008247
A;Accession: A23895
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity
Matches 10; Conserv
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1 RENLRIALRY 10

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C:Species: Homo sapiens (man)
C:Species: Homo sapiens (man)
C:Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 16-Feb-1997
C:Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 16-Feb-1997
C:Accession: B30345
R:Haysahi, H: Ennis, P.D.; Ariga, H.; Salter, R.D.; Parham, P.; Kano, K.; Takiguchi, J. Immunol. 142, 306-311, 1989
A.Title: HLA-B51 and HLA-B452 differ by only two amino acids which are in the helical A:Recence number: A30345; MUID: 89080265
A:Accession: B30345
A:Accession: B30345
A:Accession: B30345
A:Residues: 1-362 - AAIV
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Reywords: transmembrane protein
F:220-285/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       class I histocompatibility antigen Gogo-B0103 heavy chain precursor - lowland gorilla C; Species: Gorilla gorilla (lowland gorilla)
C; Species: Gorilla gorilla gorilla (lowland gorilla)
C; Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C; Accession: JH0541
R; Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
J. Exp. Med. 174, 1491-1509, 1991
A; Title: Gorilla class I major histocompatibility complex alleles: comparison to huma A; Reference number: JH0534; MUID: 92078860
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C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
C; Styorids: transmembrane protein
F; 1-24/Domain: signal sequence #status predicted <SIG>
F; 25-362/Product: class I histocompatibility antigen heavy chain, Gogo-B0103 #status
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A;Experimental source: EBV-transformed B cell
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F;299-362/Domain: intracellular #status predicted <INT>
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0.01;
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R.Hayashi, H.; Ooba, T.; Nakayama, S.; Sekimata, M.; Kano, K.; Takiguchi, M. Immunogenetics 32, 195-199, 1990
A;Title: Allospecificities between HLA-Bw53 and HLA-B35 are generated by substitution A;Reference number: A45834; MUID:91033941
A;Accession: A45834
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Tissue Antigens 43, 209-218, 1994
A; Mitle: HLA-B15: a widespread and diverse family of HLA-B alleles.
A; Reference number: 138421; MUID:94367483
                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-362 KHAY>
A; Cross-references: GB:M58636; NID:g187756; PIDN:AAA36228.1; PID:g187757; GB:M33574
A; Note: this allele is designated B*5301
'Species: Homo sapiens (man)
Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 23-Jul-1999
Accession: A45834
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:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 6p21.3-6p21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;1-24/Domain: signal sequence #stens predicted <SIG>
F;220-285/Domain: immunoglobulin homology <IMA
F;110/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Molecule type: mRNA
A;Residues: 1-562 <RES>
A;Cross-references: GB:L15005; NID:g493154; PIDN:AAA56832.1; PID:g493155
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100.0%; Pred. No. 0.01;
.ive 0; Mismatches 0; Indels
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Pred. No. 0.01;
Mismatches
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity
Matches 10; Conserv
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C;Superfamily: clas
C;Keywords: glvror*
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Class I histocompatibility antigen Gogo-B0102 heavy chain precursor - lowland gozilla (Species: Gozilla gozilla (lowland gozilla)

C. Species: Gozilla gozilla gozilla (lowland gozilla)

C. Species: Gozilla gozilla (lowland gozilla)

C. Stacession: JH0540

R. Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.

J. Exp. Med. 174, 1491-1509, 1991

A; Title: Gozilla class I major histocompatibility complex alleles: comparison to human a stacession: JH0540

A; Reference number: JH0540

A; Reference number: JH0540

A; Residues: 1-362 claw>
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                                                                                                                                                                                      to human
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                                                      C. Accession: J00394

R. Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
J. Exp. Med. 174, 1491-1509, 1991

A. Title: Gorilla class I major histocompatibility complex alleles: comparison to humber: J0034; MUID: 92078860

A. Reference number: J40534; MUID: 92078860

A. Recession: J4053

A. Molecule Gorilla class I major histocompatibility complex alleles: comparison to humber: J40534; MUID: 92078860

A. Molecule type: DNA

A. Residues: 1-362 <LAW>
A. Residues: 1-362 <LAW>
A. Residues: 1-362 <LAW>
A. Consor-references: EMBL: X60255; NID: 922865; PIDN: CAA42807.1; PID: 922866

A. Experimental source: EMBL: X60255; NID: 92941; 338/1; 349/1

C. Genetics: A. Title: Cass I histocompatibility antigen; immunoglobulin homology

C. Keywords: transmembrane protein

F. 12-24/Domain: signal sequence #status predicted <SIG>
F. 25-362/Product: class I histocompatibility antigen heavy chain, Gogo-B0101 #statu F; 25-114/Domain: alpha-2 <AL2>
F; 25-114/Domain: alpha-2 <AL2>
F; 220-288/Domain: alpha-3 <AL2>
F; 220-288/Domain: alpha-3 <AL3>
F; 220-288/Domain: intracellular #status predicted <INT>
F; 220-288/Domain: intracellular #status predicted <INT>
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                                   30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
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RESULT 14 A45834 MHC class I histocompatibility antigen HLA-B53 alpha chain precursor

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# GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

February 8, 2000, 00:59:49; Search time 63.71 Seconds (without alignments) 4.688 Million cell updates/sec

US-08-653-294-8 49 1 RENLRIALRY 10

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

82229 seqs, 29864866 residues Searched:

82229 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

SwissProt_38:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	1B01_PANTR 1B01_GORGO	1B02_GORGO	1B15_HUMAN	1B47_HUMAN		1B53_HUMAN	1B54_HUMAN	1B60_HUMAN	1B62_HUMAN	HLAH_HUMAN	1A23_HUMAN	1A24_HUMAN	1B05_HUMAN	1B41_HUMAN	1B42_HUMAN	1A25_HUMAN	1A32_HUMAN	1B40_HUMAN	1A04_GORGO	HAIK_MOUSE	VP19_HSV6U			1B16_HUMAN	1B18_HUMAN	1B19_HUMAN	1B29_HUMAN	1B45_HUMAN	MASY_ECOLI	HA1Y_MOUSE
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                                     RESULT 3
1B02_GORGO STANDARD; PRT; 362 AA.

AC 930380;
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0102 ALPHA CHAIN PRECURSOR.
OC GOTILIA gorilla (Lowland gorilla).
CLASS (Bukryote; Metazoa; Chordata; Cranlata; Warmmalla; Mammalla; Hominidae; Gorilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAWLOR D. A., WARREN E., TAYLOR P., PARHAM P.;
"Gorilla class I major histocompatibility complex alleles: comparison
to human and chimpanzee class I.";
to human and chimpanzee class I.";
J. Exp. Med. 174:1491-1509(1991).
-i- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
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01-APR-1993 (Rel. 25, Last annotation update)
01-APR-1993 (Rel. 25, Last annotation update)
02-APR-1993 (Rel. 25, Last annotation update)
03-APR-1993 (Rel. 25, Last sequence update)
03-APR-1993 (Re
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R PFAM: PF00047; 19:1.

R PFAM: PF00129; MHC_I; 1.

R MHC_I: Transmembrane; Glycoprotein; Signal.

FT SIGNAL 1 24 CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0102 ALPHA CHAIN.

FT CHAIN 25 114 EXTRACELLULAR ALPHA-1.

FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.

FT DOMAIN 207 298 EXTRACELLULAR ALPHA-3.

CONNECTING PEPTIDE.
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-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
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MEDLINE; 92078860.
LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
"Gorilla class I major histocompatibility complex alleles: comparison to human and chimpanzee class I.";
J. Exp. Med. 174:1491-1509(1991).
-:- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMONE SYSTEM.
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P30379;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
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PIR; JH0539; JH0539.
HSSP; P03989; 1HSA.
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                                                                                                                             VEGA M.A., EZQUERRA A., ROJO S., APARICIO P., BRAGADO R.,
LOPEZ DE CASTRO J.A.;
"Structural analysis of an HLA-B27 functional variant: identification
"Structural analysis of an HLA-B27 functional variant: identification
"Structural analysis of an HLA-B27 functional variant: identification
of residues that contribute to the specificity of recognition by
cytolytic T lymphocytes.";
Proc. Natl. Acad. Sci. U.S.A. 82:7394-7398(1985).
-I-FONCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
-I-SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
  SEQUENCE FROM N.A.
PARHAM P., ARNETI K.L., ADAMS E.J.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
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EMBL; 138504; AAA69724.1; USESP; PO3989; 1HKPR.
HSSP; PO3989; 1HSA.
MIM; 142830; PRSOCSTE: PSO0290; IG_MRC; 1.
PRAM; PF00047; 19; 1.
MRC I; Transmembrane; Glycoprotein; Signal.
SIGNAL.
                                                                                      86-107 AND 171-181.
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MEDLINE; 86042671
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1D 1847_HUMAN
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DT 01-FEB-1996
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DE HLA CLASS I
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                                                                                 LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
"Gorilla class I major histocompatibility complex alleles: comparison
to human and chimpanzee class I.";
J. Exp. Med. 174:1491-1509(1991).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
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SEEMANN G.H.A., REIN R.S., BROWN C.S., PLOEGH H.L.;
"Gene conversion-like mechanisms may generate polymorphism in human class I genes.";
EMBO J. 5:547-552(1986).
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PROSTIE; PSUULSOU.
PFAM: PF00129; MHC_I; 1.
MHC_I; Transmenbrane; Glycoprotein; Signal.
BY SIMILARITY.
SIGNAL 25 362 CASS I HISTOCOMPATIBILITY ANTIGEN,
GOGO-BOLIO3 ALPHA CHAIN.
"""PACTELLULAR ALPHA-1.
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01-APR-1993 (Rel. 25, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2702 ALPHA CHAIN
PRECURSOR (B-27K) (B27.2).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                 THE IMMUNE SYSTEM.
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100.0%; Pred. No. 0.0037;
ive 0; Mismatches 0; Indels
  Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
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EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
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                                         SEQUENCE FROM N.A. MEDLINE; 92078860.
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SEQUENCE FROM N.A.
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P10317;
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HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2702 ALPHA CHAIN.

EXTRACELLULAR ALPHA-1. EXTRACELLULAR ALPHA-2. EXTRACELLULAR ALPHA-3. CONNECTING PEPTIDE.

CYTOPLASMIC TAIL.
BY SIMILARITY.
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01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-49(B-21) B*4901 ALPHA CHAIN
PRECURSOR.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
100.0%; Score 49; DB 1; Length 362; 100.0%; Pred. No. 0.0037; ive 0; Mismatches 0; Indels
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                                                                                                                          MEDLINE; 89080265.
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TAKRGOCHI M.;
"HLA-B51 and HLA-Bw52 differ by only two amino acids which are in the
helical region of the alpha 1 domain.";
J. Immunol. 142:306-311(1989).
                 ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
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reaction: frequency and nature of errors produced in amplification.";
Proc. Natl. Acad. Sci. U.S.A. 87:2833-2837(1990).
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EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-2.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDILINE; 89233295.
POHLA H., KUON W., TABACZEWSKI P., DOERNER C., WEISS E.H.:
POHLA H., KUON W., TABACZEWSKI P., DOERNER C., WEISS E.H.:
"Alielic variation in HLA-B and HLA-C sequences and the evolution of the HLA-B alleles.";
Immunogenetics 29:297-307(1989).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
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PFAM; PF00129; MHC_I; 1.
PFAM; PF00129; MHC_I; 1.
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AAA59620.1; JOINED.
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PIR; A30548; A30548.
HSSP; P30491; IA1M.
MIM; 142830; --
PROSITE; PS00290; IG_MHC; 1.
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                                                                                                             SEQUENCE FROM N.A.
MEDLINE; 90207291
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                                                                                                         REVISION TO 78.
MEDILNE: 93056529.
HILDEBRAND W.H., MADRIGAL J.A., BELICH M.P., ZEMMOUR J., WARD F.E.,
WILLIAMS R.C., PARHAM P.;
"Serologic cross-reactivities poorly reflect allelic relationships in
the HIA-B12 and HIA-B21 groups. Dominant epitopes of the alpha 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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01-NOV-1990 (Rel. 16, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-51(B-5) B*5101 ALPHA CHAIN
PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-49(B-21) B*4901 ALPHA CHAIN, EXTRACELLUIAR ALPHA-1. EXTRACELLUIAR ALPHA-2. EXTRACELLUIAR ALPHA-3. CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                         욘
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-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Pred. No. 0.0037;
.ive 0; Mismatches 0; Indels
                                   PARHAM P., LAWLOR D.A., LOMEN C.E., ENNIS P.D.;
Diversity and diversification of HLA-A,B,C alleles.";
J. Immunol. 142:3937-3950(1989).
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PFAM; PF00129; MHC_I; 1.
PFAM; PF00129; MHC_I; 1.
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PROSITE; PS00290; IG_MHC; 1.
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Matches 10; Conservative
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362 AA;
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 SEQUENCE FROM N.A. MEDLINE; 89235215.
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P18464;
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                                                                                                                 SECUENCE FROM N.A.
MEDLINE; 89080265.
MEDLINE; 89080265.
MEDLINE; 890802655.
TAKIGUCHI M.;
TAKIGUCHI M.;
"HIA-BASI and HIA-BWS2 differ by only two amino acids which are in the helical region of the alpha i domain.";
J. Immunol. 142:306-311(1989).
-!- FONGTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
THE IMMUNE SYSTEM.
-!- SUBGUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-52(B-5) B*5201 ALPHA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-52(B-5) B*5201 ALPHA CHAIN. EXTRACELLULAR ALPHA-1. EXTRACELLULAR ALPHA-2. EXTRACELLULAR ALPHA-3. CONNECTING PEPTIDE.
                               HIA-B OR HIAB.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
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EMBL; M22793; AAA59645.1; JOINED.
EMBL; M22794; AAA59645.1; JOINED.
EMBL; M22795; AAA59645.1; JOINED.
EMBL; M22796; AAA59645.1; JOINED.
EMBL; M22797; AAA59645.1; JOINED.
EMBL; M22798; AAA59645.1; JOINED.
PIR; B30345; B30345.
PIR; B30548; B30548.
HSSP, P90491; JAIM.
MIN; 142830; -.
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362 AA;
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P30491;
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1B54_HUMAN
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                                                                                     01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-51(B-5) B*5104 ALPHA CHAIN
PRECIRSOR.
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EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
CONNECTING PEPTIDE.
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BELICH M.P., MADRIGAL J.A., HILDEBRAND W.H., ZEMMOUR J., WILLIAMS R.C., LUZ R., PETZL-ERLER M.L., PARHAM P.; Unusual H.A.B alleles in two tribes of Brazilian Indians."; Nature 357:326-329(1992).

-- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS THE IMMUNE SYSTEM.

-- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HSSP, P30491; 1AlM.
MIM; 142830; -.
PROSITE; PS00290; IG_MHC; 1.
PFAM; PF00047; ig; 1.
PFAM; PF00129; MHC_1; 1.
MHC_I; Transmembrane; Glycoprotein; Signal.
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1B53_HUMAN
ID 1B53_HUMAN
AC P30490;
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P30489;
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                                                                                                                                                                                                 MEDLINE; 90207291.

ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;

"Rapid cloning of HLA-A,B cDNA by using the polymerase chain
reaction: frequency and nature of errors produced in amplification.";

Proc. Natl. Acad. Sci. U.S.A. 87:2833-2837(1990).
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                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE; 9106747.
ISAMAT M., GIRDLESTONE J., MILSTEIN C.;
"Nuclectide sequence of an HLA-BW57 gene.";
Nuclectide Acids Res. 18:6702-6702(1990).
-II-CIDEL ACIDS INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-II-SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
     01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-57(B-17) B*5701 ALPHA
CHAIN PRECURSOR (BW57.1).
                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Pred. No. 0.0037;
rative 0; Mismatches 0; Indels
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EMBL; X5711; CAA39244.1; --
PIR; S12622; S12622.
PIR; D35997.
HSSP, P30491; 1A1M.
MIM; 142830; --
PROSITE; PS00290; IG_MHC; 1.
PRAM; PF00147; 19; 1.
PFAM; PF00129; MHC_1; 1.
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Best Local Similarity 100.
Matches 10; Conservative
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362 AA;
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1B61_HUMAN
ID 1B61_HUMAN
AC P30497;
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SIGNAL
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BW-53 B*5301 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
                                                                                                                                                                                                                                                                                                     "Allospecificities between HLA-Bw53 and HLA-B35 are generated by substitution of the residues associated with HLA-Bw4/Bw6 public epitopes.";
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-53 B*5301 ALPHA CHAIN
PRECURSOR.
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                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PFAM; PF00047; 19; 1.
PFAM; PF00129; MHC_L; 1.
MHC I; Transmembrane; Glycoprotein; Signal; 3D-structure. SIGNAL
                                                                                                                             SEQUENCE FROM N.A.
MEDLINE; 91033941.
HATASHI H.; OOBA T., NAKAYAMA S., SEKIMATA M., KANO K.,
TAKIGUCHI M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 25-302.
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Best Local Similarity 100.
Matches 10; Conservative
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PDB; 1A1M; 08-APR-98.
PDB; 1A1O; 08-APR-98.
MIM; 142830; -.
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362 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-58(B-17) B*5801 ALPHA CHAIN. EXTRACELLULAR ALPHA-1. EXTRACELLULAR ALPHA-2. EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                   INOUE T., OGAWA A.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
-!- SUBDNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
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THEAL HIAH CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN H PRECURSOR

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                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Pred. No. 0.0037;
Mismatches 0; Indels
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PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
24
                                                                                SEQUENCE FROM N.A.
MEDLINE; 86008247.
WAYS J.P., COPPIN H.L., PARHAM P.;
"The complete primary structure of HLL."
J. Biol. Chem. 260:11924-11933(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M11799; AAA59628.1; -.
EMBL; AB008102; BAA22916.1; -.
PIR; A23895; HLHUB8.
HSSP; P30491; 1A1M.
MIM; 142830; -.
PROSITE; PS00290; IG_MHC; 1.
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Best Local Similarity 100.

Matches 10; Conservative
    sapiens (Human)
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362 AA;
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01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-57(B-17) B*5702 ALPHA CHAIN
PRECURSOR (BW57.2).
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                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE; 93056508.
MADRIGAL J.A., BELIO.
LITTLE A.-M., ZEMMOUR J., ENNIS P.D., WARD F.E., PETZL-ERLER M.L.,
LITTLE A.-M., ZEMMOUR J., ENNIS P.D., WARD F.E., PETZL-ERLER M.L.,
MARTELL R.W., DU TOIT E.D., PARHAM P.;
"Distinctive HLA-A.B antigens of black populations formed by
internal lelic conversion.";
J. Immunol. 149:3411-3415(1992).
-: FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE INMUNE SYSTEM.
-: SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
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01-MAR-1989 (Rel. 10, Last sequence update)
115-JUL-1998 (Rel. 36, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-58(B-17) B*5801 ALPHA
CHAIN PRECURSOR.
HLA-B OR HLAB.
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                                                                                                                                          Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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628C2156 CRC32;
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PFAM; PF00129; MHC_1; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
SIGNAL 1 24
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Best Local Similarity 100.
Matches 10; Conservative
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P10319;
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MICROGLOBULIN).
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                              MALISSEN M., MALISSEN B., JORDAN B.R.; "Exon/intron organization and complete nucleotide sequence of an HLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 79:893-897(1982).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS
-!- THE IMMUNE SYSTEM. COULD BE THE PRODUCT OF A PSEUDOGENE.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND. A BETA CHAIN (BETA-2-
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01-APR-1993 (Rel. 25, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTICEN, A-23(A-9) ALPHA CHAIN
PRECURSOR.
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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EXTRACELLUIAR ALPHA-1.
EXTRACELLUIAR ALPHA-2.
EXTRACELLUIAR ALPHA-3.
CONNECTING PEPTIDE.
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PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS00290; IG_MHC; 1.
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Matches 10; Conservative
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MIM; 142800; -.
PROSITE; PS00290; I
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P30447;
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8, 2000, 00:59:49

Search completed: February Job time: 3778 sec

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A-23(A-9) ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
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EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
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PFAM: PF001047: 19: 1.
PFAM: PF00129: MHC_I: 1.
MHC I: Transmembrane: Glycoprotein; Signal.
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PROSITE; PS00290; IG_MHC; 1.
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Gorilla gorilla gorilla (Lowland gorilla).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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100.0%; Score 49; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches 0; Indels
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CAO K., BURDETT L., ZHANG G., FERNANDEZ-VINA M.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AF017320; AAB70286.2;
                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
MIC CLASS I ANTIGEN (FRAGMENT).
HLA-B.
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046657;
041-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
MHC CLASS I ANTIGEN HLA-H ORTHOLOG (FRAGMENT).
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89 AA; 10606 MW; 99D11089 CRC32;
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SEQUENCE FROM N.A.
CHANDNAXINGYOND D., SIRIKONG M., LONGTA K., SRINAK D., RUNGROUNG E.,
CHANDNAXINGYOND D., SIRIKONG M., LONGTA K.,
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: 190421, AABSO144.1;
EMBL: 190420; AABSO144.1;
PEMBL: 190420; AABSO144.1;
PEMBL: 190420; ARC_I: 1.
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SEQUENCE FROM N.A.
CHANDANAYINGYONG D., SIRIKONG M., LONGTA K., SRINAK D., RUNGROUNG E.,
BEJCHANDRA S., BLASCZYK R., GROSSE-WILDE H.;
                                               "An intronic mutation responsible for a low level of expression of a HIA-AA*24 allele.";
Tissue Antiquens 50:340-346(1997),
EMBL: Z72423: CAA96533.1;
PFAM: PF00129; MHC_I; 1.
LAFORET M., FROELICH N., PARISSIADIS A., BAUSINGER H., PFEIFFER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapions (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I HLA-B (FRAGMENT).
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Last annotation update)
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138 138
138 AA; 15610 MW; B8417FAO CRC32;
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19909 MW; CAAE5641 CRC32;
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01-JAN-1998 (TrEMBLrel. 05, Le
01-NOV-1998 (TrEMBLrel. 08, La
MHC CLASS I HLA-B (FRAGMENT).
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172 AA;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MHC CLASS I HISTOCOMPATIBILITY ANTIGEN-B (HLA-B-27KSH) (FRAGMENT).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Score 49; DB 7; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches 0; Indels
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TISSUB-LEUKOCYTE;
PETERSDORF E.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U18659; AAB60357.1; -..
MIM; 142830; -...
PFAM; PF00129; MHC_I; 1.
                                                                                                                   GRIMSLEY C., MATHER K.A., OBER C.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF02217: AAC99794.1; -.
PFAM; PF00129; MHC_I; 1.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAY-1999 (TrEMBLrel. 10, Last annotation update)
HUMAN LEUKOCYTE ANTIGEN PRECURSOR (FRAGMENT).
   Eutheria; Primates; Catarrhini; Hominidae; Gorilla
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90 AA; 10689 MW; SESF2495 CRC32;
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   PFAM; PF00129; MHC_I; 1
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                                                                           172 1
172 AA;
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AC 019771
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
CHANDANAYINGYONG D., SIRIKONG M., LONGTA K., SRINAK D., RUNGROUNG E.,
CHANDANAYINGYONG D., SIRIKONG M., LONGTA K.,
BEJCHANDRA S., JUJI T., TOKUNAGA K.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U90419; AAB50143.1; -.
EMBL; U90418; AAB50143.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
CHANDAXINGYONG D., SIRIKONG M., LONGTA K., SRINAK D., RUNGROUNG E.,
CHANDAXINGYONG D., SIRIKONG M., LONGTA K., SRINAK D., RUNGROUNG E.,
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: U90425; AAB50146.1; -.
EMBL: U90424; AAB50146.1; JOINED.
PFAM; PF00129; MHC_1: 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Primates, Catarrhini, Hominidae, Homo.
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100.0%; Pred. No. 0.02;
tive 0; Mismatches 0; Indels
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases. EMBL: U90423; AAB50145.1; -. EMBL. U90422; AAB50145.1; JOINED. PFAM: PF00129; MHC_1: 1.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
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172 AA; 19909 MW; CAAE5641 CRC32;
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HLA-B.
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Best Local Similarity 100.
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68 RENLRIALRY 77
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                 Query Match 100.0%; Score 49; DB 7; Length 172; Best Local Similarity 100.0%; Pred. No. 0.02; Matches 10; Conservative 0; Mismatches 0; Indels
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BLASCIXK R.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; X96473; CAA65327.1; -
PFAM; PF00129; MHC_I; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC HLA-#51 PROTEIN (FRAGMENT).
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I HLA-B (FRAGMENT).
172
19909 MW; CAAE5641 CRC32;
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172 172
172 AA; 19942 MW; 1A73E47D CRC32;
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100.0%; Pred. No. 0.02;
.ive 0; Mismatches
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Pred. No. 0.02;

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                          0; Indels
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PETERSDORF E.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
EMBL, 1028759; ABB60367.1; -.
HSSP; P10318; 1ROG.
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                 029694;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MHC CLASS I HLA-B ANTIGEN (FRAGMENT).
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01-JAN-1998 (TrEMBLrel. 05; Last sequence update)
01-NOY-1999 (TrEMBLrel. 12, Last annotation update)
MHC CLASS I HLA-A (FRAGMENT).
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180 180
180 AA; 20811 MW; CECC3537 CRC32;
Best Local Similarity 100.0%; Pred. No. 0.0 Matches 10; Conservative 0; Mismatches
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Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Mammalia;
Eutheria: Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                  Query Match 100.0%; Score 49; DB 7; Length 172; Best Local Similarity 100.0%; Pred. No. 0.02; Matches 10; Conservative 0; Mismatches 0; Indels
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100.0%; Score 49; DB 7; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 0; Indels
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CHANDANZINGYONG D., SIRIKONG M., LONGTA K., SRINAK D.,
SIRIBOONRIT U., RUNGROUNG E., BEJCHANDRA S.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: U906614, AAA56244.1; -.
EMBL: U906613; AAB50244.1; JOINED.
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CHANDANAYINGYONG D., SIRIKONG M., LONGTA K., SRINAK D.,
SIRIBOONRIT U., RUNGROUNG E., BEJCHANDRA S.;
SUDMITTED (1977) to the EMBL/GenBank/DDBJ databases.
EMBL; U90616; AAB50245.1;
EMBL; U90615; AAB50245.1;
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I HLA-B (FRAGMENT).
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
HHC CLASS I HLA-B (FRAGMENT).
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NON_TER 172 172
SEQUENCE 172 AA; 20026 MW; 4D9A1043 CRC32;
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172 172
172 AA; 20052 MW; F6214671 CRC32;
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DB 7; Length 180;

Score 49;

100.08;

Query Match

Length 172;

DB 7;

Score 49;

100.08;

Query Match

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               0; Gaps
                                                                                                                                                                                                                                                          Homo saplens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                   Query Match
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Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels
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019608;
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01-JAN-1999 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MHC CLASS I HLA-A (FRAGMENT).
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Search completed: February 8, 2000, 13:17:35 Job time: 32484 sec

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i AF030927 Homo sapiens MHC cl
i AF030929 Homo sapiens MHC cl
i U59699 Human MHC class I (HL
                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota, Matazoa, Chordata, Vertebrata, Mammalia, Eutheria,
Eukaryota, Catarzhini, Hominidae, Homo.

1 (bases 1 to 250)
Rojdas-Munoz, A., Mendez, I. and Yunis, I.
Rojeas-Munoz, A., Mendez, I. and Yunis, I.
Rojear-Word, Mendez, I. and Yunis, I.
Community : The Nukak-Maku
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Rojas-Munoz, A.
Bolrect Submission
Submitted (07-0CT-1996) A. Rojas-Munoz, National Institute Of Health, Immunogenetics, Avenida El Dorado, Carrera 50, Santafe Bogota / Zona 6, COLOWBIA
Location/Qualifiers
1. .250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-0CT-1996
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Gaps: 0
Percent Identity: 100.000
                                                                                                                                            HSHLABHBA 250 bp DNA PRI H.saplens HLA-B gene, exon 2, HB(a) allele. Y08692 Y08692 I GI:1619287
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LOCUS HSHLABHBB 250 bp DNA PRI DEFINITION H.septiens HLA-B gene, exon 2, HB(b) allele.
ACCESSION Y08693.1 GI:1619288
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Locus HSHLABHBA
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gb_pr3:HS611HLA1
gb_pr3:HS639HLA1
gb_pr4:HSKM315S1
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AJ133780 Homo sapiens HLA-B gen
AJ238971 Homo sapiens HLA-B gen
AJ238073 Homo sapiens HLA-B gen
U37110 Human HLA-A24 gene, alle
U37114 Human HLA-A24 gene, alle
U37112 Human HLA-A24 gene, alle
U18987 Human MHC class I antige
U16400 Human HLA-B gene, allele
LL43528 Homo sapiens (clone K920
LL43528 Homo sapiens (clone K620
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                                                                                   About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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  OM of: US-08-653-294-8 to: GenEmbl:*
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Database: GenEmbl:*
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Database Information 1518192014
Search time (sec): 11370.480000
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                                           Date: Feb 8, 2000 4:37
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Query length: 10
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gb_pr1:HSHLABHBD
gb_pr2:HSHLABB1
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gb_pr4:AF022160
gb_pat:114590
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gb_pr2:HSHLABG1
gb_pr2:HSHLABI1
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Wed Feb

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           Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Gatarrhin; Hominidae; Homo. 1 (bases 1 to 250) Rojas-Munoz, A., Mendez, I. and Yunis, I. Molecular evolution of HLA-B locus in a small population amerindian community: The Nukak-Maku
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Eukaryota: Metazoa: Chordata: Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae: Homo.
1 (bases 1 to 250)
Rojas-Munoz, A., Mendez, I. and Yunis, I.
Molecular evolution of HIA-B locus in a small population amerindian community: The Nukak-Maku
                                                                                                                                                                      Direct Submission
Submitted (07-0CT-1996) A. Rojas-Munoz, National Institute Of
Health, Immunogenetics, Avenida El Dorado, Carrera 50, Santafe De
Bogota / Zona 6, COLOMBIA
Location/Qualifiers
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H.Saplens HLA-B gene, exon 2, HB(d) allele.
Y08694
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human.
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Rojas-Munoz,A.
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Rojas-Munoz, A.
Direct Submission
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Quality: 49.00
Ratio: 4.900
Percent Similarity: 100.000
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Submitted (07-OCT-1996) A. Rojas-Munoz, National Institute Of Health, Immunogenetics, Avenida El Dorado, Carrera 50, Santafe De Bogota / Zona 6, COLOMBIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (23-FEB-1997) Transfusion Medicine, Faculty of Medicine, Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 250)
Chandanayingng, D., Sirikong, M., Longta, K., Srinak, D., Rungroung, E., Bejchandra, S., Juji, T. and Tokunaga, K. Bis allales (B*1513)
Unpublished
2 (bases 1 to 250)
Chandanayingng, D., Sirikong, M., Longta, K., Srinak, D., Rungroung, E., Bejchandra, S., Juji, T. and Tokunaga, K.
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Gaps: 0
Percent Identity: 100.000
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                                                                         Location/Qualifiers
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US-08-653-294-8 x HSHLABD1
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AUTHORS
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AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 250)
Chandanayingyong, D., Sirikong, M., Longta, K., Srinak, D.,
Siribooniti, U., Rungroung, E. and Bejchandra, S.
Direct Submission
Submitted (25-FEB-1997) Transfusion Medicine, Faculty of Medicine,
Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /haplotype="(b)HLA-A2,B77,Cw8N,DR12(DR52),DQ7/(c)A11.1,
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                                                                                                                                                       Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 10
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Percent Identity: 100.000
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82 c 80 g 32 t
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                                                                                                                                                                                                                                                                              1 ArgGluAsnLeuArgIleAlaLeuArgTyr 10
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1. .250
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U90611.1 GI:1905865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality: 49.00
Ratio: 4.900
Percent Similarity: 100.000
                                                                                                                                                       Ratio: 4.900
Percent Similarity: 100.000
                                                                                                                                                                                                                                               Align seg 1/1 to: HSHLABB1
                                                                                                                                       49.00
                                                                                                                                                                                                    alignment_block:
US-08-653-294-8 x HSHLABB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B*51V alleles
Unpublished
                                                                                                                                                                                                                                                                                                                                         seq_name: gb_pr2:HSHLABD1
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                                                                                                                                         Quality:
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KEYWORDS
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ORIGIN
                                                            BASE COUNT
ORIGIN
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JOURNAL
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      exon
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Chandanayingyong, D., Sirikong, M., Longta, K., Srinak, D.,
Siriboonrit, U., Rungroung, E. and Bejchandra, S.
Direct Submission
Submitted (25-FEB-1997) Transfusion Medicine, Faculty of Medicine,
Siriral Hospital, Mahidol University, Prannok Road, Bangkok 10700,
Thailand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSHLABG1 250 bp DNA PRI 25-MAR-1997
Human cell line THAI DCH011 MHC class I HLA-B gene (allele
HLA-B*51V), exon 2.
U90615
                                                                                                                                                                               seg_documentation_block:
LOCUS HSHLABF1 250 bp DNA PRI 25-MAR-1997
DEFINITION Human cell line THAI DCH028 MHC class I HLA-B gene (allele
HLA-B*51V), exon 2.
                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butherla: Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 250)
Chandanayingyong, D., Sirikong, M., Longta, K., Srinak, D.,
Siriboonrit, U., Rungroung, E. and Bejchandra, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 10
Gaps: 0
Percent Identity: 100.000
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  to: 250
                                             202 CGAGAGAACCTGCGGATCGCGCTCCGCTAC 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ArgGluAsnLeuArgIleAlaLeuArgTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
  from: 1
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U90613.1 GI:1906033
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Ratio: 4.900
Percent Similarity: 100.000
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Align seg 1/1 to: HSHLABD1
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US-08-653-294-8 x HSHLABF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B*51V alleles
Unpublished
                                                                                                                                            seq_name: gb_pr2:HSHLABF1
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LOCUS
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Unpublished
C (Dases 1 to 250)
C (Anadanayingyong, D., Sirikong, M., Longta, K., Srinak, D.,
Rungroung, E. and Bejchandra, S.
Blacet Submission
Submitted (23-FEB-1997) Transfusion Medicine, Faculty of Medicine,
Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
Direct Submission
Submitted (23-FEB-1997) Transfusion Medicine, Faculty of Medicine,
Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSHLABJ1 250 bp DNA PRI 22-MAR-1997
Human cell line THAI DCH028 MHC class I HLA-B gene (allele
HLA-B*1513), exon 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa: Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 250)
ChandnayIngyong, D., Sirikong, M., Longta, K., Srinak, D.,
Rungroung, E. and Bajchandra, S.
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Percent Similarity: 100.000
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US-08-653-294-8 x HSHLABI1
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LOCUS HSHLABJ1
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                                                          Thailand
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human.
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JOURNAL
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                                                                                                                                                                                                           Chases I to 250)
Chandanayingyong, D., Sirikong, M., Longta, K., Srinak, D.,
Siriboonrit, U., Rungroung, E. and Bejchandra, S.
Direct Submission
Submitted (25-FEB-1997) Transfusion Medicine, Faculty of Medicine,
Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
Thailand
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /haplotype="(a)HLA-A11.1,B51V,Cw14,DR12(DR52),DQ7/(b)A24,
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                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 250)
Chandanayingyong, D., Sirikong, M., Longta, K., Srinak, D., Siriboonrit, U., Rungroung, E. and Bejchandra, S.
B*51V alleles
Unphilished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSHLABII 250 bp DNA PRI 22-MAR-1997
Human cell line THAI DCH011 MHC class I HLA-B gene (allele
HLA-B*1513), exon 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

L (bases 1 to 250)
Chandanayingyong, D., Sirikong, M., Longta, K., Srinak, D.,
Rungroung, E., Bejchandra, S., Blasczyk, R. and Grosse-Wilde, H.
Bl5 alleles (B*1513)
Unphilished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 250)
Chandanayingyong, D., Sirikong, M., Longta, K., Srinak, D.,
Rungroung, E., Bejchandra, S., Blasczyk, R. and Grosse-Wilde, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 10
Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                               /map="6p21"
   GI:1906037
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82 c
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Ratio: 4.900
Percent Similarity: 100.000
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US-08-653-294-8 x HSHLABG1
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LOCUS HSHLABI1
                                                         human.
Homo sapiens
   090615.1
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seq_name: gb_pr4:AF022159
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LOCUS AF022159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo saplens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 250)
Chandanayingyong, D., Sirikong, M., Longta, K., Srinak, D.,
Rungroung, E., Bejchandra, S., Juji, T. and Tokunaga, K.
Unpublished
                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
LOCUS HSHLABI1 250 bp DNA PRI 22-MAR-15
DEFINITION Human cell line THAI DCH009 MHC class I HLA-B gene (allele
HLA-B*1513), exon 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 250)
Chandanayingyong,D., Sirikong,M., Longta,K., Srinak,D.,
Rungroung,E., Bejchandra,S., Juji,T. and Tokunaga,K.
Direct Submission
                                                                                                          Gaps: 0
Percent Identity: 100.000
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Percent Identity: 100.000
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/product="MHC class I HLA-B"
83 c 80 g 32 t
/product="MHC class I HLA-B"
83 c 80 g 32 t
                                                                                          Length:
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/cell_type="lymphoblastoid"
/cell_line="THAI DCH009"
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/note="Allele: HLA-B*1513"
                                                                                                                                                                                                    to: 250
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    1. 250
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /chromosome="VI"

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                                                                                                                                                                                                    from: 1
                                                                                                                                                                                                                                                                                                                                                                                             U90418
U90418.1 GI:1905826
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                                                                                        Quality: 49.00
Ratio: 4.900
Percent Similarity: 100.000
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US-08-653-294-8 x HSHLABJ1
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US-08-653-294-8 x HSHLABT1
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1 ArgGluAsnLeuArgIleAlaLeuArgTyr 10

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2 (bases 1 to 255)
Grimal-By,C., Mather,K.A. and Ober,C.
Direct Submission
Submission
Submitted (03-SEP-1997) Fred Hutchinson Cancer Research Center,
1100 Fairview Ave. N., M374, Seattie, WA 98109, USA
1.0555
                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 255)
Grimsley,C., Mather,K.A. and Ober,C.
HLA-H: a pseudogene with increased variation due to balancing selection at neighboring loci
Mol. Biol. Evol. 15 (12), 1581-1588 (1998)
                                                                         AFU22159 255 bp DNA PRI 05-JAN-1999
Homo sapiens isolate 026 MHC class I antigen HLA-H (HLA-H)
pseudogene, partial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
LOCUS AF022160 259 bp DNA PRI 05-JAN-1999
DEFINITION Homo sapiens isolate 034 MHC class I antigen HLA-H (HLA-H)
PSEUGOGENE, partial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/isolate="026"
/db_xref="taxon:9606"
/db_oxosome="6"
/map="6p21.3"
/note="African-American individual"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 10
Gaps: 0
Percent Identity: 100.000
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/gene="HIA-H"
/note="MHC class I antigen HIA-H"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202 CGAGAGAACCTGCGGATCGCGCTCCGCTAC 231
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/gene="HLA-H"
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AF022160.1 GI:2655063
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/gene="HLA-H"
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Percent Similarity: 100.000
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US-08-653-294-8 x AF022159
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I14591.1 GI:997074
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Quality: 49.00
Ratio: 4.900
Percent Similarity: 100.000
                                                                     Ratio: 4.900
Percent Similarity: 100.000
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US-08-653-294-8 x 114590
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US-08-653-294-8 x I14591
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Locus I14591
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                                                      Quality:
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                                         alignment_scores
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E 2 (bases 1 to 259)

S Grimsley,C., Mather,K.A. and Ober,C.

Direct Submission

AL Submitted (03-SEP-1997) Fred Hutchinson Cancer Research Center,

1100 Fairview Ave. N., M374, Seattle, WA 98109, USA

1259

Location/Qualifiers

1. 259

//organism="Homo sapiens"

//solate="034"

//db_xref="taxon:9606"

//map="6p21:3"

//map="6p21:3"

//map="6p21:3"
                                     Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria: Primates: Catarrhin; Hominidae: Homo. 1 (bases 1 to 259) (arimaley,c., Mather, K.A. and Ober,c. HIA-H: a pseudogene with increased variation due to balancing selection at neighboring loci solection at neighboring loci 99083426
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Apple, R. J., Bugawan, T. L. and Erlich, H. A.
Methods and reagents for HLA class I A locus DNA typing
Patent: US 5451512-A 67 19 SEP-1995;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 49.00 Length: 10 Ratio: 4.900 Gaps: 0 Percent Similarity: 100.000 Percent Identity: 100.000
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/codon_start=1
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Sequence 67 from patent US 5451512.
114590
114590.1 GI:997073
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84 c 95 a
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/gene="HLA-H"
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Unclassified.
                             Homo sapiens
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LOCUS I14590
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                human.
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26-SEP-1995
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1 (bases 1 to 270)
Apple, K.J., Bugawan, T.L. and Erlich, H.A.
Methods and reagents for HLA class I A locus DNA typing
Patent: US 5451512-A 68 19-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 270)
Apple, R.J., Bugawan, T.L. and Erlich, H.A.
Methods and reagents for HLA class I A locus DNA typing
Patent: US 5451512-A 69 19-SEP-1995;
Length: 10
Gaps: 0
Percent Identity: 100.000
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Gaps: 0
Percent Identity: 100.000
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Sequence 69 from patent US 5451512.
114592 16:997075
                                                                                                                                                                                                                                                                            114591 270 bp DNA
Sequence 68 from patent US 5451512.
114591
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                                                                                                                          Align seg 1/1 to: I14590 from: 1 to: 270
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                                                                                                                                                                               222 CGAGAGAACCIGCGGAICGCGCTCCGCTAC 251
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1 84 c 95 q
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alignment_scores:
Quality: 49.00 Length: 10
Ratio: 4.900 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block: US-08-653-294-8 x I14592

Align seg 1/1 to: I14592 from: 1 to: 270

us-08-653-294-8.rge

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Carcinoembryonic antigen CE Carcinoembryonic antigen CE CEA protein encoding cDNA. Human cytomegalovirus (HCMV
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03-MGG-1990; 207329.
03-MGG-1990; JP-207329.
03-MGG-1990; JP-207329.
03-MGG-1990; JP-207329.
05-MGG-1990; JP-207329.
06-MGG-1990; JP-207329.
07-MGG-1990; JP-207329.
08-MGG-1990; JP-207329.
08-MGG-1990; JP-207329.
08-MGG-1990; JP-207329.
08-MGG-1990; JP-207329.
09-MGG-1990; JP-2073
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Human leukocyte antigen; transgenic; germ cells; somatic cells;
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19-MAR-1991 (first entry)
Sequence encoding HLA-B51 antigen.
Probe; HLA class I DNA; immunogen; ss.
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ID Q01834 standard; DNA; 1086 BP.
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US-08-653-294-8 x Q29167
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N_Geneseq_36:Q54352
N_Geneseq_36:T46062
N_Geneseq_36:V70153
N_Geneseq_36:T85076
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270 | Hid-Bw 52 exon 2 alpha-1 domain 1086 | Sequence encoding HiA-B51 anti 1086 | Sequence encoding HiA-B51 anti 1089 | HiA-Bw52 gene for production of 1056 | Sequence encoding the human him of 1056 | Sequence of genomic DNA encoding 553 | HiA-By7 consensus sequence. De 35100 | KSHV LUR DNA (nucleotides 70, 137507 | Sequence and N-termin 1011 | Beta-glucuronidase-contg inser 1011 | Braphylococcus aureus contig inser 1011 | Braphylococcus aureus contig inser 1011 | Braphylococcus aureus contig inser inser 1011 | Braphylococcus aureus contig inser inser in 11309 | Borrella burgdorferi polynuc 1011 | Braphylococcus aureus cour 1011 | Braphylococcus aureus co
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Staphylococcus aureus ribonuci
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H6/CEA expression cassette fro
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Carcinoembryonic antigen cDNA.
Heat-resistant barley beta-amy
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-Q=/cgn1_1/USPTO_spool/US08653294/runat_04022000_160701_15807/app_query.fasta.1

-Q=/cgn1_1/USPTO_spool/US08653294/runat_04022000_160701_15807/app_query.fasta.1

-Q=/cgn1_1/USPTO_spool/US08653294/runat_0402000_16000

-GAPEXT=4.000 -MINMATCH=0.100 -MODEL-0.000 -MODEXT=0.000

-GAPEXT=4.000 -QAREXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500

-FGAPOP=6.000 -DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500

-TRANS-human40.cdi -LIST=45 -DOCALIGN-200 -THR_SCORE-pct

-ALIGN=15 -MODE-LOCAL -OUTFWT=pfs -NORM=ext -MINLEN-0

-MAXLEN-1000000 -USER-US08653294 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
                                                                                                                                                      4.5,
                                                                                                                                                  Results were produced by the GenCore software, version Copyright (c) 1993-2000 Compugen Ltd.
       out_format : pfs
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Database sequences: 311585
Database length: 125096042
Search time (sec): 590.520000
                                                                   Date: Feb 8, 2000 1:27 PM
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Query length: 10
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N_Geneseq_36:012114
N_Geneseq_36:X33945
N_Geneseq_36:N70935
N_Geneseq_36:N70935
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N_Geneseq_36:V73804
N_Geneseq_36:V19941
N_Geneseq_36:T85000
N_Geneseq_36:X51732
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N_Geneseq_36:Q05916
N_Geneseq_36:V09025
N_Geneseq_36:Q43182
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Geneseq_36:043183
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Sequence
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rakiguchi M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New DNA for class 1 human leucocyte antigens and derived probes and transformed cells, useful for DNA typing, as immunogens etc.
Claim 2; ppl1-12; 23pp; English.
The HLA class I DNA can be used a source of probes for use in DNA typing. Transformed cells, which are useful as immunogens, can be obtained by introducing these DNAs into eucaryotic cells.
Sequence 1086 BP; 333 A; 335 C; 358 G; 170 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QUOSON-1991 (first entry)
03-GAM-1991 (first entry)
HLA-B51 gene for production of monoclonal antibodies.
Alloptype specific monoclonal anti-HLA antibodies; hybridomas; transgenic animals; HLA-B51 gene; ss.
transgenic animals; HLA-B51 gene; ss.
key
1. 73
exon
/*tag= a
/*mumber=1
exon
74. .343
                Length: 10 terror terror terror terror terror 10 terror terror terror 10 terror terror 100.000 lignment block.
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Gaps: 0
Percent Identity: 100.000
                                                                                                                                                       to: 1086
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                                                                                                                                                                                                                294 CGAGAGAACCTGCGGATCGCGCTCCGCTAC 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    294 CGAGAGCTGCGGATCGCGCTCCGCTAC 323
                                                                                                                                                                                                                                                                                                                                                                                      Sequence encoding HLA-Bw52 antigen.
Probe; HLA class I DNA; immunogen; ss.
                                                                                                                                                                                              1 ArgGluAsnLeuArgIleAlaLeuArgTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ArgGluAsnLeuArgIleAlaLeuArgTyr 10
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1. .1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-AUG-1989.
11-AUG-1988; JP-200758.
(OLYU) Olympus Optical Co., Ltd.
                                                                                                                                                       from: 1
                                                                                                                                                                                                                                                                                                              seq_documentation_block:
ID Q01822 standard; DNA; 1086 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
ID Q05693 standard; DNA; 1089 BP.
AC Q05693;
                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                       seq_name: N_Geneseq_36:Q01822
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Ratio: 4.900
Percent Similarity: 100.000
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                                                                                                                                                       Align seg 1/1 to: Q01834
                                                                                              alignment_block:
US-08-653-294-8 x Q01834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-08-653-294-8 x Q01822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kano K, Takiguchi;
WPI; 90-046289/07.
P-PSDB; R03142.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                       .9-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-FEB-1990
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Taxayoull m, and an anti- HLA antibodies prodn. - using Allotype specific monoclonal anti- HLA antibodies prodn. - using hybridoms derived from transgenic animals carrying HLA gene and immunised with HLA antigen of different allotype Disclosure; Fig 1 A-G; 20pp; English.

The human HLA-B51 gene was injected into fertilised mouse eggs and these introduced into the uterus of a pseudo pregnant mouse.

The young were tested to ensure incorporation of the gene into the chromosome, and one of them mated 3 times with a normal male to produce 16 young, seven of which carried the HLA-B51 gene.

The transgenet offspring were fused with HLA antigen.

The spleen lymphocytes were fused with myeloma cells. Hybridomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JAN'1991 (first entry)
MIA-EW52 gene for production of monoclonal antibodies.
Alloptype specific monoclonal anti-HLA antibodies; hybridomas; transgenic animals; HLA-EW52 gene; ss.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality: 49.00 Length: 10 Ratio: 4.900 Gaps: 0 Percent Similarity: 100.000 Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            335 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             295 CGAGAGAACCTGCGGATCGCGCTCCGCTAC 324
                                                                                                                                                                                                         /note="alpha 3-domain"
896. .1012
                     'note="alpha 1-domain'
                                                                                                             note="alpha 2-domain
320. .895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ArgGluAsnLeuArgIleAlaLeuArgTyr 10
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ID Q05701 standard; DNA; 1089 BP.
AC Q05701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224 A;
                                                                                                                                                                                                                                                                                              1013. .1042
/*tag= f
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1043. .1089
/*tag= g
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07-FEB-1990; 102424.
08-FEB-1989; JP-029313.
(OLYU ) OLYMPUS OPTICAL KK.
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/number=1
74. .343
/*tag= b
                                           .619
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                                                                                                                                                                                                                                                                        'number=5
/number=2
                                                                                         'number=3
                                                                                                                                                                                 /number=4
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                                                                      /*tag=
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US-08-653-294-8 x Q05693
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Valuation .

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seq_name: N_Geneseq_36:N70935
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US-08-653-294-8 x X33945
                                                                                                                                  alignment_block:
US-08-653-294-8 x Q12114
                                                                                                                                                                                                                                                seq_documentation_block:
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Ratio:
Percent Similarity:
                                                                             alignment_scores:
Quality:
Ratio:
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 800000g
                                                                                                                                                                                                                                                            The spleen imphocytes were fused with myeloma cells (P3x63-Ag8.653). Hybridomas producing antibodies were selected. Sequence 1089 BP; 223 A; 336 C; 359 G; 171 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human leukocyte antigen; probe; major histocompatibility complex;
MHC; class I; ss.
Homo saplens.
                                                                                                                                                                                                                                                       Allotype specific monoclonal anti- HLA antibodies prodn. - using hybridomas derived from transgenic animals carrying HLA gene and immunised with HLA antigen of different allotype bisclosure; Fig 1 A-G; 20pp; English.

The human HLA-Bw52 gene was introduced into mouse L cells and then these cells used to immunise one of the transgenic mice (See Q05693).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HLA-BW53 gene, DNA probe and transformant cells - used for immunisation, identifying specificity of antiserum etc.
                                                                                                                                                                                                                                                                                                                                                                                           Gaps: 0 Gaps: 0 Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to: Q05701 from: 1 to: 1089
                                                                         /note="alpha 3-domain"
896. .1012
/*tag= e
'note="alpha 1-domain"
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                                   /note="alpha 2-domain'
520. .895
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1. .1089
/*tag= a
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ID Q12114 standard; DNA; 1089 BP.
AC Q12114;
                                                                                                          /number=5
1013. .1042
/*tag= f
/number=6
1043. .1089
/*tag= g
/number=7
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22-SEP-1889; 247697.
22-SEP-1989; JP-247697.
(OLYU ) OLYMPUS OPTICAL KK.
WPI: 91-182991/25.
P-PSDB; R12463.
                                                                                                                                                                                  EP-383183-A.
22-AUG-1990.
27-EB-1990.
08-FEB-1989; JP-029313.
(OLYU ) OLYMPUS OPTICAL KK.
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         .619
                              /number=3
                                                                      /number=4
                                                                                                                                                                                                                                                                                                                                                                                            Quality: 49.00
Ratio: 4.900
Percent Similarity: 100.000
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                                                           /*tag=
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US-08-653-294-8 x Q05701
                                                                                                                                                                                                                                       Takiguchi M;
WPI; 90-255479/34.
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                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores
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P-PSDB: 10.20.5.
New isolated human genes
Claim 2; Page 126-129; 184pp; English.
This sequence represents a human gene of the invention, that is induced
This sequence represents a human gene of the invention, tesignated HCMV-inducible
genes (cig or cigs). The invention also relates to genes that are
repressed in the presence of HCMV infection, designated HCMV-repressible
genes (crg or crgs). The products can be used to obtain agents which can
be used for anti-viral therapy, particularly anti-HCMV therapy. They can
also be used for the development of drugs that would allow for higher
dosage IFN treatments without the concomitant toxicity normally
associated with administering high levels of IFN. The products can also
be used for detection, diagnosis and drug screening.
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Claim 1; Page 1; 11pp; Japanese.

Probes comprising part of the sequence can be used to identify class I genes. The DNA can be expressed for immunisation of animals and prodn. of monoclonal antibodies specific for the HIA-BW53 antigen. See also J03112485 and J03112486.
Sequence 1089 BP; 222 A; 337 C; 356 G; 174 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 10
Gaps: 0
Percent Identity: 100.000
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3.889 Gaps: 0
90.000 Percent Identity: 70.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ArgGluAsnLeuArgIleAlaLeuArgTyr 10
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2-5EP-1997; U5-05975.
08-5EP-1997; U5-05978.
(UYPR-) UNIV PRINCETON.
CONG J, SChenk T, Zhu H;
WPI: 99-43759/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouality: 49.00
Ratio: 4.900
Percent Similarity: 100.000
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T61639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mrna
                                                                                                                                                                                                                                                                                                                                                                                                                                mrna
                                                                                                                                                                                                                                                                                                            The DNA may be used as a hybridisation probe for detecting the HLA B27 gene, e.g. for assessing susceptibility to rheumatic disorders such as anytylosis spondylitis, or may be used to transform cells for prodn. of HLA B27. The HLA B27 may be used to detect HLA B27 antibody in human serum, or to produce mono- or polyclonal HLA B27
                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-APR-1991 (first entry)
Sequence of genomic DNA encoding human histocompatibility antigen
HIA-B 27.
 LU-APR-1991 (first entry)
Sequence encoding the human histocompatibility antigen HLA B27.
Rheumatic disorder; genetic screening; diagnosis;
ankylosing spondyittis; ss.
Homo sapiens.

    and diagnostic reagents contg.

                                                                                                                                                                                                                                                       162 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ankylosing spondylitis; rheumatic disorder; diagnosis;
                                                                                                                                                                                                                                                                                          Length: 10
Gaps: 0
Percent Identity: 70.000
                                                                                                                                                                                                                                                       344 G;
                                                                                                                                                                                                                                                                                                                                                        from: 1 to: 1026
                                                                                                                                                                                                                                              antibodies for use in immunoassay.
Sequence 1026 BP; 213 A; 307 C;
                                                                                                                                   (BEHW ) BEHRINGWERKE AG.
Riethmuller G, Meo T, Welss E, Szots H;
WPI: 87-157893/23.
P-PSDB; P70590.
                                                                                                                                                                                                                                                                                                                                                                                          223 CGAGAGGACCTGCGGACCCTGCTCCGCTAC 252
                                                                                                                                                                                                                                                                                                                                                                         1 ArgGluAsnLeuArgIleAlaLeuArgTyr 10
                                                                      Location/Qualifiers
1. .1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                      DNA coding for antigen HLA B27 such DNA, antigen or antibody Claim 2; Page 4; 5pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
ID N70225 standard; DNA; 3874 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            518. .590
/*tag= a
720. .989
/*tag= b
1090. .1506
/*tag= c
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...3041
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2450. .2566
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4.250
80.000
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                                                                                                        28-NOV-1985; 542024.
28-NOV-1985; DE-542024.
21-DEC-1985; DE-545576.
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3148. .
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US-08-653-294-8 x N70935
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21-NOV-1986; 116139.
seg_documentation_block
                                                                                                                                                                                                                                                                                          Quality:
Ratio:
                                                                                                                                                                                                                                                                                                            Percent Similarity:
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                                                                                        DE3542024-A
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                                                                                                 04-JUN-1987
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P-PSDB; P70155.

DNA coding for human histocompatibility antigen HLA-B 27 - useful for diagnosis and antigen and antibody prodin.

Claim 1: p6: 13pp; German.

THe DNA may be used to detect the HLA-B 27 gene (opt. mutated) in human genetic material. The HLA-B 27 may be used to detect anti-HLA-B 27 antibodies in human serum. The antibodies may be used to determine HLA-B 27 levels in human serum, e.g. for diagnosis of rheumatic disorders, esp. ankylosing spondylitis.

Sequence 3874 BP; 751 A; 1094 C; 1171 G; 858 T;
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Detecting pre-disposition to seronegative spondylarthropathies -
from the absence of a C residue at a specific position in the
finanting region of the HLA B27 allele
Claim 1; Page 52-56; 68pp; English,
Genetic predisposition to seronegative spondyloarthropathies (SNSA)
is detected by determining the absence of a cytosine nucleotide in
the 3' flanking region (see also T61647-48) of an HLA-B gene at a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "3' flanking region diagnostic for genetic predisposition to SNSA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUN-1997 (first entry)
Lath B27 consensus sequence.
HLA B27; seronegative spondylarthropathy; ankylosing spondylitis;
Reiter's syndrome; arthritis; acute anterior uveitis; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "3' flanking region diagnostic for genetic predisposition to SNSA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note "HLA-B27 3' flanking region, downstream of
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/note* "absence of cytosine at this site
indicative of a predisposition to SNSA"
01-JAN-1985; DE-542024.
21-DEC-1985; DE-545576.
(BEHW) BEHRINGWERKE AG.
Szots H, Weiss E, Dorner C, Lang M, Meo T, Riethmuller WPI; 87-171469/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 10
Gaps: 0
Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 3874
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3968. .6653
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16-406-1995.
01-SEP-1995: US-522942.
(CEDA-) CEDARS SINAI MEDICAL CENT.
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ID T61639 standard; DNA; 6553
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4.250
80.000
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US-08-653-294-8 x N70225
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Ratio:
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Mrit; 37-097-44.70.

Rapos1's sarcoma-associated herpes virus nucleic acid - encodes
di:hydro:folate reductase and is useful for treatment, prophylaxis
or diagnosis of Kapos1's sarcoma

PT or diagnosis of Kapos1's sarcoma

Disclosure; Column 125-156; 109pp; English.

This sequence is a fragment of the Kapos1's sarcoma-associated
herpesvirus (KSHV) LUR (long unique region). This fragment contains
coding regions for ORF54, ORF54, ORF56 which encodes a transactivator
(LCTP), K8, ORF52, ORF53, ORF54 which encodes durpase, ORF55, ORF56
which encodes DNA replication protein I, ORF57 which encodes immediated
carly protein II (IEP-II), K9 which encodes transactivator
crossembly/DNA maturation protein, ORF59 which encodes a samplication protein or semally rich encodes a large ribonucleotide reductase, ORF62 which encodes tegument protein II. KSHV is a new human

CI, ORF64 which encodes tegument protein III. KSHV is a new human
Herpesvirus (HHV8) believed to cause Kapos1's sarcoma (KS) which is the
most common form of neoplasm occurring in persons with adquired immune
deficiency syndrome (AIDS). The DHFR protein is useful for vaccination,
prophylaxis, diagnosis and treatment of a subject with Kapos1's sarcoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KSHV LUR DNA (incleotides 70, 201-105,300).

Kaposi's sarcoma; acquired immune deficiency syndrome; AIDS; DHFR; Bcl-2; diaphydroclate reductase; LUR; long unique region; vaccine; prophylaxis; diagnosis; treatment; Hransactivator; LCTP; durpase; IEP-II; DNA replication protein I; immediated early protein II; vIRFI; ICSBP; phosphoprotein; DNA replication protein II; ribonucleotide reductase; sascembly/DNA maturation protein; tegument protein; ds.

Kaposi's sarcoma-associated herpesvirus.
position corresponding to nucleotide 4495 of the HLA-B27 consensus sequence given in T61639. Probes and primers (see also T61640-46) based on this region can be used in diagnostic assays to detect the genetic predisposition to SNSA, and permit the distinction of B274 individuals who are resistant to SNSA from B274 normal individuals who are resistant to such the distinction of B274 sequence 6553 BP; 1443 A; 1619 C; 2017 G; 1474 T;
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29-NOV-1996; 770379.
29-NOV-1996; US-770379.
29-NOV 1996; US-770379.
CUYCO ) UNIV COLUMBIA NEW YORK.
BOHERZKY RA, Chang Y, Edelman IS, Moore PS, Russo JJ;
WPI; 99-069741/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8650
                                                                                                                                                                                                                               Length: 10
Gaps: 0
Percent Identity: 70.000
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Gaps: 0
Percent Identity: 77.778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10010 C;
                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: T61639 from: 1 to: 6553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1102 CGAGAGGACCTGCGGACCCTGCTCCGCTAC 1131
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ArgGluAsnLeuArgIleAlaLeuArgTyr 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
ID     V73804 standard; DNA; 35100 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V73804;
25-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34.00
4.250
88.889
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4.250
80.000
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US-08-653-294-8 x T61639
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Ratio:
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Ratio:
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/product- macrophage inflammatory protein II complement (27137. .27424)
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                                                                                                                                                                                                                                                                                                                                                                                                     /product interferon regulatory factor 99500. .90541
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8699. .11236
/*tag= b
                       to: 35100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product capsid protein IV complement (123808. .127296)
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complement (21548. .21832)
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complement (58976. .60175)
                                                                                                                                                                                                                                                                                                                                                            /product glycoprotein M complement (69412. 69915)
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                       Align seg 1/1 to reverse of: V73804 from: 1
                                               σ
                                        1 ArgGluAsnLeuArgIleAlaLeuArg
                                                                                               V19941 standard; DNA; 137507 BP
V19941;
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alignment_block:
US-08-653-294-8 x V73804/rev
                                                                      seq_name: N_Geneseq_36:V19941
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US-757669.
US-686243.
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                                                                                       seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9804576-A1
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                                                                                                                                                                                                                                                                                             CDS
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US-686350

25-JUL-1996;

Percent Similarity:

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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X51732;
                                                                                                                                                                                                                                                                                                                                     source
Proparation of vaccines for treatment of, HIV patients

Proparation of vaccines for treatment of, HIV patients

Proparation of vaccines for treatment of, HIV patients

Example 1: page 135-203; 230pp; English.

This sequence represents the long unique region and terminal repeat of

This sequence represents the long unique region and terminal repeat of

the Kaposi's sarcoma-associated herpes virus (KSHV), KSHV is also known

as human herpes virus 8 (HHV8). This sequence contains the DNAs of the

Invention which encode KSHV polypeptides selected from: (a) viral

CC (a) viral IRF 1; (d) complement-binding protein; glycoproteins B, M or L;

CC (c) viral IRF 1; (d) complement-binding protein; glycoproteins B, M or L;

CC (d) capsid protein IV encoded by ORF65; and (e) immediate early protein

CC (d) capsid protein IV encoded by ORF65; and (e) immediate early protein

CC (d) capsid protein; belied probes for the nucleic acid, proteins

CC (d) capsid protein IV encoded by ORF65; and (e) immediate early protein

CC (d) capsid protein antipodies (Aa)) specific for the proteins are useful for

CC (d) capsid protein and belied proteins can be treatment of HHV8 infection,

CC (d) capsid protein can be used for prophylaxis or treatment of HHV8 infection,

CC (d) fiferentiate between lymphomas, and HHV8 may be implicated in many

CC (d) differentiate between lymphomas, and HHV8 may be implicated in many

CC (a) differentiate between lymphomas, and animals containing the

CC (a) date used for antiviral drugs, e.g. dihydrofolate reductase gene

CC (a) deal manue status of a patient infected with HIV. HHV8 derived protein

CC (a) e.g. treating rheumatoid arthritis. This sequence is stated as containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31375 T;
                                                                                                                                     New nucleic acid encoding Kaposi's sarcoma associated herpes virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Type II topoisomerase database reference sequence SEQ ID NO:182. Detection: identification: TopoII; contamination; food; human; animal; plant; plant; soil; water; PCR; polymerase chain reaction; ds. Sphingomonas capsulatum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35758 G;
                                                                       13-NOV-1996; US-748640.
(UYCO ) UNIY COLUMBIA NEW YORK.
Bohenzky RA, Chang Y, Edelman IS, Moore PS, Russo JJ;
WPI; 98-130615/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to reverse of: V19941 from: 1 to: 137507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity: 77.778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37795 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73775 CGGGAGAATCTCCGGTGTTCTCTGCGA 73749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ArgGluAsnLeuArgIleAlaLeuArg 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32579 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
ID T85000 standard; DNA; 423 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-1990; 548138.
06-JUN-1995; US-470179.
05-JUL-1990; US-548138.
13-AUG-1993; US-106482.
(UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-NOV-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.00
4.250
88.889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-653-294-8 x V19941/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: N_Geneseq_36:T85000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137507 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97-362925/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
                                         10-OCT-1996;
13-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T85000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Huang
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Detection and identification of organisms - using DNA primers to amplify signature segment of organism's type II topoisomerase Calaim 17-178; IIAPP; English.

A method has been produced for selectively amplifying DNA segments of one or more species of organisms in a sample. The method involves: (a) providing a database containing reference sequences, comprising a subunit sequence of a signature region of a macromolecule selected from a type II topoisomerase (Topoil), or a homoloque, where each reference sequence is specific to a different species of a chosen group, and the macromolecule comprises lst and 2nd conserved regions adjacently flanking the signature region; and (b) making an extract of DNA molecules, and selectively amplifying DNA segments of the signature constructed to bind a DNA encoding the macromolecule, to produce amplified DNA segments. The present sequence represents a DNA fragment constructed to bind a DNA encoding the macromolecule, to produce amplified DNA segments. The present sequence represents a DNA fragment constanting a signature sequence for Sphingomonas capaulatum. The method can be used to identify all of the different organisms present in a single sample without using multiple probes. It can accurately distinguish and similar and related species, and can be used with, e.g. contaminated food products, tissue or fluid samples from diseased humans, animal or plants, soil samples and water samples from any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated human genes and the secreted polypeptides they encode - useful for diagnosis and treatment of e.g. neurological disorders. tumours, immune disorders, inflammation or haematological disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted protein; cancer; immune disorder; infection; inflammatory disorder; skin disorder; tumour; atherosclerosis; restenosis; autoimmune disorder; Alzheimer's disease; peripheral neuropathy; trauma; spinal cord injury; allergy; hematopoietic disorder; skeletal disorder; neurological disorder; arthritic disorder; asthma; immunodeficiency disease; AIDS; transplant rejection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps: 0
Gaps: 0
Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC.
Brewer LA, Ebner R, Lafleur DW, Moore PA, Olsen HS,
Rosen GA, Ruben SM, Shi Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to reverse of: T85000 from: 1 to: 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding a human secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    366 CGGCAGAACCIGCGGCTCGTGCTCCGC 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ArgGluAsnLeuArgIleAlaLeuArg 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X51732 standard; DNA; 978 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio: 3.667
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-653-294-8 x T85000/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: N_Geneseq_36:X51732
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12-SEP-1997; US-058666.
12-SEP-1997; US-058667.
12-SEP-1997; US-058973.
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05-SEP-1997; US-057663
05-SEP-1997; US-057669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-SEP-1998; U18360
12-SEP-1997; US-058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence 423 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 99-204988/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9911293-A1.
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claim 1; Page 170; 215pp; English.

X51701-55 encode human secreted proteins. The polynucleotides and the teating or ameliorating medical conditions, e.g. by protein or generating or ameliorating medical conditions, e.g. by protein or generating or ameliorating medical conditions, e.g. by protein or generating or ameliorating medical conditions and iso be diagnosed by determining the macount of the new polyneptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are constructed for each polynucleotide, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, immune disorders, infection, inflammatory disorders, skin disorders, tumours, atherosclerosis, restenosis, autoimmune disorders, Alzheimer's disease, peripheral neuropathies, trauma, spinal cord injuries, allergy, hematopoietic disorders, skeletal disorders, neurological disorders, arthritic disorders, asthma, immunodeficiency disease, AIDS and transplant rejection. The polypeptides are also useful for identifying their beinging partners.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1: Page 12; 11pp; English.

E.coli transformed with expression vectors contg this sequence produce BG at a high level (BG = 50% of total cellular protein).

The efficient BG promoter sequence can be placed upstream of DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_type=imperfect 26bp dyad
/note="possible repressor binding function"
231. .552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="confers high expression activity"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Efficient prokaryotic expression system -
using DNA coding for part or all of the amino acids of
Escherichia coli beta-glucuronidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-051-1990 (first entry)
Beta-glucuronidase-contg insert of E.coli plasmid pBG1
E.coli MS371 beta-glucuronidase (BG);
prokaryotic expression system; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
502. 1011
4489- a
485. .495
/*tag- b
//abel- strong RBS
//note-"start and end not defined"
                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: 978
                                                                                                                                                                                                                                                                                                                             197 G;
                                                                                                                                                                                                                                                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to reverse of: X51732 from: 1
                                                                                                                                                                                                                                                                                                                             256 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 AGGGAGGTGAGAATCCAACTGCGGTGG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
ID N80055 standard; DNA; 1011 BP.
                                                                                                                                                                                                                                                                                                                             285 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                    Quality: 33.00
Ratio: 3.667
Percent Similarity: 90.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: N_Geneseq_36:N80055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JAN-1988.
26-DEC-1984; 686344.
26-DEC-1984; US-686344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (REPL-) Repligen Corp.
Anilionis A, Palmer JL;
WPI; 88-049643/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; P80057
                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US4721671-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_rna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N80055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
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CC coding for other proteins eqinsulin. Fusion proteins are then CC produced at high levels.
CC The region from 231-552 or any part of it can be used in an expression system to enhance prodn of proteins.
SQ Sequence 1011 BP; 245 A; 220 C; 253 G; 293 T;
```

SQ Sequence 1011 BP; 245 A; 220 C; 253 G; 293 T; alignment_scores:

alignment_scores:

Quality: 33.00

Percent Similarity: 90.000

Percent Identity: 60.000

alignment_block:
US-08-653-294-8 x N80055/rev

Align seg 1/1 to reverse of: N80055 from: 1 to: 1011

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us-08-653-294-8.rst

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1 R33700 yh78d08.rl Soares pla
1 AA786878 m6h06a1.rl Aspergil
1 AQ188490 HS_3228_B2_G04_MR C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: heart; normalized directionally cloned cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Construction of a normalized directionally cloned cDNA library adult heart and analysis of 3040 clones by partial sequencing Genomics 35 (1), 231-235 (1996)
                                                                                                                                         seq_documentation_block:
LOCUS
LOCUS
C03945
DEFINITION C03945 Human heart cDNA (YNAKamura) Homo sapiens cDNA clone
3NHC2454, mRNA sequence.
ACCESSION C039454
                                                                                                                                                                                                                                                                                                                                                              Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 232)
Tanaka,T., Ogiwara,A., Uchiyama,I., Takagi,T., Yazaki,Y. and Nakamura,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block: 255 bp mRNA EST 10-DEC-1996 LOCUS AA151891 255 bp mRNA DEFINITION zoolff06.rl Stratagene colon (#937204) Homo sapiens CDNA clone DEFINITION 5001f06.rl Stratagene colon (#937204) Homo sapiens CDNA clone IMAGE:566435 5' similar to 9b:M15497_cds1 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-24(A-9) A*2401 (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Oct 24, 1995 this sequence version replaced gi:1040105
Contact: Yusuke Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.232
/Organism="Homo sapiens"
/db_tratef="taxon:9606"
/clone="3NHC2454"
/clone=lib="Human heart cDNA (YNAKamura)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 49.00 Length: 10 Ratio: 4.900 Gaps: 0 Percent Similarity: 100.000 Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Institute of Medical Science
University of Tokyo
4-6-1, Shirokanedai, Minato-ku, Tokyo 108,
TEL: 81-3-5449-5372
Fax: 81-3-5449-5433
     414
418
418
203.39
205.59
205.59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: yusuke@ims.u-tokyo.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ArgGluAsnLeuArgIleAlaLeuArgTyr 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40 CGAGAGAACCTGCGGATCGCGCTCCGCTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="adult"
128.97
128.89
128.89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from adulí heart"
77 c 68
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AA151891.1 GI:1720754
                                                                                                                                                                                                                                                                                  C03945.1 GI:1467196
  35.00
35.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: gb_est10:AA151891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-08-653-294-8 x C03945
                                                                                                    seq_name: gb_est8:C03945
                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sednence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25
                                                                                                                                                                                                                                                                                                                                    human.
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gb_est3:R33700
gb_est19:AA786878
gb_gss10:AQ188490
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
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AA837121 od19905.sl NOI_CGAP_GC
AA332511 EST36483 Embryo, 8 wee
A9302 yw25c11.rl Morton Fetal
AQ833080 HS_5499_A2_H02_SP6E RF
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-0-Cgn1_1/USPTO_spool/US08653294/runat_04022000_160700_15770/app_query.fasta.1

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-MINMATCH-0.100 -LOOPCL-0.000 -LOOPEXT-0.000 -GGAPDF4.500

-GGAPEXT-0.000 -YGAPOP-10.000 -YGAPEXT-0.500 -FGAPOP-6.000

-FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500 -DELOP-6.000

-LIST-45 -DOCALIGN-200 -THR_SCORE-pct -ALIGN-15 -MODE-LOCAL

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-OUTPWT-pfs -NORM-ext -MINLEN-0 -MAXIELEN-1000000 -USER-US08653294
                                                                                                 About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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gb_est27:A1466429
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Tel: 272-20-8856
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Faxi: 315 close is available royalty-free through LLNL; contact the
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This close is available royalty-free through LLNL; contact the
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This considered overall poor quality
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 1.
Location Qualifiers

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AA265158 GI:1898964
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I (bases 1 to 255)
Hiller, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
Radidis, E., Moore, B., Moris, M., Parsons, J., Prange, C., Rifkin, L.,
Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Weg, J.,
Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primetes; Catarrhini; Hominidae; Homo.
1 (bases 1 to 283)
Claudio,J.O., Liew,C.C., Dempsey,A.A., Cukerman,E., Stewart,A.K.,
Na,E., Atkins,H.I., Iscove,N.N. and Hawley,R.G.
Identification of sequence-tagged transcripts differentially
                                                                                                                                                                                         Generation and analysis of 280,000 human expressed sequence tags Genome_Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                    On May 8, 1995 this sequence version replaced g1:800234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 others
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Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 CGAGAGAACCTGCGGATCGCNCTCCGCTAC 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ArgGluAsnLeuArgileAlaLeuArgTyr 10
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Percent Similarity: 100.000
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US-08-653-294-8 x AA151891
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                                                                                                                                                                      and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                 97044478
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COMMENT
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KEYWORDS
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/note="Vector: Lambda Zap Express (Stratagene); Site_1:
CooRis Site_2: XhoI; Unidirectional cloning sites:
ECORI. Site_2: XhoI; Unidirectional cloning sites:
ECORI.-Abol. mRNA was purified from KGl-a cell line,
was synthesized using an XhoI-OligodT linker primer. EcoRI
adaptors were ligated, followed by digestion with XhoI for
directional cloning into predigested Lambda Zap Express"
1 c 88 g 40 t
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Unpublished (1995)
On Apr 14, 1993 this sequence version replaced gi:785255.
Contact: Jun Takeda
Institute for Molecular and Cellular Regulation, Gunma University
3-39-15 Showa-machi, Maebashi Gunma 371, Japan
                                                                                                                    Contact: Hawley RG
Contact: Hawley RG
Contact: Hawley RG
Contact: Hawley RG
Contact: Hawley RG
Contact: Hawley RG
Contact: Hawley RG
Contact: Hawley Research Laboratories
The Toronto Hospital
CRCS-424, 67 College St., Toronto, Ontario MSG 2M1, Canada
Tel: 416 3403834
Fax: 416 3403834
Fax: 416 3403836 MHC class I HIA-Bw gene. Clone was randomly
ploked from KGlas primary library.
Seq primar: 5' GAAATTAACCCTCATTAAAGGG 3'
High quality sequence stop: 283.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib=*KG1-a Lambda Zap Express cDNA library"
/cell_type="promyeloblast"
/cell_line="KG1-a"
expressed within the human hematopoietic hierarchy Genomics 50 (1), 44-52 (1998)
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Gaps: 0
Percent Identity: 100.000
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Location/Qualifiers
1. 375
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Mary Contract Contrac

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Quality:
Ratio:
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/db_xref="taxon:9606"
/clone_lib="Human pancreatic islet"
/clone_lib="Human pancreatic islet"
/note="vector: Lambda ZAPII; Site_1: Eco RI; Site_2: Xho
I; mRNN was prepared from normal adult human islets. cDNA
was directionally synthesized from the Xho I in the vector
to the EcoRI site. cDNA was size fractionated to remove
sequences <loop by in size." 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
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Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 618)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NGI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NGI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NGI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

CGAP/PRIGAP), Tumor Gene Index.

Unpublished (1998)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert Strausbergénih.gov

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
LOCUS AI399260

LOCUS AI399260

DEFINITION QY27007 x1 NCLCGAP_Brn23 Homo sapiens cDNA clone IMAGE:2013205 3'
Similar to gb:D32129 HLA CLASS I HISTOCOMPATIBILITY ANTICEN,
AW -66(A-10) A*6601 ALPHA (HUMAN); mRNA sequence.

VERSION AI359260.1 GI:4110881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. 618
/organism="Homo sapiens"
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/clone="IMAGE:2013205"
/clone_lib="NGLCGAP_Brn23"
/tissue_type="91ioblastoma (pooled)"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                Gaps: 0 Percent Identity: 100.000
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High quality sequence stop: 458.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              306 CGAGAGAACCTGCGGATCGCGCTCCGNTAC 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ArgGluAsnLeuArgIleAlaLeuArgTyr 10
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Ratio: 4.900
Percent Similarity: 100.000
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US-08-653-294-8 x D82221
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 748)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NATIONAL Gancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

Tumor Gene Index

Unpublished (1997)

On Mar 16, 1998 this sequence version replaced gi:2961758.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausbergenih.gov

Life Technologies catalog #: 11548-013

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                            into
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/db_xref="taxon:9606"
/db_made:124421"
/clone_lib="NcI_CGAP_Pan1"
/tissue_type="adenocarcinoma"
/lab_host="DH108"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: Sal1; Site_2: Not1; Cloned unidIrectionally. Primer: Oligo dT. Average insert size 1.72 kb. Life Technologies catalog #: 11548-013"
T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatina Bonaldo."
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LOCUS AI696864 748 bp mRNA EST 03-JUN-1999

DEFINITION wc74h11.x1 NC1_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2324421

Similar to qb:M28205 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,

B-511B-5) B*5101 ALPHA (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                          Length: 10
Gaps: 0
Percent Identity: 100.000
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Gaps:
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High quality sequence stop: 424.
Location/Qualifiers
1. 748
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Ratio: 4.900
Percent Similarity: 100.000
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to: AA147151
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     Align seg 1/1
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IMAGE:588587 5' similar to gb:M64740 HLA CLASS I HISTOCOMPATIBILITY
ANTIGEN, A-24(A-9) A*2402 ALPHA (HUMAN);, mRNA sequence.
AAA147151. GI:1716526
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I (bases 1 to 581)

Hillar, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hulfman, M., Kucaba, T., Lacy, M., Le, M., Mardis, E., Moore, B., Morris, M., Passons, J., Prange, C., Rikin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .581

/organism="Homo sapiens"
/db_xref="dcBs:462089"
/db_xref="taxon:9606"
/clone="IMAGE:588587"
/clone="IMAGE:588587"
/clone="IMAGE:588587"
/clone="IMAGE:588587"
/clone="Image:588587"
/lab_host="Sourcelis (kanamydin resistant)"
/note="Organ: colon; Vector: pBluescript SK-; Site_1:
pBluescript SK-; Site_1: pBluescript SK-; Site_1: pBluescript SK-; Site_1: pBluescrip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Generation and analysis of 280,000 human expressed sequence tags (enome Res. 6 (9), 807-828 (1996)
     Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 10
Gaps: 0
Percent Identity: 90.000
                                                                                                                                                                                                                                                                                      to: 748
                                                                                                                                                                                                                                                                                                                                                                                                                                               137 CGAGAGAACCTGCGGATCGCGCTCCGCTAC 166
                                                                                                                                                                                                                                                                                                                                                                                            1 ArgGluAsnLeuArgIleAlaLeuArgTyr
                                                                                                                                                                                                                                                                                      from: 1
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Ratio: 4.500
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                Align seg 1/1 to: AI696864
     Percent Similarity: 100.000
                                                                                                                 alignment_block:
US-08-653-294-8 x AI696864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: gb_est10:AA147151
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US-08-653-294-8 x AA147151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
LOCUS AA147151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
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VERSION
KEYWORDS
SOURCE
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JOURNAL
MEDLINE
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
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/ (18sue_type="pooled frontal lobe"
/ dev_stage="adult"
/ dev_stage="adult"
/ lab_host="souR (kanamycin resistant)"
/ note="Crgan: brain; Vector: Bluescript SK-; Site_1:
ECORI; Stanley Neuropathology Consortium
(www.stanleylab.org) brains S-58, S-65, S-67, S-78
Random + oligo-dr primed into EcoRI site of ZAP II Vector.
Mass excised. Avg insert length 1.9kb. Custom library
provided by Dr. Nancy Johnston [(410) 614-3918,
nli@welchlink.welch.jhu.edu].
30 a 140 c 136 g 58 t
                                                                                                                                                                           seq_documentation_block:

LOCUS
A1124815
A1124815
DEFINITION am56606.x1 Johnston frontal cortex Homo sapiens cDNa clone
INAGE:1539586 3' similar to gb:M24038_cds1 HLA CLASS I
HISTOCOMPATIBILITY ANTIGEN, BW-44(8-12) B*4402 (HUMAN); contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[ (bases 1 to 414)]
Hillieri, Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Marthi, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Washg-NCI human EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
On Jan 17, 1998 this sequence version replaced gi:1899887.
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                      MER22.t3 TAR1 repetitive element ;, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Johnston frontal cortex"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 10
Gaps: 0
Percent Identity: 90.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .414
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1539586"
                                   152 CGAGAGAACCTGCGGATCNCGCTCCGCTAC 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           284 CGAGAGAACCTGCGCACCGCGCTCCGCTAC 313
1 ArgGluAsnLeuArgIleAlaLeuArgTyr 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: AI124815 from: 1
                                                                                                                                                                                                                                                                                                                                                                         AI124815
AI124815.1 GI:3593329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44.00
4.889
90.000
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                                                                                                                    seq_name: gb_est23:A1124815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
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LOČUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

FEATURES

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Homo sapiens
Bukaryota, Mantazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Primates: Catarrhini; Hominidae; Homo.
1 (bases 1 to 522)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Mahairas, G.G., Wallace, T.C., Smith, K., Swartzell, S., Adams, M.D. and
Hood, L.
The WashU-Merck EST Project
Unpublished (1955)
Contect: Wilson RX
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Email: est@wasbon.wustl.edu
Insert Size: 1875
High quality sequence stops: 384 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1875 Std Error: 0.00
Seq primer: M33RPl
High quality sequence stop: 384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
LOCUS AQ164696.

DIA BASS 16-OCT-1998
DEFINITION HS.3006.B2_D07_T7 CIT Approved Human Genomic Sperm Library D Homo Sapiens genomic clone Plate=3006 Col-14 Row=H, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="GDB:399148"
/db_xref="taxon:9606"
/clone="IMAGE:26801"
/clone=lib="Soares infant brain INIB"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouality: 42.00 Length: 9
Ratio: 4.667 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 286 CGAGAGAACCTGCGGATCGCGCTCCGC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQ164696
AQ164696.1 GI:3562891
                                                                                                                                                                                                                                                                                                                                                                                  1. .459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: gb_gss9:AQ164696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-08-653-294-8 x R13904
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                                                                                                                                                                                                                                                                                                                                                                                         source
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KEYWORDS
SOURCE
ORGANISM
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ORIGIN
    TITLE
JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo saplens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/dclone_lib="human pancreatic islet"
/note="vector: Lambda ZAPII; Site_1: Eco RI; Site_2: Xho
I; mRNA was prepared from normal adult human islets. cDNA
was directionally synthesized from the Xho I in the vector
to the EcoRI site. cDNA was size fractionated to remove
sequences <100 bp in size."
8 others
                                                                                                                                                                                                                                                                                                                                               Human pancreatic islet ESTs
Unpublished (1995)
On Apr 14, 1993 this sequence version replaced g1:785206.
Contact: Jun Takeda
Institute for Molecular and Cellular Regulation, Gunma University
3-39-15 Showa-machi, Maebashi Gunma 371, Japan
Tel: 272-20-8856
Fax: 272-20-8896
                                                                       D82189 415 bp mRNA EST 09-FEB-1996 HUMHEC4524 Human pancreatic islet Homo sapiens cDNA similar to HLA-B, mRNA sequence.
D82189 1 GI:1183662
                                                                                                                                                                                                                                                                   Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 415)
Takeda,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 459)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hulrman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YE3904 459 bp mRNA EST 12-APR-199
YE62c03.rl Soares infant brain lNIB Homo saplens cDNA clone
IMAGE:26801 5' similar to gb:M64742_cds1 HLA CLASS I
HISTOCOMPATIBILITY ANTIGEN, A-23(A-9) A*2301 (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 10 Gaps: 0 Percent Identity: 90.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: D82189 from: 1 to: 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: jtakeda@sb.gunma-u.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    279 CGAGAGCTGNGGATCGCGCTCCGNTAC 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ArgGluAsnLeuArgIleAlaLeuArgTyr 10
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R13904
R13904.1 GI:766980
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4.778
90.000
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US-08-653-294-8 x D82189
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LOCUS R13904
                                                      seq_documentation_block:
                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: gb_est2:R13904
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       seq_name: gb_est6:D82189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
Ratio:
Percent Similarity:
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                                                                                                                                                                                                                         human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human.
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BASE COUNT ORIGIN

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

DEFINITION

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seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                     seq_name: gb_est1:T24384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         castor bean.
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KEYWORDS
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                                                      BASE COUNT
ORIGIN
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COMMENT
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon.9606"
/db_aref="plate=3006 Col=14 Row=H"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. 1 (bases 1 to 325)
Lee, N.H., Quackenbush, J., Mason, T.M., Quackenbush, J., Karlavage, A.R. and Adams, M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
                                                                                                                                                                                                                                                                                                                                   /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Co11 DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene Index
houbblished (1998)
On Jan 17, 1998 this sequence version replaced g1:1900396.
Contact: Lee, NH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
99380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
High Throughput Sequencing Center
High Throughput Sequencing Center
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Fear: (206) 616-3887
Faar: (206) 616-3887
Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                       4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 10
Gaps: 0
Percent Identity: 80.000
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2
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/db_xref="taxon:10118"
/clone="RBRAV89"
                                                                                                                                                                                                                                                                                                                                                                     186 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1
                                                                                                                                                                                               High quality sequence stop: 522.
                                                                                                                                           Sequence Tagged Connector
Plate: 3006 row: H column: 14
Class: BAC ends
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    .325
    /organism="Rattus sp."

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                                                                                                                                                                                                               Location/Qualifiers
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AI007865.1 GI:3221697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.
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US-08-653-294-8 x AQ164696/rev
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4.556
90.000
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Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                       163
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ORIGIN
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/clone_ib="lambdaZAPST"
/clone_ib="lambdaZAPST"
/note="Vector: lambdaZAPII; Site_1: ECORI; Site_2: XhOI;
Poly(A)+ RNA was purified from developing stage III to
stage V (Greenwood & Bewley, Can. J. Bot. 60:1751-1760,
1982) endosperm plus embryo of immature castor fruits.
cDNA was synthesized and cloned into lambdaZAPII according
to plustructions of the manufacturer (Stratagene):
synthesis was primed from the poly(A) tail, and cloned
directionally into XhoI (3') and EcoRI (5') sites. In few
cases, sequence data indicated that this directionality
was reversed. Partial cDNA clones predominate. "
102 t 7 9 tothers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ricinus communis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids I; Malpighiales; Euphorbiaceae;
/clone_llb-"Normalized rat brain, Bento Soares"
/note="Organ: brain; Vector: pT7T3Pac; Site_l: EcoRI;
Site_2: NotI"
a 61 c 76 g 81 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124384 351 bp mRNA EST 28-JUL-1995 crs1519 lambdaZAPST Ricinus communis cDNA clone pcrs1519, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carnegle Institution, 290 Panama St, Stanford, CA 94305
Tel: 4153251521
Email: crs@andrew.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 351)
vandeLoo,F.J., Turner,S. and Somerville,C.
Expressed sequence tags from developing castor seeds
Plant Physlol. 108, 1141-1150 (1995)
Contact: Somerville CR
Carnegie Institution
                                                                                                                                                                                                                               Percent Identity: 70.000
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Gaps: 0
Percent Identity: 80.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                    to: 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207 AGGAAGAATGTACGGTTGGCATTGAGATAC 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ArgGluAsnLeuArgIleAlaLeuArgTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:3988"
/clone="pcrs1519"
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                                                                                                                                                                                                                                                                                                                                                                                                                                    from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence.
T24384
T24384.1 GI:689202
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Percent Similarity: 100.000
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Ratio: 4.000
Percent Similarity: 100.000
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US-08-653-294-8 x AI007865
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The state of the state of

1

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// Organism="Rattus norvegicus"
// Organism="Rattus norvegicus"
// Strain="Sprague-DawLey"
// Astrain="Sprague-DawLey"
// Ab xref="Laxon:10116"
// Ab xref="Laxon:10116"
// Ab host="UI-R-A0"
// Ab host="dult"
// Ab host="bH10B (Life Technologies)"
// Ab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: msoares@blue.weeg.ulowa.edu
The sequence tag present in the cDNA between the NotI site and the oligo-dr track served to identify it as a clone from the normalized adult Brain library. cDNA Library Preparation: M. Fatima Bonaido, Ph.D. Clone distribution: clones will be available through Research Genetics This clone is also available through the I.M.A.G.E. Consortium at LiMi. (info@image.lini.gov). IMAGE ID=176300 The following repetitive elements were found in this cDNA sequence: 4-126, >(TAAAA)#Simple_repeat
Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:

LOCUS AA817822 540 bp mRNA EST 03-JUL-1999

DEFINITION UI-R-A0-ae-d-07-0-UI.S1 UI-R-A0 Rattus norvegicus CDNA clone
UI-R-A0-ae-d-07-0-UI 3' similar to gb|U92535|BTU92535 Bos taurus

neuronal axonal membrane protein (NAP-22) mRNA, complete cds, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
I (bases 1 to 540)
Bonaldo, M.E., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On Feb 17, 1998 this sequence version replaced gi:2887702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 10 Gaps: 0 Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
                                                                                    from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Res. 6 (9), 791-806 (1996)
97044477
                                                                                                                                                                                                                                                         303 AGACAAAATTGAGGATTGCACTAAGATAC 274
                                                                                                                                                                    1 ArgGluAsnLeuArgIleAlaLeuArgTyr 10
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                                                                                to reverse of: T24384
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US-08-653-294-8 x T24384/rev
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Rattus norvegicus
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Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                  seq_name: gb_est26:AA817822
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                                                                                    Align seg 1/1
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VERSION
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TITLE
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On Feb 19, 1999 this sequence version replaced gi:4146293.
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3687
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RFCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.biffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@tesgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 928 row: N column: 15
Seg primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia, Butherla, Primates; Catarrhini, Hominidae, Homo.

1 (bases I to 562)

Mahalras, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                        HS_5352_B1_G08_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=928 Col=15 Row=N, genomic survey sequence. AQ570343
AQ570343.1 GI:4963563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomic sequence of BAC ends"
5 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .562
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=928 col=15 Row=N"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      562
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Gaps: 0
Percent Identity: 70.000
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111 c 114 g 175
                                                                   to: 540
                                                                                                                                    340 AGGAAGAATGTACGGTTGGCATTGAGATAC 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 562.
Location/Qualifiers
                                                                                                             1 ArgGluAsnLeuArgIleAlaLeuArgTyr 10
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                                                                   from: 1
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                                                                 to: AA817822
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Ratio: 3.900
Percent Similarity: 100.000
alignment_block:
US-08-653-294-8 x AA817822
                                                                                                                                                                                                   seq_name: gb_gss14:AQ570343
                                                                                                                                                                                                                                               seq_documentation_block:
LOCUS AQ570343
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KEYWORDS
SOURCE
ORGANISM
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and

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378 AAAGAACACCTACGGTTAGCATTAAGATAC 349

us-08-653-294-8.rst

Amino acid sequenc Human Cdn-2. New n Bak-2 protein. Scr BGP. DNA having ge S. aureus gidB pro S. aureus gidB pro Human lymphocyte a Human lymphocyte a

Peptide B2702.84-7 Immunomodulating d Mutant of the firs

Run on:

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R92909 standard; peptide; 20 AA.
R92909;
16-MAY-1996 (first entry)
HIA-B2702 CIL modulating peptide (B2702.84-75/75-84(T)).
Cytocoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
Immunosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HIA-B2702.
Synthetic,
W09525979-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-ARV-1997.
23-ARV-1997, U06705.
22-ARV-1996, US-651650.
22-MAY-1996, US-651650.
Clayberger C, Krensky AM;
WPI; 98-018220/02.
NOVel immunomodulatory peptide-type compound - useful for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transplant rejection
Claim 10: Page 36: 41pp; English.
The present sequence is an immunomodulatory peptide, which
The present sequence is an immunomodulatory peptide, which
Comprises a Class I HAA-B alpha-1 domain sequence. It can be used
in a pharmaceutical composition together with a subtherapeutic dose
of an immunouppressant, to extend the period of acceptance of a
transplant from a major histocompatibility complex (MHC) unmatched
donor, i.e. to inhibit transplant rejection. It can also be used in
the treatment of autoimmune diseases.
Peptides using the D-form amino acids are more effective
immunomodulators than their diastereomers or enantiomers.
                                                                                                                                                                                                                                                                                                                                                                   Immunomodulatory peptide.'
Immunomodulator; Class I HLA-B alpha-1 domain; inhibition;
Iransplant rejection; treatment; autoimmune disease.
Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 100.0%; Score 49; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 0.00011; Matches 10; Conservative 0; Mismatches 0; Indels
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/note= "at least one of
D-1somer
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W33798
W33799
W62901
W51846
R77877
R77877
W74405
W88359
W88359
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W47266;
22-MAY-1998 (first entry)
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Sequence
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RESULT
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B. thaliana ethyle
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Carbonic anhydrase
Carbonic anhydrase
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HLA-B2702 CTL modu
HLA-B2702 84-751/7
Peptide B2702.84-7
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Immunomodulating d
Peptide B2702.84-7
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Immunomodulatory p
EHV-4 gC. Nucleic
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Immunomodulatory p
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HLA-B2702 CTL modu
HLA-B2702 CTL modu
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Immunomodulatory p
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1.933 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
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                                 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                    188963 seqs, 23686106 residues
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Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                       8, 2000, 01:29:37
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Listing first 45 summaries
                                                                                      protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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W33779
W33792
W47268
W47270
R92910
R92908
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W73117
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W73120
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R92909
R92911
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R69849
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R21416
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W94245
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R20796
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seq length: 1000000
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Result

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Gaps

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Example 15; Page 36; 80pp; English.

R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of r83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of feature is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HLA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs) of the patient.
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HIA-B2702 84-75-84 palindrome.
HIA-B2702 84-75-84 palindrome.
HIA: p74: alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic I lymphocyte; CTL; differentiation;
                                                                                                                                                                                                        HLA-B2702 CTL modulating peptide (B2702.84-75/75-84).
Cytocoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
immnosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HLA-B2702.
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Example: Page 112, 29pp; English.
Example: Page 112, 29pp; English.
R95413, and R95415-R95431 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the HIA-R3702 84-77-84 palindrome. These sequences can be used to isolate the protein p74 from a T-cell lysate. P74 is a T-cell surface membrane, protein associated with T-cell activation in mammalian T-cells, and is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 49; DB 1; Length 20; 100.0%; Pred. No. 0.00024; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Krensky AM, Parham P;
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18-MAY-1995.
10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                   05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR
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                                                                                                                              R92907 standard; peptide; 20 AA.
R92907;
                                                                                                                                                                                  (first entry)
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Best Local Similarity 100.
Matches 10; Conservative
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05-APR-1994; US-222
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YRLAIRLNER 10
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WPI; 95-358582/46.
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WO9513288-A1.
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WO9526979-Al.
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R83061-R83085, R83090-R83096 and R92207-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HLA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLS)
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HLA-B2702 CTL modulating peptide (B2702.84-75/84-75).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
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R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence class I major histocompatibility complex (MHC) antigens. This sequence is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC HLA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited peeriod of time (compared to the lifetime administration for current treatments). The peptides particularly
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WPI; 95-358582/46.
Extension of acceptance period of transplants from MHC unmatched Annor hosts - using Class I B75-84 MHC antigen of the recipient
                                                                                                                                Extension of acceptance period of transplants from MHC unmatched donor hosts – using Class I B75-84 MHC antigen of the recipient
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100.0%; Pred. No. 0.00024;
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100.0%; Pred. No. 0.00024;
iive 0; Mismatches 0;
                                                                               Krensky AM, Parham P;
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05-APR-1995; U04349.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                 (STRD ) UNIV LELAND STANFORD JUNIOR
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
                           US-222851
05-APR-1995; U04349
05-APR-1994; US-222
                                                                               Clayberger C, Krer
WPI; 95-358582/46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          patient.
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RESULT R92911

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Sequence

of the

Gaps

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also immunologically cross reactive with the heat shock protein Hsc70.

p74 is found in a limited number of cell types, but is particularly expressed on B and T cells. p74 can be isolated by lysis of a suitable cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HLA-B2702 palindromic peptide.

Compositions comprising the extracellular fragment of p74 combined with HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate compounds can be screened for their effect on the cytolytic activity of T-cells, by combining them with the extracellular portion of p74 and cetermining the amount of binding between the candidate compound and p74. Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCs), by adding to the with p74 for the binding of the p74 in an amount sufficient to compete with p74 for the binding of the p74 ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PER 24-MAY-1997; U08689.

PE 22-MAY-1997; U08689.

PE 22-MAY-1997; U08689.

RAY-1997; US-STAD-10 STANFORD JUNIOR.

PE 24-MAY-1997; US-STAD-10 STANFORD JUNIOR.

PE 25-MAY-1997; US-STAD-10 STANFORD JUNIOR.

PE 25-MAY-1996; US-STAD-10 STANFORD JUNIOR.

PE 25-MAY-1996; US-STAD-10 STANFORD JUNIOR.

PE 38-086530/08

New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or treating autoimmune diseases

Claimal 16; Page 35; 41pp; English.

PT treating autoimmune diseases

CC dimer peptide of the invention. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal and activity, including the N-terminal acylated and/or C-terminal and activity, including the N-terminal acylated and/or C-terminal and activity, including the N-terminal acylated type compound comprises the formula; A-B, where the peptide-type compound comprises the formula; A-B, where the peptide-type compound comprises the formula; A-B, where the peptide-type compound comprises and activity acquence in the brackets may peptide type bond within the brackets. The compounds comprise amino acid; as82 - R or L; as83 - G or R; and activity activity activity contains of interest to activate CTLS. They can also inhibit the compounds comprises (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antigened peptide contains of interest to activate CTLS. They can also inhibit the compounds of protleration of T cells in response to anti-CD3. The peptide contains used for preventing rejection of transplants or for treating autoimmune contains and lupus erythematosis.

Per protleration and also be used for detection and diagnosis.
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Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 49; DB 1; Length 20; 100.0%; Pred. No. 0.00024; Ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W33778 standard; peptide; 20 AA. W33778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-JUN-1998 (first entry)
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Best Local Similarity 100.
Matches 10; Conservative
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Sequence 20 AA;
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WO9744351-A1.
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Score 49; DB 1; Length 20; Pred. No. 0.00024;

100.0%;

Query Match Best Local Similarity

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treating autoimmune diseases

Estatural unital usus preventing rejection of transplants or treating autoimmune diseases

Claim 16: Page 35: 41pp: English.

This sequence represents a specifically claimed immunomodulating

This sequence represents a specifically claimed variant is

claimed which has immunomodulating activity, including the N-terminal

claimed which has immunomidated or esterified forms of up to 60

amino acids, where the peptide-type compound comprises the formula; A-B,

W; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = E or

N; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = E or

N; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81 = C or

Hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and as

represents amino acid; The sequence in the brackets The

compounds comprise amino acid sequences related to a class I HiA-B

alphal domain (positions 79-84). They can be used to inhibit the

proteins of interest to activate CILs. They can also inhibit the

cused for preventing rejection of transplants or for treating autoimmune

cused for preventing rejection of transplants or for treating autoimmune

cused for preventing rejection and diagnosis.

The products can also be used for detection and diagnosis.
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   Gaps
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Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
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Peptide B2702.84-75/75-84T tested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-MAY-1997.
22-MAY-1997.
24-MAY-1997.
24-WAY-1996; US-653294.
24-WAY-1996; US-653294.
Bellow R, Clayberger C, Krensky AM;
WPI; 98-086530/08.
New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or
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Indels
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Mismatches
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Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
                                                                    1 YRLAIRLNER 10
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WO9744351-A1.
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WO9744351-Al
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19-JUN-1998
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Krensky AM, Parham P;
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Best Local Similarity 90.0
Matches 9; Conservative
                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transplant rejection
                                                Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                          1 YRLAIRLNER 10
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| YRLLIRLNER 10
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A);
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WO9526979-A1.
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Synthetic.
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PR (STRD ) UNIV LELAND STANFORD JUNIOR.

PR Bellow R, Clayberqer C, Krensky AW;

WIL: 99-086330/08.

New immunomodulating dimer peptide(s) - based on a Class I HLA-B

PT alpha-1 domain, used for preventing rejection of transplants or

Incating autoimmune diseases

Example 1; Page 19; 41pp; English.

PT Example 1; Page 19; 41pp; English.

PR Example 1; Page 19; 41pp; English.

CC C-terminal amidated or esterilied forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B = 1 condition and a rapressents amino acid sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a Class I HLA-B alphal domain (positions of a tany peptide type bond within the brackets. The compounds comprise amino acid sequences related to a Class I HLA-B alphal domain (positions of a class I hey can be used to inhibit cytotoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be activate CTLs. They can also inhibit the proliferation of T cells in cativate CTLs. They can also inhibit the proliferation of T cells in cativate CTLs. They can also inhibit end of a control of transplants or for treating autoimmune diseases, e.g. diabetes, conserved the control of transplants or for treating autoimmune diseases, e.g. diabetes, conserved the control of transplants or for treating autoimmune diseases, e.g. diabetes, control of transplants or for treating autoimmune diseases, e.g. diabetes, control of transplants or for treating autoimmune diseases, e.g. diabetes, control of transplants or for
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Claim 10; Page 36; 41pp; English.
The present sequence is an immunomodulatory peptide, which
The present sequence is an immunomodulatory peptide, which
comprises a Class I HiAh-B alpha-I domain sequence. It can be used
in a pharmaceutical composition together with a subtherapeutic dose
of an immunosuppressant, to extend the period of acceptance of a
transplant from a major histocompatibility complex (MHC) unmatched
donor, i.e. to inhibit transplant rejection. It can also be used in
the treatment of autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel immunomodulatory peptide-type compound - useful for inhibiting
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/note= "at least one of the amino acids is D-isomer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunomodulatory peptide.
Immunomodulator; Class I HLA-B alpha-1 domain; inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 49; DB 1; Length 20; 100.0%; Pred. No. 0.00024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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Peptides using the D-form amino acids are more effective immunomodulators than their diastereomers or enantiomers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transplant rejection; treatment; autoimmune disease.
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Clayberger C, Krensky AM:
WPI; 98-018220/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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22-MAY-1996; US-651650.
22-MAY-1997; U08689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 10; Conserv
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                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel immunomodulatory peptide-type compound - useful for inhibiting
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The present sequence is an immunomodulatory peptide, which comprises a Class I HIA-B alpha-1 domain sequence. It can be used in a pharmaceutical composition together with a subtherapeutic dose of an immunosuppressant, to extend the period of acceptance of a transplant from a major histocompatibility complex (MHC) unmatched donor, i.e. to inhibit transplant rejection. It can also be used in the treatment of autoimmune diseases.
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    .10
    /note= "at least one of the amino acids is the

                                                                                                                                                                                                                                                                                                                                                                                                                 Immunomodulatory peptide.
Immunomodulator; Class I HLA-B alpha-1 domain; inhibition;
transplant rejection; treatment; autoimmune disease.
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Pred. No. 0.0013;
1; Mismatches 0; Indels
   Length 10;
                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptides using the D-form amino acids are more effective immunomodulators than their diastereomers or enantionmers.
   Score 44; DB 1;
Pred. No. 0.0013;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-NOV-1997.
23-ARR-1997; U06705.
22-MAY-1996; US-651650.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM;
WPI; 98-018220,02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-OCT-1995.
05-APR-1995; U04349.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM, Parham P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                               W47270 standard; peptide; 10 AA.
W47270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R92910 standard; peptide; 20 AA.
89.8%;
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90.0%;
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with 97-1940/A27.

While of Compens. Comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CILS.

Example, Page 12: 29pp; English.

Example, Page 13: 20pp; English.

Example of English in Expressed on B and T cells.

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                                                                                               12-NOV-1996 (first entry)
12-NOV-1996 (first entry)
12-NOV-1996 (Affact entry)
12-NOV-1996 (Affact entry)
12-NOV-1996 (Affact entry)
12-NOV-1996 (Affact entry)
13-NOV-1996 (Affact entry)
14-NOV-1996 (Affact entry)
15-NOV-1996 (Affact entry)
16-NOV-1996 (Affact entry)
17-NOV-1996 (Affact entry)
18-NOV-1996 (Affact ent
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Peptide B2702.84-75775-84 tested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or treating autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             adding to the mix the extracellular portion of p74, in an amount sufficient to compete with p74 for the binding of the p74 ligand. Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 44; DB 1; Lengtn 20, Pred. No. 0.0028;
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100.0%; Pred. No. ...
0; Mismatches
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22-MAY-1997; U08689.
24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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98-086530/08.
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W33791;
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                                            R95430 standard; peptide;
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10-NOV-1994; U12985
10-NOV-1993; US-1504
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Best Local Similarity
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WPI; 95-194027/25
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WO9744351-A1.
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WPI; 98-08
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W33791
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                                                                                                                                 Example 15; Page 36; 80pp; English.

R83061-R83085, R83090-R83306 and R92907-R92913 represent fragments of class I major histocompatibility complex (MRC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MRC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MRC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs) Sequence 20 AA;
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R83061-R83085, R83090-R83096 and R92207-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (comparated to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CLLs)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-MAY-1996 (first entry)
16-MAY-1996 (first entry)
16-MAY-1996 (TL MODULALING PEPtide (B2702.84-75(T)/75-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HLA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                        MHC unmatched
the recipient
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Pred. No. 0.0028;
0; Mismatches 1; Indels
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WPI; 95-358582/46.
Extension of acceptance period of transplants from
donor hosts - using Class I B75-84 MHC antigen of
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(STRD ) UNIV LELAND STANFORD JUNIOR.
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90.0%;
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Matches 9; Conservative
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05-APR-1995; U04349.
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WPI; 95-358582/46.
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RESULT R92908

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Example 1; Page 19; 41pp; English.

Peptides W33784-98 and W3378-9 were assayed for their immunocdulating activity. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or C-terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B = (R aa76-71L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino acid. The sequence in the brackets any optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a class I HLA-B alphal domain (positions of a can peptide type bond within the brackets. The compounds comprise amino acid sequences related to a class I HLA-B alphal domain (positions of 10-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be activate CTLS. They can also inhibit the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of fransplants or for treathing autoimmune diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosis. The products can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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ö Gaps ö Score 44; DB 1; Length 20; Pred. No. 0.0028; 0; Mismatches 1; Indels Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative

1 YRLAIRLNER 10 1 YRLATRINER 10 ò g

19-JUN-1998 (first entry)
Peptide B2702.84-75r/75-84T tested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain; W33793 standard; peptide; 20 AA

(STRD ) UNIV LELAND STANFORD JUNIOR. Beulow R, Clayberger C, Krensky AM; 24-MAY-1996; US-653294. 27-NOV-1997. 22-MAY-1997; U08689. Beulow R, Clayberd WPI; 98-086530/08 Homo sapiens. WO9744351-A1. ynthetic 

New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or treating autoimmune diseases. Example 1; Page 19; 41pp; English.

Peptides W33784-98 and W33778-9 were assayed for their immunomodulating

crivity. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or c-terminal andiated or esterilied forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B = (R aa76-71L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = D. S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino acid; aa81 = a or L; aa83 = G or R; and aa represents amino acid; acadences related to a Class I HIA-B alphal domain (positions of a many peptide type bond within the brackets. The compounds comprise amino acid sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a Class I HIA-B alphal domain (positions of 19-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes. rheumatoid arthritis and lupus erythematosis. The products can also be uged for detection and diagnosis.

20 Sequence

Gaps ö Length 20; 1; Indels Score 44; DB 1; Pred. No. 0.0028; Mismatches 89.88; Conservative Query Match Best Local Similarity

1 YRLAIRLNER 10

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(without alignments)
4.008 Million cell updates/sec

US-08-653-294-9 49 1 YRLAIRLNER 10 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

142080 seqs, 47169319 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

PIR_62:* 1: pir1: Database :

pir1:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description			glycoprotein gp13		hypothetical prote	ethylene receptor	zinc-finger protei	probable flagellar	flagellar switch p	-	DNA-directed RNA p				hypothetical prote	¥	tegument protein -	ribosomal mobile e			hypothetical prote		probable UDP-N-ace	RNA polymerase-ass	hypothetical prote	probable seryl-tRN	conserved hypothet	hypothetical prote	hypothetical prote	14
SUMMARIES	B45343	VGBEEH	B46114	A30889	S74416	T16992	JC2069	D71922	H64592	JE0369	S58820	S67177	S43275	S43277	S62557	WZBEZ4	T09326	A21047	TVFFR3	C64941	D72317	T01392	B71041	JC6088	S44541	B72500	D72213	806696	0	A48246
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Length	485	468	468	846	185	741	1214	123	123	465	654	661				2077	2078	144	182	321	377	395	418	444	445	463	538	584	624	738
% Query Match	73.5	69.4	O	σ	67.3	7	~	65.3	S	'n	S	'n.	ഗ	65.3	S	S	S	E	3	S.	3	3	3	63.3	3	3	m	B	•	63.3
Score	36	34	34	34	33	33	33	32	32	32	32	32	32	32	32	32	32	31	31	31	31	31	31	31	31	31	31	31	31	31
Result No.	1	7	m	4	r.	9	7	80	σ		11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30

cell wall enzyme h conserved hypothet probable membrane	trypsin (EC 3.4.21 probable transcrip ribosomal protein 2-methylthio-N6-1s Holliday junction	hypothetical prote conserved hypothet carbonate dehydrat hypothetical prote methionine adenosy	probable cell divi conserved hypothet
D69934 F71321 S64994	B25528 H64752 T12615 D70202 A72217	H70693 H71358 A35795 F71196 S74736	T11665 G69130
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132 176 201	252 252 306 346	336 345 377 409	517 610
61.2 61.2 61.2	61:2 61:2 61:2 61:2 61:2 61:2 61:2 61:2	61.2 61.2 61.2 61.2	61.2
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## ALIGNMENTS

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Glycoprotein gpl3 precursor - equine herpesvirus 4
N;Alternate names: glycoprotein gC
C;Species: equine herpesvirus 4
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C;Accession: B45343
R;Nicolson, L; Onions, D.E.
Virology 179, 378-387, 1990
A;Title: The nucleotide sequence of the equine herpesvirus 4 gC gene homologue.
A;Reference number: A45343; MUID:91021040
A;Title: The nucleotide sequence of the equine herpesvirus 4 gC gene homologue.
A;Reference number: A45343; MUID:91021040
A;Title: The nucleotide sequence of the equine herpesvirus 9 gC gene homologue.
A;Residues: 1-485 AIIC>
A;Coss-references: GB:M58031; NID:9330894; PIDN:AAA46083.1; PID:9330896
C;Superfamily: herpesvirus glycoprotein F
C;Superfamily: herpesvirus glycoprotein F
C;Superfamily: squance #status predicted <SIG>C;Reywords: glycoprotein gpl3 #status predicted <GGP>F;1-30/Domain: signal sequence #status predicted <GGP>F;1-30/Domain: signal sequence #status predicted <GGP>F;1-30/Domain: slynal sequence #status predicted <GGP>F;1-30/Domain: slynal sequence #status predicted <GGP>F;0,61,66,67,72,108,116,147,220,225,286/Binding site: carbohydrate (Asn) (covalent)

Score 36; DB 1; Length 485; Pred. No. 6.1; 1; Mismatches 2; Indels 73.5%; Scor 70.0%; Pre-Query Match 73.5 Best Local Similarity 70.6 Matches 7; Conservative

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Gaps ö

1 YRLAIRLNER 10

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120 YRLEIHLNOR 129 g

Valerant ap13 precursor - equine herpesvirus 1

N; Alternate names: glycoprotein gC
C; Species: equine herpesvirus 1

X; Note: host Equus cabalius (domestic horse)
C; Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 24-Sep-1999
C; Date: 30-Jun-1989
C; Date: 30-Jun-1989
Experimental source: strain Kentucky T431
A; Otto: 63, 4189-4198, 1989

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C;Species: Drosophila melanogaster
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 20-Aug-1999
C;Accession: A30889
R;MacKrell, A.J.; Blumberg, B.; Haynes, S.R.; Fessler, J.H.
Proc. Natl. Acad. Sci. U.S.A. 85, 2633-2637, 1988
A;Title: The lethal myospheroid gene of Drosophila encodes a membrane protein homolog
A;Reference number: A30889; MUID:88190122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: S74446
C;Accession: S74446
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:D64001; GB:AB001339; NID:g1001102; PID:d1010985; PID:g100119
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA (Accession No. AF04747)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
S7416
hypothetical protein sll0687 - Synechocystis sp. (strain PCC 6803)
C.Species: Synechocystis sp.
A; Variety: PCC 6803
C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 21-Aug-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ethylene receptor homolog - apple tree
C;Species: Malus domestica (apple tree)
C;Date: 20-Sep.1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16992
                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GB:J03251; NID:g157954; PIDN:AAA28714.1; PID:g157955
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                                 integrin beta chain precursor - fruit fly (Drosophila melanogaster)
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A;Accession: S74416
A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: FlyBase:mys
A;Cross-references: FlyBase:FBgn0004657
C;Superfamily: integrin beta chain; laminin-type EGF-like homol
C;Superfamily: integrin oytoskeleton; transmembrane protein
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A;Title: Isolation and characterization of a broccoli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 33; DB 2;
Pred. No. 9.5;
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Pred. No. 29;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
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Best Local Similarity 66.7%;
Matches 6; Conservative
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A; Accession: T16992
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-846 <MAC>
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162 RLALRVNEK 170
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A; Residues: 1-185 <KAN>
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C(Keywords: glycoprotein; transamebrane protein
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-468/Product: glycoprotein gp13 #status predicted <WAI>
F:46,57,62,92,100,131,203,208,269/Binding site: carbohydrate (Asn) (covalent) #status pr
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C; Keywords: glycoprotein; transmembrane protein
C;F:30-Vomain: signal sequence #status predicted <SIG>
F:31-468/Product: glycoprotein gpl3 #status predicted <GPT>
F:32-451/Domain: transmembrane #status predicted <TMN>
F:46,57,62,92,100,131,203,208,269/Binding site: carbohydrate (Asn) (covalent) #status pr
A.Title: Expression in recombinant vaccinia virus of the equine herpesvirus 1 gene encod
A;Reference number: A32980; MUID:89382761
A;Accession: A32980
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Species: equine herpesvirus 1
Note: host Equus caballus (domestic horse)
Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:M86664; NID:9330791; PIDN:AAB02451.1; PID:9330808
A;Experimental source: strain Ab4p
R:Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.
Virology 189, 304-316, 1992
A;Title: The DNA sequence of equine herpesvirus-1.
                                                                                     A; Molecule type: DNA
A; Residues: 1-48 eGUO>
A; Residues: 1-48 eGUO>
A; Cross-references: GB:M86664; NID:9330791; PIDN:AAB02451.1; PID:9330808
R; Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.
submitted to GenBank, March 1992
A; Description: The DNA sequence of equine herpesvirus-1.
A; Reference number: A36805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Reference number: A41831; MID:92295566
A:Contents: annotation; possible protein-coding frames
A:Note: neither amino acid nor nucleotide sequence is given
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Pred. No. 16;
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A; Title: DNA sequence and transcriptional analy A; Reference number: A46114; MUID:93212524
A; Accession: B46114
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Best Local Similarity
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Best Local Similarity
Matches 7; Conserv
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|104 YRLKIYLNOR 113
                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-468 <TEL>
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C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 26-Aug-1999
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 26-Aug-1999
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 26-Aug-1999
R;Tomb, JF.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKe
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weldman, J.M.; Fujii, C.; Bowman, C.; Watthey,
A. Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Accession: H64520; MuD:97394467
A;Accession: H64520; Mulli:97394467
A;Accession: H64520; Mulli:9739467
A;Accession: H64520; Mulli:9739467
A;Accession: H64520; Mulli:9739467
A;Accession: H64520; Mulli:9739467
A;Cossion: H64520; Mulli:9739
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DNA-directed RNA polymerase (EC 2.7.7.6) III chain RPC82 - yeast (Saccharomyces cerev
DNA-tlternate names: DNA-directed RNA polymerase C chain RPC82; DNA-directed RNA polyme
C;Species: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Arabidopáis thaliana (mouse-ear cress).
C;Date: 23-011-1999 #sequence_revision 23-011-1999 #text_change 20-Sep-1999
C;Accession: JRD369
R;Mullaney, E.J.; Ullah, A.H.J.
Blochem: Biophys, Res. Commun. 251, 252-255, 1998
A;Title: Identification of a histidine acid phosphatase (phyA)-like gene in Arabidops A;Reference number: JRD369
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10;
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                                                                            65.3%; Score 32; DB 2;
100.0%; Pred. No. 10;
.ive 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches
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60.0%; Pred. No. 41;
ive 2; Mismatches
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A.Residues: 1-465 < MULD.
C.Superfamily: yeast acid phosphatase
C.Reywords: phosphoric monoester hydrolase
                                                                                Query Match 65.3
Best Local Similarity 100.
Matches 7; Conservative
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128 YQLGIRVRER 137
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                        102 LAIRLNE 108
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| 102 LAIRLNE 108
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A; Status: preliminary
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A. Molecule type: mRNA
A. Cross references: GB:M91585
C. Comment: This is a nuclear protein with broad tissue distribution, but is especially a c. Superfamily: unassigned bromodomain proteins: bromodomain homology
C. Superfamily: unassigned bromodomain proteins: bromodomain homology
C. Keywords: DNA binding; phosphoprotein; transcription regulation; zinc finger
F: 553-708/Domain: bromodomain homology cBRO>
F: 5100, 304, 317, 320/Binding site: zinc (Cys) #status predicted
F: 300, 333, 350, 352/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F: 380, 333, 444, 447/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F: 410, 413, 444, 447/Binding site: zinc (His, Cys, Cys, His) #status predicted
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C; Species: Helicobacter pylori
C; Species: Helicobacter pylori
C; Species: Helicobacter pylori
C; Species: Helicobacter pylori
C; Species: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 26-Aug-1999
C; Accession: D71922
B; Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Tavan, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A; Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-123 <ARN>
A;Cross-references: GB:AE001485; GB:AE001439; NID:g4155057; PIDN:AAD06097.1; PID:g415506
A;Experimental source: strain J99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Species: Homo sapiens (man)

C; Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 12-Sep-1997

C; Accession: JC2069

R; Thompson, K.A.; Wang, B.; Argraves, W.S.; Giancotti, F.G.; Schranck, D.P.; Ruoslahti, Blochen. Blophys. Res. Commun. 198, 1143-1152, 1994

A; Title: BR140, a novel zinc-finger protein with homology to the TAF250 subunit of TFIID
A; Reference number: JC2069; MUID:94161726
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Pred. No. 70;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                Length 741
                                                                                                                                                                                                                                                                                                                    1; Indels
A;Cross-references: EMBL:AF032448; NID:g3411050; PID:g3411051
A;Experimental source: cultivar Granny Smith; ripening fruit
C;Genetics:
A;Note: ETR1
                                                                                                                                                                                                                                Score 33; DB 2
Pred. No. 41;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: fliN
C;Superfamily: flagellar motor switch protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N; Alternate names: bromodomain protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    zinc-finger protein, BR140 - human
                                                                                                                                                                                                                                67.3%;
50.0%;
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Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                Query Match
Best Local Similarity 50.0
Matches 5; Conservative
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A; Molecule type: DNA
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A;Cross-references: EMBL:L25663; NID:g409762; PID:g409764
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: S43277
R; Cambareri, E.B.; Helber, J.; Kinsey, J.A.
Rol. Genet. 242, 658-665, 1994
A; Title: Tad1-1, an active LINE-like element of Neurospora crassa.
A; Reference number: S43274; MUID: 94203179
A; Accession: S43277
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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C;Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 31-oct-1997
C;Accession: S6557
R;Odell, C.; Churcher, C.M.
Submitted to the EMBL Data Library, November 1995
A;Reference number: S62546
A;Reference number: S62546
A;Reference number: DAA
A;Reference number: DAA
A;Reference number: S62557
A;Reference number: S62557
A;Reference number: S62567
A;Refe
                                                                                                                           C.Species: Neurospora crassa
C.Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.Species: Neurospora crassa
C.Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Sep-1997
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R;Cambareri, E.B.; Helber, J.; Kinsey, J.A.
Mol. Gen. Genet. 242, 658-665, 1994
A;Title: Tad1-1, an active LINE-11ke element of Neurospora crassa.
A;Reference number: S43274; MUID:94203179
A;Accession: S43275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein 2 - Neurospora crassa retrotransposon Tad3-2
                                                                                         Neurospora crassa retrotransposon Tad1-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1154;
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Pred. No. 1.1e+02;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                               A, Molecule type: DNA
A, Residues: 1-1154 <CAN>
A, Cross-references: EMBL:L25662; NID:g409759; PID:g409761
C, Genetics:
A, Mobile element: retrotransposon Tad1-1
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Pred. No. 1.1e+02;
1; Mismatches 2
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66.7%;
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66.7%;
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Best Local Similarity 66./
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Best Local Similarity 66.7
Matches 6; Conservative
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A; Residues: 1-1154 <CAM>
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1136 YRLAVELEE 1144
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A; Introns: 124/3
                                                                                         hypothetical
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Accession: S72046
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A;Cross-references: EMBL:275183; NID:g1420615; PID:e252121; PID:g1420616; MIPS:YOR275c
A;Experimental source: strain S288C
R;Cheret, G.; Bernardi, A.; Sor, F.
Yeast 12, 1059-1064, 1996
                                                                                                                                                                                                                                                                                                                             Cross references: EMBL:U25841; NID:g786295; PID:g786307; MIPS:YPR190c
Chlannilkulchai, N.; Stalder, R.; Riva, M.; Carles, C.; Werner, M.; Sentenac, A.
51. Cell. Biol. 12, 4433-4440, 1992
Title: RPCB2 encodes the highly conserved, third-largest subunit of RNA polymerase
Reference number: S31298; MUID:93024385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cross-references: EMBL:X89633; NID:q1279694; PID:e189401; PID:g1279701
Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Accession: S61177; S72046
R;Cheret, G.; Sor, F.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67169
Date: 28-Nov-1995 #sequence_revision 19-Jan-1996 #text_change 23-Apr-1999
Accession: S58820; S31298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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C;Keywords: leucine zipper; nucleotidyltransferase; transcription
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Residues: 1-661 <CHW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        yeast (Saccharomyces cerevisiae)
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                                                                                  R.Miller, N. submitted to the EMBL Data Library, April 1995
A.Description: The sequence of S. cerevisiae cosmid 9677.
A.Reference number: S58816
A.Accession: S58820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecule type: DNA
Residues: 1-636, 'L',638-654 <CHI>
:Cross-references: EMBL:X63500; NID:94383; PID:94384
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Pred. No. 60;
3; Mismatches
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Pred. No. 59;
4; Mismatches
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50.0%;
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Best Local Similarity 50.0%;
Matches 5; Conservative
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Best Local Similarity 50.0.
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312 YKIALRLTEQ 321
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Residues: 1-654 <MIL>
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A; Note: YOR275c
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us-08-653-294-9.rpr

Query Match 65.3%; Score 32; DB 2; Length 1402; Best Local Similarity 87.5%; Pred. No. 1.3e+02; Matches 7; Conservative 0; Mismatches 1; Indels

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1 YRLAIRLN 8 |||| ||| 25 YRLADRLN 32 δy

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Search completed: February 7, 2000, 11:54:22 Job time: 24332 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

February 8, 2000, 00:59:49; Search time 63.71 Seconds (without alignments) 4.688 Million cell updates/sec Run on:

US-08-653-294-9 49 1 YRLAIRLNER 10

Title: Perfect score: Sequence: Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

82229 seqs, 29864866 residues Searched:

82228 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

SwissProt_38:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

IES		Description	P2259	P12889 equine	P11584 drosoph	P55201	P32349 sacch		P30002	P52340 herpes	P76254 escheri		P15255	P49333	P54162		P77300		074306		049190	051761	056313			P7287	P32786	013014	043187	P4610	05530	P14020	05995	044248	U P40758 bacillus su
SUMMARIES		a	VGLC_HSVE	VGLC_HSVEB	ITBX_DROME	BR14_HUMAN	RPC3_YEAST	ATCX_SCHPO	TEGU_HSV6G	TEGU_HSV6U	YEAX_ECOLI	PAF1_YEAST	65KD_ZYMMO	ETR1_ARATH	YPDO_BACSU	TRYP_MOUSE	YAGI_ECOLI	RL5A_SCHPO	RL5B_SCHPO	RL5_HELAN	RL5_BOMMO	MIAA_BORBU	RUVB_THEMA	AC11_HUMAN	CAH1_CHLRE	METK_SYNY3	RRN6_YEAST	BAK2_HUMAN	IPYR_SOLTU	PCP_BACAM	CYSH_SYNP7	DPM1_YEAST	RL5_NEUCR	RL5_ANOGA	YCBA_BACSU
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NCAP_SENDZ NCAP_SEND5	NCAP_SENDF LAG3_HUMAN Y107_METJA	MYPH_CHICK HYCE_ECOLI SKB1_SCHPO	NUC2_SCHPO CRPI_PERAM MCM5_CAEEL
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## ALIGNMENTS

Gaps ö Query Match
73.5%; Score 36; DB 1; Length 485;
Best Local Similarity 70.0%; Pred. No. 3.2;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Indels

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ITBX_DROME
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=KENTUCKY D;
MEDLINE; 89382761.
GUO P., GEBEL B., DAVIS S., PERKUS M.E., LANGUET B., DESMETTRE P.,
ALLEN G., PAOLETI E.,
"Expression in recombinant vaccinia virus of the equine herpesvirus 1
gene encoding glycoprotein gpl3 and protection of immunized
                                                                                                                                                                                                                                                                                                                   encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-ERBUNCKY D;
MEDLINE: 93212524.
MATSUMURA I., SMITH R.H., O'CALLAGHAN D.J.;
"DNA sequence and transcriptional analyses of the region of the equine herpesvirus type 1 Kentucky A strain genome encoding glycoprotein C.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALLEN G.P., COOGLE L.D.;
"Characterization of an equine herpesvirus type 1 gene encaptoprotein (gpl3) with homology to herpes simplex virus glycoprotein (gr.; cr.; cr.; virol. 62:2850-2858(1988).
                                                                              P12889; P36321;
01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-0CT-1989 (Rel. 13, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
GLYCOPROTEIN C PRECURSOR (GLYCOPROTEIN 13).
GC OR GP13 OR 16.
Equine herpesvirus type 1 (strain Ab4p) (EHV-1), and Equine herpesvirus type 1 (strain Kentucky D) (EHV-1).
Viruses; dSDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                           STRAIN-AB4P,
MEDLINE, 92295566.
TELFORD E.A.R., WATSON M.S., MCBRIDE K., DAVISON A.J.;
The DNA sequence of equine herpesvirus-1.";
Virology 189:304-316(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; H36796; VGBEA1.
PIR; A28149; VGBEEH.
PIR; B46114; B46114.
Glycoprotein; Transmembrane; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Virol. 63:4189-4198(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L07272; AAA46078.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M29234; AAA46085.1;
EMBL; S57839; AAB25944.1;
                                                                        STANDARD;
             1 YRLAIRLNER 10
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-KENTUCKY D;
MEDLINE; 88275055.
                                                                                                                                                                                                  SEQUENCE FROM N.A.
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VGLC_HSVEB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MACKRELL A.J., BLUMBERG B., HAYNES S.R., FESSLER J.H.;
"The lethal myospheroid gene of Drosophila encodes a membrane protein
homologous to vertebrate integrin beta subunits.";
Proc. Natl. Acad. Sci. U.S.A. 85:2633-2637(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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                                                                                                                                                                                                                                                                                             Length 468;
                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1989 (Rel. 12, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
INTEGRIN BETA-SUBUNIT MYOSPHEROID PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       846 AA
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POTENTIAL.
GLYCOPROTEIN
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E -> K (IN I
V -> A (IN I
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Pred. No. 8
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PROSITE; PS00243; INTEGRIN_BETA; 3.
PROSITE; PS00122; EGF_1; UNKNOWN_2.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
PFAM; PF00362; Integrin_B; 1.
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70.08;
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Best Local Similarity 70.0.
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104 YRLEIYENQR 113
                                                                                                                                                                                                                                            468 AA;
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P11584;
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MEDLINE; 94161726.
THOMPSON K.A., WANG B., ARGRAVES W.S., GIANCOTTI F.G., SCHRANCK D.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RUGSLAHII E.;
"BR140, a novel zinc-finger protein with homology to the TAF250
subunit of TFIID.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                 INTEGRIN BETA-SUBUNIT MYOSPHEROID.
Integrin; Cell adhesion; Transmembrane; Glycoprotein; Repeat; Extracellular matrix; Cytoskeleton; Signal.
SIGNAL 1 23 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB 1; Length 846;
Pred. No. 16;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. Biophys. Res. Commun. 198:1143-1152(1994).
-!- FUNCTION: UNKNOWN. POSSIBLE TRANSCRIPTION ACTIVATOR.
-!- SUBCELLULAR LOCATION: NUCLERR (PROBABLE).
-!- TISSUE SPECIFICITY: HIGH LEVELS IN TESTIS.
-!- SIMILARITY: CONTAINS 1 BROMODOMAIN.
                                                                                                    EXTRACELLULAR (POTENTIAL)
POTENTIAL.
                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
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CYSTEINE-RICH REPEATS.
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9906C2F9 CRC32;
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(Rel. 34, Last sequence update)
(Rel. 36, Last annotation update)
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PROSITE; PS00633; BROMODOMAIN_1; FALSE_NEG.
PROSITE; PS50014; BROMODOMAIN_2; 1.
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PFAM; PF00439; bromodomain; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M91585; AAB02119.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996 (Rel. 34, Cree 01-OCT-1996 (Rel. 34, Last 15-JUL-1998 (Rel. 36, Last PEREGRIN (BR140 PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          718
846 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162 RLALRVNEK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 RLAIRLNER 10
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P55201;
                                                                                                                                                                                                                                                                                                                         REPEAT
CARBOHYD
CARBOHYD
                                                                                                          DOMAIN
TRANSMEM
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CARBOHYD
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WILSON R., WATERSTON R.; Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
-1. FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-S288C / AB972;
JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DU Z.,
STRAIN-S288C / AB972;
SAVELLO A., FULTON L., GATTUNG S., GRECO T., KIRSTEN J., KUCABA T.,
HALLSWORTH K., HAWKINS J., HILLIER L., JIER M., JOHNSON D.,
JOHNSTON L., LANGSTON Y., LATREILLE P., LE T., MARDIS E., MENEZES S.,
MILLER N., NHAN M., PAULEY A., PELUSO D., RIFKEN L., RILES L.,
TAICH A., TREVASKIS E., VIGNATI D., WILCOX L., WOHLDMAN P., VAUDIN M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- MISCELLANEOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES ARE FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE II FOR 5S AND TRNA GENES.
                                                                                                                                                                                                                                                                                                                                                                                                                                               RPC3_YEAST STANDARD; PRT; 654 AA.
P32349; Q06591;
01-0CT-1993 (Rel. 27, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
NAM-DIRECTED RNA POLYMERASE III 74 KD POLYPEPTIDE (EC 2.7.7.6) (C74).
RPC3 OR PPC92 OR PPG97.11.
Saccharomyces cerevisiae (Baker's 9reat).
Eukaryota; Fungi; Ascomycota; Hemlascomycetes; Saccharomycetales;
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBSTRATES.
CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE
                                      DNA-binding; Activator; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "RPC82 encodes the highly conserved, third-largest subunit of RNA polymerase C (III) from Saccharomyces cerevisiae."; Mol. Cell. Biol. 12:4433-4440(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNA(N).
SUBDUIT: RNA POLYMERASE III CONSISTS OF ABOUT 15 DIFFERENT
SUBDUITS. THIS SUBDUIT IS THE THIRD LARGEST COMPONENT OF RNA
POLYMERASE III.
                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE; 93024385.
CHIANNILKULCHAI N., STALDER R., RIVA M., CARLES C., WERNER M.,
                                                                                                                                                                                                                             Score 33; DB 1; Length 1214;
Pred. No. 38;
2; Mismatches 2; Indels
                                                                        47 C2H2-TYPE.
296 C4-TYPE.
333 C4-TYPE.
400 C4-TYPE.
715 BROMODOMAIN.
; 137542 MW; B3E44584 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                   67.3%;
PFAM; PF00628; PHD; 1.
PFAM; PF00855; PWWP; 1.
Transcription regulation;
                                                                                                                                                                                                                                 Query Match 67.3
Best Local Similarity 60.0
Matches 6; Conservative
                                                                        21
276
276
317
386
40
645
1214 AA;
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                                                                                                                                                                                                                                                                                                                1 YRLAIRLNER 10
                                                        Zinc-finger.
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                                                                            ZN_FING
ZN_FING
ZN_FING
ZN_FING
DOMAIN
SEQUENCE
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RPC3_YEAST
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25 YRLADRLN 32
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P52340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
             Query Match
                                                                                                                   RESULT 7
TEGU_HSV6G
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TEGU_HSV6U
                                   Matches
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                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=972;
ODELL C., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
Submitted (Nov-1995) to the EMBL/Genbank/DDBJ databases.
-!- FUNCTION: THIS MAGNESIUM DEPENDENT ENZYME CATALYZES THE
HYDROLYSIS OF ATP COUPLED WITH THE TRANSPORT OF CALCIUM
                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: ATP + H(2)0 = ADP + ORTHOPHOSPHATE.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
                                                           fransferase; DNA-directed RNA polymerase; Transcription; Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Calcium transport; Transmembrane; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 PHOSPHORYLATION (BY SIMILARITY).
159355 MW; DEDEAD76 CRC32;
                                                                                                                                        Score 32; DB 1; Length 654;
Pred. No. 32;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                            01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PROBABLE CALCIOM-TRANSPORTING ATPASE (EC 3.6.1.38).
                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Archiascomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                 502 LEUCINE-ZIPPER.
537 V -> L (IN REF. 1).
74016 MW; 9E17F4F8 CRC32;
                                                                                                                                                                                                                                                                        PRT; 1402 AA.
                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces pombe (Fission yeast).
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PFAM; PF00122; E1-E2_ATPASE; 2.
                                                                                                                                           65.3%;
            EMBL; X63500; CAA45072.1; -. EMBL; U25841; AAB64619.1; -.
                                                                                                                                        Query Match 65.3
Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; 267757; CAA91777.1;
                                                                                                                                                                                                                                                                        STANDARD;
                                                                                  602
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1238
1280
569
                                  PIR; S31298; S31298.
SGD; L0001693; RPC82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (E1-E2 ATPASES).
                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces.
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                                                                                            637 6
654 AA;
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312 YKIALRLTEQ 321
                                                                                                                                                                                       1 YRLAIRLNER 10
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                       Nuclear protein.
DOMAIN 581
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1218
1260
569
1402
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                                                                                                                                                                                                                                                                   ATCX_SCHPO
Q09891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase;
                                                                                             CONFLICT
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MOD_RES
SEQUENCE
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                                      Gaps
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Length 1402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2077;
                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                    Herpes simplex virus (type 6 / strain GS).
Viruses; dSDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Roseolovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Herpes simplex virus (type 6 / strain Uganda-1102). Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
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Pred. No. 1.1e+02;
DB 1;
73;
                                                                                                                                                                                                    TEGU_HSV6G STANDARD; PRI; 2077 AA. P30002; 01-APR-1993 (Rel. 25, Created) 01-APR-1993 (Rel. 25, Last sequence update) 1-OCT-1996 (Rel. 34, Last annotation update) LARGE TEGUMENT PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
10-CCT-1996 (Rel. 34, Last annotation update)
LARGE TEGUMENT PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2077 AA
                                      0; Mismatches
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 Score 32;
                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Betaherpesvirinae; Roseolovirus.
65.3%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; S57540; AAB19786.1; -.
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50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 65.3
Best Local Similarity 50.0
Matches 5; Conservative
                                    7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H40511; WZBEZ4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |::|: |||:
495 YKVAVLLNEK 504
                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 YRLAIRLNER 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 95266321.
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EMBL; X76053; CAA53642.1; --
EMBL; Z36148; CAA65243.1; --
PIR; S44541; S44541.
S91155; S93135.
SGD; L0002621; PAFI.
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270
278
309
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70 YQIAVRLEE 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 94378722
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                                                                                                                                                                                                                                                                                                                                                                                                            Iron-sulfur; E
NP_BIND
NP_BIND 11
METAL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
PAF1_YEAST
ID PAF1_YEAST
AC P38351;
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SEQUENCE
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"The DNA sequence of human herpesvirus-6: structure, coding content, and genome evolution."; Virology 209:29-51(1995).
-!- FUNCTION: TEGUMENT PROTEIN.
-!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36, EHV-1 24, EBV BPLF1, HVS-1 64, VZV 22, AND HCMV UL48.
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ITOH T. AIBA H., BABA T., FUJITA K., HAYASHI K., INADA T., ISONO K., KASAHI H., KINURA S., KITAKAWA M., KITAGAWA M., MAKINO K., MIKI T., MALOBUCHI K., MORI H., MORIN T., MOTOMURA K., NAKADE S., NAKAMURA Y., NASHIMOTO H., NISHIO Y., OSHIMA T., SAITO N., SAMPEI G., SEKI Y., SIVASUDARAM S., TACAMI H., TAKEDA J., TAKEMOTO K., WADA C., YAMAMOTO Y., HORIUCHI T.; TA SCHOOL T., TAKEDA J., TAKEMOTO Y., WADA C., TAKEDA DNA SEQUENCE OF THE ESCHETICHIA COLI K-12 GENOME COLIESPONDING to the 40.1-50.0 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=RIZ / MG165;
STRAIN=RIZ / MG165;
BLATINE; 97426617.
BLATINER F.R., FLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,
RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
RALEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
MAU B., SHAO Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- COFACTOR: FWN (BY SIMILARITY).
-i- SUBUNIT: PROBABLE HETERODIMER OF YEAW AND YEAX.
-i- SIMILARIY: IN THE C-TERMINAL, BELONGS TO THE 2FE2S PLANT-TYPE
FERREDOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete genome sequence of Escherichia col1 K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 32; DB 1; Length 207
Pred. No. 1.1e+02;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YEAX_ECOLI STANDARD; PRT; 321 AA.
P76254; 007972; 007970;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
PUTATIVE DIOXYGENASE BETA SUBUNIT YEAX (EC 1.-.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X83413; CAA58411.1; -.
SEQUENCE 2077 AA; 239946 MW; 36FCF7B1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -! - SIMILARITY: BELONGS TO THE PDR/VANB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65.3%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 50.۰۰
میر S; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Res. 3:379-392(1996
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495 YKVAVLLNEK 504
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oved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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SIMILARITY).
SIMILARITY).
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PAFI OR YBR279W OR YBR2016.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SHI X., WADE P., BURTON 2., JAEHNING J.A.;
Unpublished observations (XXX-1995).
-!- FUNCTION: RNA POLYMERASE II ASSOCIATED PROTEIN IMPORTANT FOR
TRANSCRIPTION.
-!- SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of
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                                                                                                                                                                                                                                                                                       PFAM; PF00111; fer2; 1.
PFAM; PF00175; oxidored_fad; 1.
Hypothetical protein; Oxidoreductase; Flavoprotein; FMN; NAD; Iron-sulfur; Electron transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BY
(BY
(BY
(BY
                                                                                                                                                                                                                                                                                                                                                                                                FMN (BY SIMILARITY).
NAD (BY SIMILARITY).
IRON-SULFUR (2FE-2S) (1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOLMSTROEM K., BRANDT T., KALLESOE T.;
The sequence of a 32,420 bp segment located on chromosome II from Saccharomyces cerevisiae.";
Yeast 10:S47-S62(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 31; DB 1
Pred. No. 24;
3; Mismatches
  modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                        EMBL, AE000274; AAC74873.1; --
EMBL, D90824; CAB21531.1; --
EMBL, D90824; CAB21524.1; --
HSSP, P33164; 2PIA.
ECOGENE; EG13510; YEAX.
PROSITE; PS00197; 2FE2S_FERREDOXIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35661 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 55.6%;
Matches 5; Conservative
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                                                                                                                                                                                                           -i- TISSUE SPECIFICITY: LEAVES, ROOTS, STEMS, FLOWERS AND SEEDLINGS.
-i- PTM: ACTIVATION PROBABLY REQUIRES A TRANSFER OF A PHOSPHATE GROUP
BETWEEN A HIS IN THE TRANSMITTER DOMAIN AND A ASP OF THE RECEIVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus subtilis chromosome region between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A->V: IN ETR1-3; ETHYLENE INSENSITIVITY.
I->F: IN ETR1-1; ETHYLENE INSENSITIVITY.
A->T: IN ETR1-1; ETHYLENE INSENSITIVITY.
A->T: IN ETR1-2; ETHYLENE INSENSITIVITY.
                                                                                                                               -I- FUNCTION: MAY ACT EARLY IN THE ETHYLENE SIGNAL TRANSDUCTION PATHWAY, POSSIBLY AS AN ETHYLENE RECEPTOR, OR AS A REGULATOR OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sensory transduction; Phosphorylation; Transmembrane; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOROKIN A.V., AZEVEDO V., ZUMSTEIN E., GALLERON N., EHRLICH S.D.,
                        CHANG C., KWOK S.F., BLEECKER A.B., MEYEROWITZ E.M.; "Arabidopsis ethylene-response gene ETR1: similarity of product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the serA and kdg loci cloned in a yeast artificial chromosome.";
Microbiology 142:2005-2016(1996).
-!- SIMILARITY: TO E.FAECALIS CELL WALL ENZYME EBSB.
                                                                                                                                                                                                                                                                                                                  SIMILARITY: TO PROKARYOTE SENSORY TRANSDUCTION PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996 (Rel. 34, Created)
1-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
HYPOTHETICAL 14.7 KD PROTEIN IN BCSA-DEGR INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMITTER DOMAIN (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.3%; Score 31; DB 1; Length 738; 40.0%; Pred. No. 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RECEIVER DOMAIN (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FD593871 CRC32;
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PHOSPHORYLATION
PHOSPHORYLATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFAM; PF00072; response_reg; 1. PFAM; PF00512; signal; 1. PFAM; PF01590; GAF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 A
82565 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L24119; AAA70047.1; -.
                                                                                                                                                                                                                                                                                         DOMAIN (BY SIMILARITY).
                                                                           two-component regulators.
Science 262:539-544(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Sequence analysis of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 40.0
nes 4; Conservative
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43
76
106
353
659
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MEDLINE; 96349105.
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62
65
102
738 AA;
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  MEDLINE; 94024007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996 (
01-OCT-1996 (
15-DEC-1998 (
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SEQUENCE
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DOMAIN
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YPDQ_BACSU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-ATCC 10988 / ZMI;
MISAMA N., NAKAWURA K.;
"The nucleotide sequence of the 2.7 kilobase pair plasmid of Zymomonas mobilis ArCc 10988";
J. Biotechnol. 12:63-70(1989).
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosida II; Brassicales; Brassicaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 584;
                                                                                                      Length 445;
                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
Transcription; Nuclear protein.
SEQUENCE 445 AA; 51800 MW; 9259106B CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1990 (Rel. 14, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) 65 KD PROTEIN (ORF 1). Zymomonas mobilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
ETRI PROTEIN (EC 2.7.3..).
                                                                                                 Score 31; DB 1
Pred. No. 34;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 46;
                                                                                                                                                                                                                                                                                                                                                                                             584 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 31;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1990 (Rel. 14, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65793 MW;
                                                                                                 63.3%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X14438; CAA32611.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFAM; PF01076; Mob_Pre; 1.
                                                                                                 Query Match 63.3
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    584 AA;
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Best Local Similarity
Matches 6; Conserv
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359 YRSKIRINE 367
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                           288 LAIRLNDK 295
                                                                                                                                                                                                           3 LAIRLNER 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 YRLAIRLNE 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid pZM2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        806696
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                                                                                                                                                                                                                                                                                                                                                                                                65KD_ZYMMO
P15255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ETR1_ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zymomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                          RESULT 11
65KD_ZYMMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ETR1_ARATH
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RECOCCOS BETTTE

(AUTO-) (BY SIMILARITY).

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Gaps

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Indels

us-08-653-294-9.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STEVENSON B.J., HAGENBUCHLE O., WELLAUER P.K.;
Stevence organisation and transcriptional regulation of the mouse elastase II and trypsin genes.";
elastase II and trypsin genes.";
Nucleic Acids Res. 14:8307-8330(1986).
-!- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: ARG-, LYS-,
-!- SUBCELDULAR LOCATION: EXTRACELJULAR.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRYPSIN.
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Serine protease; Digestion; Pancreas; Zymogen; Signal
                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                  Score 30; DB 1; Length 132;
Pred. No. 15;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTIVATION PEPTIDE
                                                                                                                                                       EMBL; L77246; AAA96618.1; -.
EMBL; 299115; CAB14117.1; -.
EMBL; P00647; CAB14117.1; -.
SUBTILIST; BG11608; YPDQ.
PFAM; PF00075; TRASEH; 1.
PFAM; PF00075; TRASEH; 1.
SEQUENCE 132 AA; 14670 MW; 7A8ACE92 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
TRYPSINOGEN PRECURSOR (EC 3.4.21.4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    246 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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EMBL; X04577; CAA28245.1; -.
PIR; B25528; B25528.
HSSP; P00763; IDPO.
MGD; MGI:102759; TRY2.
PROSITE; PS00134; TRYPSIN_ER; 1.
PROSITE; PS00135; TRYPSIN_ER; 1.
PRAM; PF00089; LYPPSIN_ER; 1.
Hydrolase; Serine protease; Digestic
                                                                                                                                                                                                                                                                                                                      61.2%;
85.7%;
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 85.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-A/J;
MEDLINE; 87066713
                                                                                                                                                                                                                                                                                                                                                                                                               125 AIRLNEK 131
                                                                                                                                                                                                                                                                                                                                                                                         4 AIRLNER 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRYP_MOUSE
P07146;
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ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
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TRYP_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                              SPECIFICITY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN PERR-ARGF INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE; 97426617.
BLATINER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,
RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
SCHRAMM S., DUNCAN M., ALLEN E., ARAUJO R., APARICIO A., CHUNG E.,
DAVIS K., FEDERSPIEL N., HYMAN R., KALMAN S., KOMP C., KURDI O.,
LASHKARI D., LEW H., LIN D., NAMATH A., OEFNER P., ROBERTS D.,
      (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ECOGENE; EG13349; YAGI.

PROSITE; PS01051; HTH_ICLR_FAMILY; 1.

PFAM; PF01614; LC1R; 1.

Hypothetical protein; Transcription regulation; DNA-binding.
DNA_BIND 25 45 H-T-H MOTIF (POFENTIAL).

SEQUENCE 252 AA; 27838 MW; 3D954295 CRC32.
                                                                                                                                                                                                                                                                                                                                                             Score 30; DB 1; Length 246;
Pred. No. 29;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
      RELAY SYSTEM
RELAY SYSTEM
                                                                                                                                                                                                                                                                          BD975983 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               252 AA.
CHARGE RELAY S'
CHARGE RELAY S'
CHARGE RELAY S'
BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
REQUIRED FOR SI
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                                                                                                                                                                                                                                                                          26203 MW;
                                                                                                                                                                                                                                                                                                                                                             61.2%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                      246 AA;
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67 YRIQVRLGE 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 YRLAIRLNE 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GREGOR J., DAVIS
MAU B., SHAO Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGULATORS.
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                              ACT_SITE
DISULFID
DISULFID
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DISULFID
DISULFID
DISULFID
SITE
      ACT_SITE
                                                                                                                                                                                                                                                                      SEQUENCE
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YAGI_ECOLI
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Score 30; DB 1; Length 252; Pred. No. 30;

61.2%; 60.0%;

Query Match Best Local Similarity

2; Indels 2; Mismatches 6; Conservative Matches

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0; Gaps

1 YRLAIRLNER 10 |||| ::| || 62 YRLGMKLVER 71

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Search completed: February 8, 2000, 00:59:50 Job tlme: 3779 sec

099493 acropyrum p 016917 caenorhabdi 098160 little cher 09x294 thermotoga 081768 arabidopsis

Q9YAG3 016917 Q98160 Q9X294 081768 004325

001914 090933 09XE40 032370 046302

004325 arabidopsis 0049230 brassica ol 001914 caenorhabdi 090933 gallus gallu 090933 gallus gallu 090933 conspilosect 046302 clostridium 081521 forsythia x 040796 physalis cr 081481 treponema p 01230 saccharomyc P7615 mycobacteri 083189 treponema p 085943 sphingomona 0859512 pyrococcus 905965 amycolatops 059512 pyrococcus 095964 streptomyce

040796 040796 0813181 012530 0831815 0831815 085943 085912 095655

ALIGNMENTS

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STRAIN-NS80567;
MEDLINE; 98264497.
TELFORD E.A.R., WATSON M.S., PERRY J., CULLINANE A.A., DAVISON A.J.;
"The DNA sequence of equine herpesvirus-4.";
J. Gen. Virol. 79:1197-1203(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-NS80567;
TELFORD E.A., WATSON M.S., PERRY J., CULLINANE A.A., DAVISON A.J.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
Submitted (OCT-1997) i. .
PRIEL; AF030027; AAC59530.1; .
PRINTS; PRO00668; GLYCPROTEINC.
SEQUENCE 485 AA; 52539 MW; 8DF52A42 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 91021040.
NICOLSON D., ONIONS D.E.;
"The nucleotide sequence of the equine herpesvirus 4 gC gene homologue.";
Virology 179:378-387(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Equine herpesvirus 4.
Viruses; dSDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 039258 PRELIMINARY; PRT; 485 AA.
039258;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1999 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
COUNTERPART OF HSV-1 GENE UL44 AND VZV GENE 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 73.5%; Score 36; DB 12; Best Local Similarity 70.0%; Pred. No. 13; Matches 7; Conservative 1; Mismatches 2;
                                                                    1 YRLAIRLNER 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-NS80567;
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RESULT
039258
DDT BENERAL BE
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P99736 caenorhabdi
055192 synechocyst
062436 cucumis mel
081122 malus domes
041103 anycolatops
045107 helicobacte
035306 helicobacte
035306 helicobacte
031288 buchnera ap
09543 parameclum
004509 arabidopsis
012033 saccharomyc
04170 aeromonas h
01375 neurospora
063055 human herpe
06179 neurospora
06179 neurospora
063756 trypanosoma
057369 trypanosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9zt98 arabidopsis
                                                                                                                        8, 2000, 13:17:35; Search time 209.03 Seconds (without alignments) 3.317 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                                                                          225878
                                   Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
               GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                                                     225878 seqs, 69334122 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Listing first 45 summaries
                                                                                         protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   039258
P90736
055192
081122
044103
025306
031288
031288
004509
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001375
001379
069055
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027369
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Gapop 10.0 , Gapext 0.5
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sp_invertebrate:*
sp_mammal:*
sp_mhc:*
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sp_virus:*
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sp_phage:*
sp_plant:*
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sp_bacteria:*
sp_fung1:*
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                                                                                                                                                                                                                                        1 YRLAIRLNER 10
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                                                                                                                                                                                                                                                                                                                                                                                                            seq length: 0 seq length: 1000000
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                                                                                                                            February
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Match 1
                                                                                                                                                                                                     Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                             Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB
Maximum DB
                                                                                         OM protein
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                                                                                                                            Run on:
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Gaps

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Length 485; 2; Indels

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01-NOV-1998 (TrEMBLEEL. 08, 01-NOV-1998 (TrEMBLEEL. 08, 01-NOV-1999 (TrEMBLEEL. 12, ETHYLENE RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | ||||: |:
671 YELAIRIREK 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 YRLAIRLNER 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||||:|: :|
35 YRLALRILOR 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 YRLAIRLNER 10
                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-FRUIT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cucumis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    082436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MENDEL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               081122
081122;
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"Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome.";
DIA Res. 2:153-166(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-BRISTOL N2;
JONES S.J.M.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases -! - SIMILARITY: WEAK, TO DYNEIN HEAVY CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TABATA S.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                             01-JAN-1999 (TrEMBLrel. 09, Created)
01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
HYPOTHETICAL 305.8 KD PROTEIN B0365.7 IN CHROMOSOME V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             055192;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
HYPOTHETICAL 20.8 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35; DB 5; Lei
Pred. No. 1.3e+02;
2; Mismatches 1;
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EMBL; 281028; CAR02695.1; -
EMBL; 281096; CAR02695.1; JOINED.
EMBL; 281096; CAR03163.1; JOINED.
EMBL; 281028; CAR03163.1; JOINED.
WORMPEP; B0365.7; CE07724.
Hypothetical protein.
SEQUENCE. 2632 AA; 305774 MM; 4F3356EF CRC32;
                                                                                                                                                                              PRT; 2632 AA.
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
120 YRLEIHLNOR 129
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557 YRSAVRINE 565
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MEDLINE; 96127529.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMS M.;
                                                                                                                                                                       P90736
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                                                                                                                                     "Sequence analysis of the genome of the unicellular cyanobacterium Synechocysis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).
EMBL; D64001; BAA10334.1; -.
Hypothetical protein.
SEQUENCE 185 AA; 20830 MW; 365A078D CRC32:
MEDLINE; 97061201.
KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S.
SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
TABATA S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cucumis melo var. reticulatus (netted muskmelon).
Sukaryota, Viitdiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
core eudicots; Rosidae; eurosids 1; Cucurbitales; Cucurbitaceae;
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                                                                                                                                                                                                                                                                                                                                                                                         Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
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Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                         Score 33; DB 2;
Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82657 MW; 183F5227 CRC32;
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88;
                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33025; Cucme; 2316; 33025
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PFAM; PF00512; signal; 1.
SEQUENCE 740 AA; 82657 MW;
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                                                                                                                                                                                                                                                                                                                                                                                         67.3%;
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01-NOV-1999 (TremBlrel. 12
PUTATIVE ETHYLENE RECEPTOR
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STRAIN-26695,
MEDLINE, 97394467.
TOMB J.-F., WHITE O., KERLAVAGE A.R., CLAYTON R.A., SUTTON G.G.,
TOMB J.-F., WHITE O., KERCHUM K.A., KLENK H.-P., GILL S., DOUGHERTY B.A.,
REISCHMANN R.D., KETCHUM K.A., KLENK H.-P., GILL S., DOUGHERTY B.A.,
NELSON K., OMACKENBUSH J., ZHOU L., KIRKNERSE S.F., PETERSON S.,
LOFTUS B., RICHARDSON D., DODSON K., KHALAK H.G., GLODEK A.,
MCKENNEY K., FITZGERALD L.M., LEE N., ADAMS M.D., HICKEY E.K.,
BERG D.E., GOCANNE J.D., UTTERBACK T.K., PETERSON J.D., KELLEY J.M.,
COTTON M.D., WEIDMAN J.M., FUJII C., BOWMAN C., WATTHEY L., WALLIN E.,
HAYES W.S., BORODOVSKY M., KARP P.D., SMITH H.O., FRASER C.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'Genomic-sequence comparison of two unrelated isolates of the human
                                                                                                                                                                                                                                               Relicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Helicobacter pylori J99.
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.3%; Score 32; DB 2; Length 123; 100.0%; Pred. No. 22; 1ve 0; Mismatches 0; Indels
                                  01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
FLAGELLAR SWITCH PROTEIN (FLIN).
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01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
PUTATIVE FLAGELLAR MOTOR SWITCH PROTEIN.
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100.0%; Pred. No. 22;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Flagella.
SEQUENCE 123 AA; 13942 MW; 498DE0AE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
EMBL, AE001485; AAD06097.1; -
SEQUENCE 123 AA; 13966 MW; 9406C37C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 388:539-547(1997).
EMBL: AE000571; AAD07636.1; -.
TIGR: HP0584; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00956; FLGMOTORFLIN.
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 65.3
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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| 102 LAIRLNE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 LAIRLNE 9
                                                                                                                                                                                                                                                                                                                           Helicobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRUST T.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-J99
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092LP7
ACCOCCOS NEW RAY REPORTED TO THE REPORT OF T
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MEDLINE: 97490857.

PELZER S., REICHERT W., HUPPERT M., HECKMANN D., WOHLLEBEN W.;

PELZER S., REICHERT W., HUPPERT M., HECKMANN D., WOHLLEBEN W.;

"Cloning and analysis of a peptide synthetase gene of the balhimycin producer Amycolatopsis mediterranei DSM5908 and development of a gene disruption/replacement system.";

J. Blotechnol. 56:115-128(1997).

EMBL: X97860; CAA66454.1;

PROSITE; PSO0455; AMP BINDING; 1.

PRAM; PFO0501; AMP-Binding; 1.

PFAM; PFO0501; AMP-binding; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Pseudonocardineae; Pseudonocardiaceae; Amycolatopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                               LEE S.A., ROSS G.S., GARDNER R.C.;
"An apple (Malus domestica L. Borkh cy Granny Smith) homolog of the ethylene receptor gene ETR1 (Accession No. AF032448) (FGR98-125)."; Plant Physiol. 117:1126-1126(1998).
EMBL. AF032448, AAC31123.1; -...
MENDEL, 31773; MAIGO: 2316;31773.
                                  Malus domestica (Apple) (Malus sylvestris).
Bukaryota, Viridplantae; Streptophyta, Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
core eudicots; Rosidae; eurosids I; Rosales; Rosaceae; Malus.
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88;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1
1324 1324
1324 AA; 142666 MW; 2C08588E CRC32;
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Pred. No. 1.6e+02;
2; Mismatches 1;
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-CV. GRANNY SMITH; TISSUE-RIPENING FRUIT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAM; PF00072; response_reg; 1.
PFAM; PF00512; signal; 1.
SEQUENCE 741 AA; 82967 MW; D350B396 CRC32;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.3%;
50.0%;
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70.0%;
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Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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- 672 YELAVRIHEK 681
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Matches 5; Conserv
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STRAIN-CY. COLUMBIA;
VYSOTSAIA W.V.S., OSBORNE B.I., TORIUMI M., YU G., OJI O., SHEN Y.K.,
VYSOTSAIA W.S., OSBORNE B.I., TORIUMI M., YU G., OJI O., SHEN Y.K.,
RARAJO R., AU M., BUEHLER E., CONMAY A.B., CONMAY A.R., DEWAR K.,
FENG J., KIM C., KURTZ D., LI Y., SHINN P., SUN H., DAVIS R.W.,
ECKER J.R., FEDERSPIEL N.A., THEOLOGIS A.;
SUDMITTED (JUN-1997) to the EMBL/Genbank/DDBJ databases.
EMBL: ACO00132; AAB60740.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHERET G., BERNARDI A., SOR F.;
"DNA sequence analysis of the VPH1-SNF2 region on chromosome XV of saccharonyces cerevisiae.";
Yeast 12:1059-1064(1999).
-i - SIMILARITY: SOME, TO C.ELEGANS RIOE12.1.
                                                                                                   Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
core eudlocts; Rosidæe; eurosids II; Brassicales; Brassicaceæe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
HYPOTHETICAL 75-9 KD PROTEIN IN VPHI-SNF2 INTERGENIC REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHERET G., SOR F.; Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
                          01-JUL-1997 (TTEMBLrel. 04, Last sequence update)
01-NOV-1999 (TTEMBLrel. 12, Last annotation update)
HYPOTHETICAL 52.8 KD PROTEIN F21M12.26 IN CHROMOSOME I.
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Pred. No. 1.3e+02;
3; Mismatches 2;
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Pred. No. 89;
                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 468 AA; 52790 MW; E9129511 CRC32;
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661 AA; 75947 MW; 266DA004 CRC32;
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EMBL; Z75183; CAA99500.1; --
EMBL; X89633; CAA61781.1; --
SGD; S0005801; YOR275C.
Hypothetical -----
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                 Created)
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50.0%;
              01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04, 01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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Best Local Similarity کاری
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132 YQLGIRVRER 141
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MEDLINE; 97051594
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SEQUENCE 66
                                                                                                                                                                      Arabidopsis.
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                                                                                                                                                                                                                                                                                                                    VAN HAM R.C.H.J., MOYA A., LATORRE A.; "Putative evolutionary origin of plasmids carrying the genes involved in leucine biosynthesis in Buchnera aphidicola (endosymblont of aphids).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Phycodnavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 96400190.
KUTISH G.F., LI Y., LU Z., FURUTA M., ROCK D.L., VAN ETTEN J.L.;
Analysis of 76 the chlorella virus PBCV-1 330-kb genome: map positions 182 to 258.";
Virology 223:303-317(1996).
EMBL; U42580; AAC96860.1;
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Pred. No. 27;
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                                                                                                                                                                                                                                    Buchnera aphidicola.
Plasmid pBTs1.
Bacteria; Proteobacteria; gamma subdivision; Buchnera.
                                                                                                                                                                        Last sequence update)
Last annotation update)
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Last annotation update)
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Pred. No. 34;
1; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                           17953 MW; 66A38676 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     191 AA
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                                                                                                                                                        Created)
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EMBL: Y11966; CAA72698.1; -.
Plasmid.
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66.7%;
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60.0%;
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Best Local Similarity 60.0
ادم 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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                                                                                                                     PRELIMINARY;
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                                                                                                                                                     01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153 AA;
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74 YRLVVRENE 82
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| 102 LAIRLNE 108
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3 LAIRLNE 9
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RESULT 10 Q98543

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1 YRLAIRLNE 9
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DODD H.N., PEMBERTON J.M.;

"Cloning, sequencing, and characterization of the nucH gene encoding an extracellular nuclease from Aeromonas hydrophila JMP636.";

EMBL; L76304; AAB39273.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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A CAMBARET E.B., HELBER J., KINSEY J.A.;

A CAMBARET B.B., LEBER J., KINSEY J.A.;

I Tadl-1, an active LINE-like element of Neurospora crassa.";

IL MOI. Gen. Genet. 242:658-665(1994).

IR PRAM, PF00078: rvt, 1.

KW Hypothetical protein.

FT DOMAIN 1019 1022 POLY-LYS.

FT DOMAIN 1029 1034 POLY-GLU.

SQUENCE 1154 AA; 130398 MW; DF0BA680 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                            Aeromonas hydrophila.
Bacteria; Proteobacteria; gamma subdivision; Aeromonas group;
Aeromonas.
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01-NOV-1996 (TEMBLICH. 01, Last sequence update)
01-NOV-1998 (TEMBLICH. 08, Last annotation update)
HYPOTHETICAL 130.4 KD PROTEIN.
Neurospora crassa
Eukaryota: Fungi: Ascomycota: Buascomycetes; Sordariales; Sordariaceae; Neurospora.
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Best Local Similarity 60.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels
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Last sequence update)
Last annotation update)
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01-NOV-1996 (TEMBLFEL 01,
01-NOV-1998 (TEMBLFEL 08,
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AC 044070
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RESULT 15 Q01379 ID Q01379

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AC009485 Homo sapiens clo
299111 Bacillus subtilis
AJ235270 Rickettsia prowa
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Missouri 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7 or mailto:egreen@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry, an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is from a release of the human BAC library. The library contains cloned DNA from human sperm. See: Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); Kim et al., Genomics Natl. Acad. (1996). The clone is available from Research Genetics, Lic. (http://www.resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The actual start of this clone is at base position 1 of RG343P13; actual end is at 155881 of RG343P13. The orientation of this clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 155881)

Connell, M and Cordes, M.

The sequence of H. sapiens BAC clone RG343P13

Unpublished (1997)

2 (bases 1 to 155881)

Waterston, R.
                                                                                                                                                                                                                                                            20-AUG-1997
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                                                                                                                                                                                                                                      AC002465 155881 bp DNA PRI 20-A-Human BAC clone RG343P13 from 7q31, complete sequence. AC002465 GI:2337862
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St. Louis,
   190706
208230
282610
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Submitted (20-AUG-1997) Department of
University, 4444 Forest Park Avenue, S
SUBMITTED BY:
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2.7e+04
3.8e+04
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/organ1sm-"Homo sapiens"
/db_xref-"taxon:9606"
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Department of Genetics
Washington University
St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
mailto:sapiens@watson.wustl.edu
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VERSION AC002465
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   gb_htg3:AC009485
gb_ba1:BSUB0008
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168125 Sequence 3 from patent
188031 Equine herpesvirus 4 gl
AF064563 Hordeum vulgare culti
1037799 Bacillus subtilis genes
1 AE01206 Treponema pallidum s
1246241 Caenorhabditis elegans
AP012285 Bacillus subtilis md
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AP000815 Oryza sativa genomi
AC011687 Homo sapiens clone
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AL133316 Homo sapiens chromo
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AP000101 Homo sapiens genom:
AP000177 Homo sapiens genom:
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-Q=/cgn1_1/USPTO_spool/US08653294/runat_04022000_160701_15779/app
-Q=/cgn1_1/USPTO_spool/US08653294/runat_04022000_160701_15779/app
-Q=/cgn1_1/USPTO_spool/US08653294/runat_04022000_160701_15779/app
-Q=/cgn1_1/USPTO_spool/G-0.000 -LOOPEXT-0.000 -GAPOP-4.500
-QGAPEXT=0.050 -XGAPOP-10.000 -XGAPEXT-0.500 -FGAPOP-6.000
-FGAPEXT=7.000 -YGAPOP-10.000 -YGAPEXT-0.500 -DELOP-6.000
-DELEXT-7.000 -START=1 -MARRIX-blosum62 -TRANS-human40.cd1
-LISP-45 -DCALIGN-200 -THR_SCORE-PCT -ALIGN-15 -MODE-LOCAL
-OUTFNT-pfs -NORM-ext -MINLEN-0 -MAXLEN-1000000 -USER-US08653294
-NCPU-6 -ICPU-3 -NO_XLPXY -WAIT -THREADS-1
                                                                                                                                                About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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3189. .43271))
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SSSRESAFYAISSAGVYRAITRAGSQGFWKSCSCDPKKWAGAKDSKGIFDWGGCSDN
DYGTKFARAFVDAKERKGKDARALMNLHNRAGRKAYKRFLKQDCKCHGVSGCTLE
CWLAMADFRKTGDYLWRKYNGAIQVVMNQDGTGFTVANERFKKPTKNDLVYFENSPD
                                                                                                                                                                                                                                                                                                                               note="match to human EST 199653 (NID:g749390) ye67a02.rl"
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rotein P09544 (PID:g139750)"
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protein_id="AAB67043.1"
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                                                            ACO16116 60193 bp DNA HTG 20-NOV-1999
Homo sapiens clone RP11-27G6, LOW-PASS SEQUENCE SAMPLING.
ACO16116
                                                                                                                                                             Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 60193)

Birran, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens, clone RP11-27G6

Unpublished
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* sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
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LOCUS AC016116 (
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COMMENT

length

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of 786 bp in length
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Ratio: 4.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 88.889

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2 ArgLeuAlaIleArgLeuAsnGluArg 10

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DOE Joint
                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Drimates; Catarrhini; Hominidae; Homo.

Ricke,D.O., Bruce,D., Mundt,M., Doggett,N., Munk,C., Saunders,E., Goodwin,L., Bryant,J., Tesmer,J., Melncke,L., Thompson,S., Mite,S., Ueng,S., Tatum,O., Campbell,C., Fawcett,J., Maltble,M., Sequencing of Human Chromosome 16

Uppbblished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Large Scale Sequence Analysis and Annotation with the Sequence Comparison Analysis (SCAN) System Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submittad (01-103-1998) Center for Human Genome Studies, DOE JG
Genome Institute, Los Alamos National Laboratory, MS M888, Los
Alamos, NM 87545, USA
                                                                        seq_documentation_block:
LOCUS AC005365 86130 bp DNA PRI 01-AUG-1998
DEFINITION HOMO satiens chromosome 16, Pl clone 79-2A (LANL), complete sequence.
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/note="GRAIL 2 excellent exon, fi

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16275. .16548

/rpt_femily="Alu"
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/rpt_family="Alu"
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50768 AGGCTAGCAATTCGACTTAACGAGAAA 50742
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10542. .10563
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                                      seq_name: gb_pr3:AC005365
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idem 	2 excellent exon, frame 0"	3Alu" 2Alu" 214222428)	A1u 7	2 excellent exon, frame 0"	! "Alu"	MIR"		<pre>2 excellent exon, trame 1" 5</pre>	A1u."	256032851)	E : C K	Alu 3 2 excellent exon, frame 2"		A1u 562636748) 7.1"	717337468)	± : : : : : : : : : : : : : : : : : : :	DIA TARA	2 2	ndem	ייין קר. ייין קרו		l 2 excellent exon, frame 0"		2 excellent exon, frame 2"		1	227552538)	305853720)			3 	16357314)
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REFERENCE AUTHORS TITLE JOURNAL

COMMENT

ACCESSION VERSION KEYWORDS SOURCE

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S Birren, B., Fasman, K., McKernan, K., Nusbaum, C., Richardson, P., Lander, E., Allen, N., Baker, J., Baldwin, J., Barna, N., Beckerly, Rander, E., Allen, N., Baker, J., Baddwin, J., Barna, N., Beckerly, Benn, J., Boattwell, C., Brown, A., Byrne, S., Cantu, C., Cattle, A., Cerny, J., Cooke, P., Daly, M.J., Depayre, E., Devon, K., Furshigh, W., Forrest, C., Funke, R., Gage, D., Gardyna, S., Ferreira, P., Genshelmer, S., Geralgery, K., Gilmartin, T., Grant, G., Gray, D., Hagos, B., Harris, K., Horton, L., Howland, J.C., Hul, L., Jacotot, L., Kann, L., Linton, L., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., Machan, J., Nahl, R., Morras, W., Morray, J., Mychalecky, J., Nachalecky, J., Nachala, J., Betterson, K., Riley, R., Roberts, D., Rollins, G., Rossello, R., Roy, A., Sydna, R., Stange-Thomann, N., Stilwell, J., Stone, C., Strickland, C., Subramanian, A., Sydna, Wagner, A., Torruella -Miller, I., Wu, Y., Ye, W.J., Zhao, J., and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Survey, Standar, Linton, L., Nusbaum, C., Lander, E., Allen, N., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boatin, C., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boatin, C., Castle, A., Cerny, J., Cooke, P., Depayre, E., Devon, K., Dewar, K., Donelan, L., DuRette, B., Etemadi, S., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gardyna, S., Gensheimer, S., Geralgery, K., Gilmartin, T., Grant, G., Hagos, B., Harris, R., Horton, L., Howland, J. C., Hui, L., Jacotot, L., Kann, L., Macdonald, P., Marquis, N., Mcras, P., McGurk, A., McKernan, K., Meldrim, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Nachman, A., Nahf, R., Naylor, J., O'Connor, T., Paviln, B., Peterson, K., Rilay, R., Nabelts, D., Rossello, R., Subramanian, A., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wang, B., Wheeler, J., Wu, Y., Ye, W., J., and Zody, M., Direct, Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (01-MAY-1998) Whitehead Institute/MIT Center for Genome Research, 320 charles Street, Cambridge, MA 02141, USA ON MAY 1, 1998 this sequence version replaced 91:3095003. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (23-APR-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA (bases 1 to 99512)
      1 (bases 1 to 99512)
81rren,B., Fasman,K., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 17, clone hRPC.1043_H_15
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Location/Qualiflers
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complement(7069 . 7372)
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complement(7400 . 7689)
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1763. .4814
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REFERENCE
AUTHORS
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JOURNAL
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JOURNAL
                                                                                                                                                      AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dires, S.

Submitted (10-SEP-1999) Wellcome Trust Genome Campus, Hinxton, Submitted (10-SEP-1999) Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquires:

Numquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
on Sep 12, 1999 this sequence version replaced gi:5777438.

IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence work on the sequence is in progress and the release of this data is based on the understanding that the sequence may contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate segments. Unfinished: dJ1141E20 Contig_ID: 00340 acc-aL109912 Length: 18869 bp Unfinished: dJ1141E20 Contig_ID: 00679 acc-aL109912 Length: 13805 bp Unfinished: dJ1141E20 Contig_ID: 00679 acc-aL109912 Length: 1302 bp.

* NOTE: This is a 'working draft' sequence.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                          Homo sapiens chromosome 6 clone RP5-1141E20, *** SEQUENCING IN PROGRESS ***, in unordered pieces.
                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 97906)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HOMO Sapiens Chromosome 17, clone hRPC.1043_H_15, complete
sequence.
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Percent Identity: 80.000
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                                                                                                                                                                                                                                        AL109912.4 GI:5870369
HTG; HTGS_PHASE1.
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AC004606.1 GI:3097870
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LOCUS HS1141E20 97906 bp
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US-08-653-294-9 x HS1141E20/rev
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                                  seq_name: gb_htgl:HS1141E20
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LOCUS AC004606
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Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                          human.
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                   ORGANISM
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FEATURES

ACCESSION

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seq_documentation_block:
LOCUS HSJ112D6 135305 bp DNA PRI 23-NOV-1999
DEFINITION Human DNA sequence from clone 1112D6 on chromosome 6q21-22.2,
ACCESSION ALO80317
VERSION ALO80317.11 G1:5830430
EXEMPCES HTG; CPG Island.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 135305)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 99512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality: 39.00 Length: 9
Ratio: 4.333 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 77.778
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35366. 35500
/rpt_family="LiM4"
/rpt_family="LiM4"
36641. 36761
/rpt_family="Alusc"
complement(27414, .27600"
/rpt_famil
                                                                                                                      /rpt_family="MLT1A2"
complement(28827, 2022''
                                                                                                                                                  /rpt_family="Limei"
complement(29387, coerror)
'rpt fee';
                                                                                                                                                                                 rpt_family="Limb8"
0005. .3003
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0643. .30889
                                                                                                    28057. . 28462
/rpt_family="MSTA"
:complement(28466. .
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US-08-653-294-9 x AC004606/rev
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represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continue. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,
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Submitted (09-NOV-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr )
On Nov 15, 1999 this sequence version replaced gi:5777392.
IMPORTANT: This sequence is unfinished and does not necessarly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamamoto,T., Hikono,T. and Abe,S.-I.
Differential expression of annexin V during spermatogenesis in the newt Cynops pyrkhogaster
Dev. Genes Evol. 206, 64-71 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="matching EMBL:G33267; Identified using the e-PCR
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Caudata, Salamandroidea; Salamandridae, Cynops.
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Gaps: 0
Percent Identity: 60.000
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/db_xref="taxon:8330"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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10. .981
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/clone="R-370E23"
28537. .28674
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1. .1579
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Ratio: 3.900
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                                                                                                                                                                                             together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL: Sw:, SWISSPROT: IT:, TREMBL: Wp:, WORNPEP: Information on the WORNPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                             http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence is the entire insert of clone 1112b6. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.
This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 whitp://www.sanger.ac.uk/HGP/Chr6
                                                Submitted (09-SEP-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Sep 6, 1999 this sequence version replaced gi:5791529.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1112D6 is from the library RPCI-5 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-370E23 of RPCI-11 library from chromosome 14 of Homo sapiens (Human),
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/chromosome="6"
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1. .135305
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/clone="RP5-1112D6"
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KGLGTLENVIIEIMASRTAAEVKNIKETYKKEFDSDLEKDIVGDTSGNFERLLVSLVQ
ANRDPVGKVDEGQVENDAKALFDAGENKWGTDEETFISILSTRGVGHLRKVFDQYMTI
SGYQIEESIQSETGGHFEKLLLAVVKSIRSIOGYLAEVLYNSWGAGTDDQTLIRVLV
SRSEIDLFNIRQTFRKHYGKSLHAMIQSDTSGDYRNALLLLCGEIDD"
1564. 1571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing Center, Washington
4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         several contigs from automated sequence assembly concatenated together. No attempt has been made to order or orient the contigs relative to one another correctly before concatenating. At each location in the sequence where contigs have been joined, several consecutive Ns.may have been inserted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC010886 190094 bp DNA HTG 29-OCT-1999
Homo sapiens chromosome unknown clone NH0370K06, WORKING DRAFT
SEQUENCE, in unordered pieces.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
11 (bases 1 to 19004)
Sulston,J.E. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This 'working draft' quality sequence may consist of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (25-SEP-1999) Genome Sequencing Center, Washingt
University School of Medicine, 4444 Forest Park Parkway, S
MO 63108, USA
On Oct 29, 1999 this Sequence version replaced g1:6015414.
SUBMITTED BY: WUGSC
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Waterston, R.
The sequence of Homo sapiens unknown clone NH0370K06
Unpublished
Joases 1 to 190094)
Waterston, R. H.
                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 1579
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AC010886.3 GI:6139236
HTG; HTGS_PHASE1; HTGS_DRAFT.
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Washington University
St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                      to reverse of: D64134
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LOCUS AC010886 190094 bp
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Percent Similarity: 100.000
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/cloud___nrw.vnvv
/cloue_llb="unknown"
303. .999
/note="pseudogene similar to PID:g3192702 (AF064539) gp19
lbace=lophage NI5]"
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neurofilament-like protein – northern European squid"
The attached annotation was produced using a purely automated
                                                The location of this clone is unknown.

* NoTE: This is a 'working draft' sequence.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                    .528. .5741
/rpt_family="Retroviral"
5764. .6055
                                                                                                                                                    1. .190094
/organism="Homo sapiens"
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382. .6416
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4039. .14378
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2466. ,12556
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14648. .15582
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1691. .13964
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/rpt_family="AT_rich"
o680. .9725
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013. .8465
rpt_family="L1"
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2195, .12415
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/rpt_family="MIR"
.enc .7738
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777. .6902
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1819, .11974
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778. .9805
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1378. .114
                 procedure.
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19844. 21137
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ATPase alpha subunit [Cavia porcellus]"
21140. 21208
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ATPase alpha subunit [Cavia porcellus]"
1291. 21377
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22575. .23259
2/rpt_family="AcHobo"
2/277. .2436
2/rpt_family="MER1_type?"
24389. .24527
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7rpC_famlly="MER81"

24639 .24642

7rpt_famlly="Retroviral"

25101 .25578

25664 .25746
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21407. 21515
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21516. 21741
/rpt_family="L1"
21742. 22029
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1817. .33055
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rpt_family="(TAAAA)n"
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26318. .26456
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28013. .28081
28083. .28402
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                                                  'rpt_family="MaLR"
7345. .17547
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2467. .22564
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33352. .33790
                                                                                                                                rpt_family="MIR"
9455. .19583
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2030. .22059
               6897. .16924
rpt_family="L2"
6925. .17344
                                                                          /rpt_family="L2"
8834. .18940
                                                                                                       rpt_family="L2"
9127. .19274
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2070. .22315
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3056. 33351
rpt_family="L1" (8897. .16924
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LOCUS AC009685 210031 bp DNA HTG 29-SEP-1999
DEFINITION Homo sapiens chromosome 15 clone 91_E_13 map 15, *** SEQUENCING IN
ACCESSION AC009685
ACCESSION AC009685
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 210031)
Bitren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 15, clone 91_E_13
Unpublished
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* NOTE: This is a 'working draft' sequence. It currently consists of 27 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as a runs of N, but the exact sizes of the gaps are unknown.
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Gaps: 0
Percent Identity: 70.000
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37457. 37759
/rpt_family="Alu"
                                          34711. .34798
/rpt_family="MIR"
35849. .36154
rpt_family-"MIR'
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HTG; HTGS_PHASE1.
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Percent Similarity: 100.000
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This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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917 others
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Gaps: 0
Percent Identity: 77.778
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63180 t
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                            3042: contig c
gap of t
5640: contig c
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/clone_11b="RPCI-11
38965 c 38634 g
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14358: contig
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156571: contig
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Ratio: 4.222
Percent Similarity: 100.000.
                                                   3043
                                                                       5641
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ORIGIN
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bin (displaydbe-wormsecations) Sequence sobject=175B8A current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

Exceptions are indicated by an explicit note. Important: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

It may be shorter because we only sequence overlapping sections once, or longer because we only sequence overlapping sections once, or longer because we only sequence overlapping sections once, or longer because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The true left end of clone Y75B8 is at 1 in this sequence. The true left end of clone Y49E10 is at 298300 in this sequence. The true right end of clone Y79E2 is at 184511 in this sequence. The start of this sequence (1. .103) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL110501.
The end of this sequence (298300. .298406) overlaps with the start
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Direct Submission
Submitted (12-NOV-1998) Louis, MO 63110, USA. E-mail:
Jes8sanger.ac. uk or rwênematode.wustl.edu
Coding sequences below are predicted from computer analysis, usir
predictions from Genefinder (P. Green, U. Washington), and other
available information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
LOCUS CEY75BA 298406 bp DNA INV 06-SEF
DEFINITION CREMORTHS elegans cosmid Y75B8A, complete sequence.
ACCESSION AL033514
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94150718
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                                                                                                                                                                                                                                                                                                                                                                                                             22265 TATAAACTITCAATTAGACTTAATGAA 22291
                                                                                                                                                                                                                                                                                             1 TyrArgLeuAlaIleArgLeuAsnGlu 9
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Caenorhabditis elegans
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                                                                                                                                                                       to: AC009685
alignment_block:
US-08-653-294-9 x AC009685
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                                                                                                                                                                             Align seg 1/1
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IVAMIEETYLKAGVRQLERNYGAICRNVALRLABALNSDPGADVLPVWELPIOISASN
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COMPLEMENT (4515) 49365)
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EDXQQVTCEGQQVVILPDRLPSGYESLVIRNSSYRTIEKNSFRÄMELMJOIDERNNPN
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USCLOKRFFERRHIPGAMCAKKRCNMAGNIECYPSLMSONPADFVQRAFRSYELINP
VISCOCOCOSCAMPEDYRRVORTGPPPAMCOMMOMAMAPPOQUIPGPOTPOCOVOCHO
ORPNYLSYHARLAVQAPPOVITAPAPIPLPGGOMTHMPOHGLDIPYLIPTSFVQAVQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(45151. .45318,45616. .45804,47003. .47278,
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/codon_start=1
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/note="predicted using Genefinder; similar to ATPases
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Gaps: 0
Percent Identity: 70.000
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4.222
90.000
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Ratio:
Percent Similarity:
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Complement (32765. 37388)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OGROYNLGNDOSOLYSGOANFTGIPYCOAPYGNLRLOPPOPLNGFNTTLHDATYFRP
KCPOLNAGGPTNEDCLYLNYYTPQAGNTNANLSYLVLIDGSNGFSNGFCDQNOEKGII
SNLVQRQIVVVTMQYRIGALGFFTTYTNSVQSNLGMLDQVQAMFWIKTEIVNFGGNPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OITVAGGDDGACAVSAHCLSPMSQNLFNQAIVQSGSVYSCYNTPAVPTNPQVQVTTP
WRWTOOSNTGYGGAGYQUNYGYQPQFITSTSSCYNSANAQYDDSQQLAGTLGNISPDQ
WRNGQTQNIQONYGYGYBYRYDFFFWYWQPGGGARATWMIVRDTSFLBGSIDSLTTRRNIFI
IIGTVQDEDADYAFKLINTGKGSDPNNLDDWIFDFARKNKLNQTQANQVSNIISNNYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VNTGALGQQGAQVNSQYQGSGTGQQIASDQSTSLTTTQIQSYMQNGARHVRYYQFTHV
SECKBYTVPDPTGANNKRVFKGODNF FINMSET HYNDSYTFODRQVANONGQRNSDFV
KTGRVANMOTTNQORYNYCKLNYTQATQAQARQYGQQARRYFQDQVND IVRLAQNNYAMAN
NQSIPYPSASGSQISRAPGTAQAQYTNNANGGSNFHLLFQVNSFPFNG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(32765. .32938,33103. .33374,33423. .33570,
34571. .35268,35647. .35995,36141. .36364,37235. .37388))
/gene="Y75B8A.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="G1:3980026"
/translation="MAVRRLLFLTLFSAFSNVSNAQYQNONQNQOSNYVTVSCSQGSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="predicted using Genefinder; similar to Homeobox domain; cDNA EST yk403d9.5 comes from this gene; cDNA EST yk467d4.5 comes from this gene"
                                                                                                                                                                               /note="predicted using Genefinder; similar to Eukaryotic protein kinase domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="predicted using Genefinder; similar to Homeobox domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(5502. .5585,6378. .6565,6618. .6829,
8055. .8359)}
                                                                                         Joun(379. .690,1911. .2009,2717.
/gene="Y75B8A.36"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="CAA22093.1"
/db_xref="G1:3980025"
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                                                                              /gene-"Y75B8A.36"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8055. .8359))
/gene="Y75B8A.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start*1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=
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                                              gene
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinoidea; Cyprinidae; Rasborinae; Danio.

1 (bases 1 to 485)
Shimoda, N., Knapik, E.W., Ziniti, J., Sim, C., Yamada, E., Kaplan, S. and Fishman, M.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="Disalphar'IO"
/note="Vector: ml3MP19 with added BstXI site; V-type:
Phage; Genomic DNA from a single adult zebrafish of AB
strain was dispeted with Alui, CacBI, HaeIII, NlaVI, or
RsaI. Fragments in the range of 250-500 bp were gel
purified and a BstXI linker was added. The fragments were
cloned into a modified Ml3mp19 vector and transformed
into E. Coli DH5alpha. Microsatellite sequences were
screened with labeled d(CA)15 and d(GT)15 oligonucleotide
                                                                                                                                                                                                                                                               Contact: Mark C. Fishman
Cardiovascular Research Center
Massachusetts General Hospital
Mail code 1494100A, 149 13th Street, Charlestown, MA 02129, USA
Fax: 6177265806
Email: fishman@mgh.cvrc.harvard.edu
http://zebrafish.mgh.harvard.edu
primer A: TGTTTCCTGATTCGTGTTTG
Primer B: GCTACTGTTCTGTCCCACTG
STS size: 157
PCR Profile:
                                                                                                                                                                                    A genetic linkage map of the zebrafish with 2000 microsatellite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94 degrees C for 5.0 minutes 94 degrees C for 1.0 minute 58 degrees C for 1.0 minute 72 degrees C for 1.5 minute 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 8
Gaps: 0
Percent Identity: 87.500
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50 mM
10 mM
8.3.
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each 375 nM
each 200 uM
0.034 units/ul
10 ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Zebrafish AB"
/sex="F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'organism-"Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .211)
4 g
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/clone="26550"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(191. . 83 c 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain-"AB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Annealing:
Polymerization:
PCR Cycles:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermal Cycler:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Taq Polymerase:
Total Vol:
                                                                                                                                                                                                                                     Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Presoak:
Denaturation:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.625
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Primer:
zebrafish.
Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dNTPs:
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Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protocol
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primer_bind
BASE COUNT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
  SOURCE
ORGANISM
                                                                                                                  REFERENCE
AUTHORS
                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                 ALUZIZEG. 1 GI:3702098
HTG; HTGS_PHANEI.
Caenorhabditis elegans.
Caenorhabditis elegans.
Caenorhabditis elegans.
Caenorhabditis elegans.
ISM Metazoa; Nematoda; Secernentea; Rhabditida;
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditida;
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
I (bases 1 to 336538)
Secondaries; Caenorhabditis.
I (bases 1 to 336538)
AL Submitted (03-DEC-1998) Nematode Sequencing Project, Sanger Centre, Libmitted (03-DEC-1998) Nematode Sequencing Project, Sanger Centre, Hinxton, Cambridge CB10 1RQ, UK and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail:
Inxton, Cambridge Libs Sequence visualished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate
                                                                                                                                                                                                                             G46114 485 bp DNA STS 23-MAR-1999
26550_1 Zebrafish AB Danio rerio STS genomic clone Z6550 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1600 others
                                                to: 298406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 336638
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1. 33658
1. Gaganism="Caenorhabditis elegans"

/db_xref="taxn:6239"
/chromosome="III"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38.00 Length: 10
4.222 Gaps: 0
90.000 Percent Identity: 70.000
                                              to reverse of: CEY75B8A from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="Y75B8"
59632 c 61379 g 105818 t
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                                                                                                                       203587 TATCGGCTTAAATGCGCCTAAATCAACGA 203558
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                                                                                            10
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                                                                                          1 TyrArgLeuAlalleArgLeuAsnGluArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to reverse of: CEY75B8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence tagged site.
G46114
G46114.1 GI:4492405
  US-08-653-294-9 x CEY75B8A/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-08-653-294-9 x CEY75B8/rev
                                                                                                                                                                                      seq_name: gb_htgl:CEY75B8
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BASE COUNT ORIGIN

FEATURES

DEFINITION

ACCESSION VERSION KEYWORDS

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misc_feature
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                                                                                                                                                                               ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                              LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNSLMDKLVFSKIQSSLGGKVRLMITGAAPISTPVLTFFRAAMGCWVFEAYGQTECTA
GCSITSPGDWTAGHVGTPVSCNFVKLEDVADMNYFSVNNEGEICIKGNNVFKGYLKDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MLFIFNFLFSPLPTPALICLLTFGTAIFLWLINRPQPVLPLIDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YKWISYKQVSDRAEYLGSCLLHKGYKPSQDQFIGIFAQNRPEWVISELACYTYSMVAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKTQEVLDKDGWLHTGDIGRWLPNGTLKIIDRKKNIFKLAQGEYIAPEKIENVYSRSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PILQVFVHGESLRSFLIGVVVPDPESLPSFAAKIGVRGSFEELCQNQCVKKAILEDLQ
KVGKEGGLKSFEQVKSIFVHPEPFSIENGLLTPTLKAKRVELAKFFQTQIKSLYESIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNOSVGIEGGARRGAFOKNNDLILYYFSDAKTLYEVFQRGLAVSDNGPCLGYRKPNQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLYDTLGAEAIIYVINRADISVVICDTPQKATMLIENVEKDLTPGLKTVILMDPFDDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LMKRGEKCGIEMLSLHDAENLGKENFKKPMPPNPEDLSVICFTSGTTGDPKGAMLTHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIVSNMAAFLKFLEPIFQPTPEDVTISYLPLAHMFERLVQGVIFSCGGKIGFFQGDIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLPDDMKALKPTVFPTVPRLLNRVYDKVQNEAKTPLKKFLLNLAIISKFNEVRNGIIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (sites)
Olawaw_E., Iljima,H., Suzuki,T., Sasana,H., Sato,H., Kamataki,A.,
Nagura,H., Kang,M.-J., Fujino,T., Suzuki,H. and Yamamoto,T.
A novel acyl-CoA synthetase, ACS5, expressed in intestinal
epithelial cells and proliferating preadipocytes
J. Blochem. 124 (3), 679-685 (1998)
                                                                                                                                                                                 AB012933 2454 bp mRNA ROD 05-FEB-1999
Rattus norvegicus mRNA for acyl-CoA synthetase 5, complete cds.
AB012933
                                                                                                                                                                                                                                                                                                                  to: 2454
                                    485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality: 37.00 Length: 10 Ratio: 3.700 Gaps: 0 Percent Similarity: 100.000 Percent Identity: 60.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="acyl-CoA synthetase 5"
/protein_id="BAA33581.1"
                                    :
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .2454
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/db_xref="taxon:10116"
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                                  from: 1
                                                                                                                                                                                                                                                     AB012933.1 GI:3721652
acyl-CoA synthetase 5.
Rattus norvegicus CDNA to mRNA.
Rattus norvegicus
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                                  to reverse of: G46114
                                                                                         94 TACCGGCTCGCCATTAGAATCAAC 71
                                                                    1 TyrArgLeuAlaileArgLeuAsn 8
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/gene="ACS5"
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US-08-653-294-9 x AB012933/rev
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US-08-653-294-9 x G46114/rev
                                                                                                                                                                                 seq_documentation_block:
LOCUS AB012933
                                                                                                                                            seq_name: gb_ro:AB012933
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                                  Align seg 1/1
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TITLE
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MEDLINE
FEATURES
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AUTHORS
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SOURCE
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SSHTFHAHVDGIENTTPMDSTDNISEIMPNALVDSFKNENTRALTPENASKPESKYT
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                                                                                                                                              Saccharomyces cerevisiae COT1 protein gene, complete cds. M88252
                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae
Eukaryota; Fungi, Ascomycota; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.

1 (bases 1 to 2675)
Conklin, D. S., McMaster, J. A., Culbertson, M.R. and Kung, C.
COTI, a gene involved in cobalt accumulation in Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="potential metal coordination; putative" /db_xref="SGD:S0005843"
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Mol. Cell. Biol. 12 (9), 3678-3688 (1992)
92375034
                                                                                                                                                                                                                                               COT1 protein; transmembrane protein. Saccharomyces cerevisiae DNA.
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/db_xref="SGD:S0005843"
1129. .1182
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db_xref="SGD:S0005843"
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'db_xref="SGD:S0005843"
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872. .875
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1342. .1401
Location/Qualifiers
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alignment_scores:
Quality: 37.00 Length: 10
Ratio: 3.700 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 60.000

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Ethylene response (ETR) gen
A. thaliana ethylene respon
Staphylococcus aureus conti
Agaricus bisporus hypA and
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Equine dermal cells (NBL-6) were infected with EHV-4 strain 1942 viral DNA, purified and a BamHI library constructed in pUC9.

Calcium shocked E. coll pHT cells were transformed with the recombinant plasmids. Additional clones were derived from a restriction digest of pUC9 concy. The BamHI G fragment. The the gene was determined. by analysis of overlapping sequences (SEQ ID no 10. Vaccines can be prepd. using this sequence, and they may be used to protect horses against EHV-4 infection, inducing a higher level of immunity and less side-effects than other live virus vaccines.
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ID X20531 standard; DNA; 3858 BP.

AC X20531;
DE MAX-1999 (first entry)
DE Polynucleotide sequence from the genome of Treponema pallidum,
KW Treponema pallidum infection; syphilis; Borrelia infection; animal;
KW enzyme production; ds.

Treponema pallidum.

PN W09859034-A2.

PN W09859034-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid sequence encoding EHV-4 9H or 9C protein - used produce a vaccine for protection of horses against EHV-4
                                                                                                                                                                                                                                                                                                                                                                                            Equine herpes virus-4; glycoprotein gC; antigenic; vaccine; alphaherpesvirus; respiratory disease; cellular attatchment;
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52. .1509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-JAN-1992.
04-JUL-1991; G01091.
06-JUL-1990; GE-014950.
(UNIU ) UNIV OF GLASGOW.
(EQUI-) EQUINE VIROLOGY RES FOUN.
NACOLSON L. Onlons DE;
WPI: 92-056872/07.
P-PSDB; R20796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product- EHV-4_gC
      91.52
91.52
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                                                                                                                                                                                                                                                            Q20995 standard; DNA; 1560
Q20995;
                                                                                                                                                                                                                                                                                                     19-MAY-1992 (first entry)
EHV-4 gC gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                      pathogenic; ss.
Equine herpesvirus-4.
Key Locati
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US-08-653-294-9 x Q20995
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Ratio:
Percent Similarity:
   N_Geneseq_36:Q85556
N_Geneseq_36:V59031
N_Geneseq_36:V74399
N_Geneseq_36:T49073
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1560 | ERV4 4g cgene. Nucleic acid se  
3858 | Polynucleotide sequence from  
1549 | D. melanogaster tipE+ 4Kb clon  
3954 | Full length tipE protein codin  
3954 | Full length tipE protein codin  
3954 | Human secreted protein  
333 | Staphylococcus aureus contig SE  
333 | Staphylococcus aureus contig SE  
336 | Probe (14) for microbial genes  
846 | Antibiotic resistance gene blaz  
1176 | Staphylococcus aureus contig SE  
2030 | Protein disulphide isomerase  
2040 | Bacillus thuringiens  
2802 | Staphylococcus aureus contig SE  
2040 | Bacillus thuringiens  
2802 | Staphylococcus aureus contig SE  
2040 | Bacillus thuringiens  
2802 | Staphylococcus aureus contig SE  
205 | Expected fisher  
2802 | Staphylococcus aureus contig SE  
206 | Staphylococcus faecalis genome  
207 | Septendide synthase gene clu  
44377 | Platenolide synthase gene clu  
44377 | Platenolide synthase gene  
208 | Staphylococcus aureus contig SE  
209 | Staphylococcus aureus contig SE  
200 | Staphylococcus aureus contig SE  
201 | Staphylococcus aureus contig SE  
202 | Helicobacter pylori 76 kDa pol  
2038 | Ethylene response (ETR) gene  
2038 | Ethylene response (ETR) gene  
2037 | Eth
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A. thallana ethylene response
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A. thallana ethylene response
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1105.34
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Query: Us.08.653.294.9
Database: N_Geneseq_36:*
Database sequences: 311585
Database length: 125096042
Search time (sec): 590.520000
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N_Geneseq_36:X02018
N_Geneseq_36:T09975
N_Geneseq_36:X02015
N_Geneseq_36:X081895
N_Geneseq_36:X78539
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N_Geneseq_36:V37110
N_Geneseq_36:V75169
N_Geneseq_36:V22800
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N_Geneseq_36:Q14810
N_Geneseq_36:Q73061
N_Geneseq_36:Q73061
N_Geneseq_36:T828
N_Geneseq_36:T8508
N_Geneseq_36:T8508
N_Geneseq_36:T8508
N_Geneseq_36:T8508
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N_Geneseq_36:V64214
N_Geneseq_36:V77268
N_Geneseq_36:X20596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N_Geneseq_36:T77280
N_Geneseq_36:V32039
N_Geneseq_36:X20619
N_Geneseq_36:V74973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N_Geneseq_36:V07921
N_Geneseq_36:V07916
N_Geneseq_36:Q85560
N_Geneseq_36:Q85557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _Geneseq_36:020995
_Geneseq_36:X20531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N_Geneseq_36:085561
N_Geneseq_36:V59032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N_Geneseq_36:V59037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genesed_36:V5903
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us-08-653-294-9.rng

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US5871940-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                Align seg 1/1
                                                                                                                                                                                                                                                                                                                                        Wrii 3/ 109340/V03.

Wrii 3/ 109340/V03.

Wroleic acid encoding Drosophila melanogaster tipE protein - for prodn. of recombinant voltage-dependent cation channel
Example 11: Collumn 37.40: 33pp; English.

Togydy and Togyg represent the 5' and 3' untranslated regions of the Corsophila tipE protein, result in a chiyl methane sulphonate.

Mutations in the tipE protein, result in a chiyl methane sulphonate induced recessive mutation phenotype. Homologous files for the mutation paralyse rapidly at 38 degrees, and recover immediately when returned to 23 degrees. Coexpression of the full length tipE sequence, and a nucleic acid encoding a para protein results in translation products that form a functional voltage-dependent cation channel. The cation channel can be used to screen for possiticides active against insects such as Drosophila melanogaster and pest insects. The cation channel can also be used to screen for drugs for use in the treatment and prevention of parasitic infections in humans and animals, and to screen drugs for their neuroprotective effect against hypoxia, stroke, and head trauma.

Example 27.001 and 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T59978;
12-MAY-1997 (first entry)
3' untranslaged region of the tipE protein coding sequence.
Brosophila; tipE; para protein; voltage-dependent cation channel; stroke; pesticide; insecticide; insect; parasitic infection; human; head trauma; prosephila melanogaster.
Brosophila melanogaster.
US5593862-A.
                                                                                                                                                                                                                                                                                          detecting
                                                                                  WELLS 19.081273/07.

New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and the many of T. pallidum infections, particularly syphilis (21aim 1) Page 368-370; 1150pp; English.

X25500-21243 represent polynucleotide sequences from the genome of Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detection disease; related to Borrelia infections in animals, and for the production of blosynthetic products such as enzymes.

Sequence 3858 BP; 659 A; 777 C; 1306 G; 1116 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: 3858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps: 0
Percent Identity: 77.778
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to reverse of: X20531 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-JAN 1997.

14-JAN 1997.

04-OCT 1994; US-317880.

(UYNY) UNIV NEW YORK STATE RES FOUND.

Feng G, Hall LM;

WPI; 97-099467709.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
ID T59978 standard; DNA; 1549 BP.
23-JUN-1998; U13041.
24-JUN-1997; US-050667.
(HUMA-), HUMAN GENOME SCI INC.
Fraser',M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-08-653-294-9 x X20531/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: 36.00 Ratio: 4.000 Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: N_Seneseq_36:T59978
                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores
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Percent Identity: 66.667

Quality: 35.00 Ratio: 3.889 Percent Similarity: 100.000

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Screening for agents which modulate ion channel function - using host cells transformed with nucleic acids encoding the Drosophila melanogaster tipE and para proteins
Disclosure: Column 37-40; 54pp; English.

Disclosure: Column 37-40; 54pp; English.

Disclosure: Column 37-40; 54pp; English.

This sequence repersents the 3'-qry from a Drosophila melanogaster tipE+
protein which is used in a method for screening for agents which modulate
for channel function which uses host cells transformed with nucleic acid
encoding Drosophila melanogaster tipE and para proteins co-expression of
these genes in the host cell, allows the formation of a functional
voltage dependent cation channel (VDCC) in the cell. The agents
identified can be used as pesticides for the control of Drosophila
melanogaster or other insects. They can also be used to screen
hypoxia, ischemma, stroke and head trauma.

Sequence 1549 BP; 597 A; 328 C; 249 G; 375 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:

ID T59975 standard; DNA; 3954 BP.

T T59975 standard; DNA; 3954 BP.

T 12-MAY-1997 (first entry)

DE Full length tipE; protein coding sequence.

KW Drosophila; tipE; para protein; voltage-dependent cation channel; stroke; KW pesticide; insecticide; insecticide; insecticide; insecticide; parasitic infection; human; head trauma; meuroprotection; hypoxia; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Average (first entry)

21-APR-1999 (first entry)

D. melanogaster tipE+ 4Kb clone 3'-TTR.

D. melanogaster tipE+ 4Kb clone 3'-TTR.

D. melanogaster tipE+ 4Kb clone 3'-TTR.

pesticide; insect control; pharmaceutical agent; neuroprotection; hypoxia; ischaemia; stroke; head trauma; ss.

Drosophila melanogaster.

Key
                                                                                                         to: 1549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: 1549
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                                                                                                         to reverse of: T59978 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-FEB-1999.
13.-7AN-1997; 782396.
04-COT-1994; US-317880.
13.-7AN-1997; US-782396.
(UVNY) UNINY WING YORK STATE RES FOUND.
Feng G, Hall LM;
WPI; 99-166632/14.
                                                                                                                                                                               Align seg 1/1 to reverse of: X02018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TyrArgLeuAlalleArgLeuAsnGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      889 TTTCGTTTATCATTACGTTTAAATGAA
                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
ID X02018 standard; DNA; 1549 BP.
alignment_block: .
US-08-653-294-9 x T59978/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-08-653-294-9 x X02018/rev
                                                                                                                                                                                                                                                                                                                             seq_name: N_Geneseq_36:X02018
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WO9906552-A2.
                                                                                                                                                                               alignment_scores:
                                                                                                                             head trauma.
                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                    prosopila tipe protein. Mutations in the tipe protein, result in a brosopila tipe protein. Mutations in the tipe protein, result in a bethyl methane sulphonate-induced recessive mutation phenotype. Homologous flies for the mutation paralyse rapidly at 38 degrees, and recover immediately when returned to 23 degrees. Coexpression of this sequence, and a nucleic acid encoding a para protein results in translation products that form a functional voltage-dependent cation channel. The cation channel can be used to screen for pesticides active against insects such as Drosophila melanogaster and pest insects. The cation channel can also be used to screen for drugs for use in the treatment and prevention of parasitic infections in humans and animals, and to screen drugs for their neuroprotective effect against hypoxia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-APR-1999 (first entry)
D. melanogaster tipE+ genomic DNA.
tipE+; para protein; modulator; voltage dependent cation channel; VDCC; pesticide; insect control; pharmaceutical agent; neuroprotection; hypoxia; ischaemia; stroke; head trauma; ss.
Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Screening for agents which modulate ion channel function - using host cells transformed with nucleic acids encoding the Drosophila melanogaster tipE and para proteins
                                                                                                                                                                             prodn. of recombinant voltage-dependent cation channel
Disclosure; Column 29-32; 33pp; English.
This sequence represents the full length coding sequence for the
                                                                                                                                                                Nucleic acid encoding Drosophila melanogaster tipE protein - for
                                                                                                                                                                                                                                                                                                                                                                        834 T;
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps: 0 Gaps: 0 Oercent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 3954
                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                          867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from: 1
                                                                                                                                                                                                                                                                                                                                                                        960 C;
                                                                         14 JAN-1997.
04-0CT-1994; 317880.
04-CCT-1994; US-317880.
(UXNY) UNIV NEW YORK STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-JAN-1997; 782396.
04-oCT-1994; US-317880.
13-JAN-1997; US-782396.
(UNN ) UNIV NEW YORK STATE RES FOUND.
FENG 6, Hall LM;
WPI: 99-166632/14.
P-PSDB; W92459.
            Location/Qualifiers
1046. .2404
/*tag= a
/product= tipE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3290 TITCGITTATCATIACGITTAAAIGAA 3264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualiflers
1046. .2404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TyrArgLeuAlalleArgLeuAsnGlu 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to reverse of: T59975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "tipE+"
                                                                                                                                                                                                                                                                                                                                                                       1293 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
ID X02015 standard; DNA; 3954 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio: 3.889
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-08-653-294-9 x T59975/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: N_Geneseq_36:x02015
 Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                              stroke, and head trauma.
                                                                                                                                                                                                                                                                                                                                                                                                                          35.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                                                                                                                                                        3954 BP;
                                                                                                                            Feng G, Hall LM;
WPI; 97-099467/09.
                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
                                                                                                                                                    P-PSDB; W13843
                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                             US5593862-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US5871940-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X02015
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Claim 1: Page 256; 577pp: English.

X51787 to X52019 represent 5' expressed sequence tags (ESTS) for human secreted proteins, and encode the proteins given in Y12987 to Y13219, crespectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation/differentiation activity, haematopolesis regulating activity, tissue growth regulating activity, reproductive hormone regulating activity, chemotactic/ chemokinetic activity, haemostatic and thrombolytic activity, receptor/ ligand activity, tumour inhibition activity and chromoseme mapping procedures. The sequences can also be used for and chromosome mapping procedures. The sequences can also be used for
Disclosure; Fig 7A-B; 54pp; English.

This sequence encodes a Drosophila melanogaster tipE+ protein which is used in a method for screening for agents which modulate ion channel function which uses host cells transformed with nucleic acid encoding brosophila melanogaster tipE and para proteins. Co-expression of these genes in the host cell, allows the formation of a functional voltage dependent cation channel (VDCC) in the cell. The agents identified can be used as pesticides for the control of Drosophila melanogaster or other insects. They can also be used to screen pharmaceutical agents for their neuroprotective affect against e.g. hypoxia, ischaemia, stroke and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human secreted protein 5' EST SEQ ID NO: 109.

Human; secreted protein: EST; expressed sequence tag; diagnosis;

Horonsic; gene therapy; chromosome mapping; signal peptide;

upstream regulatory sequence; cytokine activity; cell proliferation;

differentiation; haematopoiesis regulation; tissue growth regulation;

reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;

thrombolytic; anti-inflammatory; tumour inhibition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell. 58 G; 67 T; sequence 278 BP; 95 A; 56 C; 58 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     834 T;
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31-JUL-1998; IB1236.
01-AUG-1997; US-905223.
Duclert A, Dumas Milne Edwards J, Lacroix B;
WPI: 99-153782/13.
P-PSDB; Y13095.
Wew isolated brain-derived nucleic acids - used to develop p which may have cytokine, immune, regulatory, haematopoiesis regulating, anti-inflammatory or tumour inhibition activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: 3954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality: 35.00 Length: 9
Ratio: 3.889 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     867 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     960 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3290 TTTCGTTTATCATTACGTTTAAATGAA 3264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TyrArgLeuAlalleArgLeuAsnGlu 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to reverse of: X02015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1293 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
ID X51895 standard; DNA; 278 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-9 x X02015/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: N_Geneseq_36:X51895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3954 BP;
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Location/Qualifiers complement (1. 31) /*tag= a /note= "primer RMM393"

BP

/codon_start= 38. .134

1. .37 /*tag= b

/*tag= c 135. .431 /*tag= d 432. .594 /*tag= e 595. .1384

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07-DEC-1996 (first entry)
Broccoli ACC synthase genomic DNA clone ACCAl.
ACC synthase; l-aminocyclopropyl-1-carboxylic acid synthase; ethylene; shelf-life; Cucumis melo; melon; transgenic plant; antisense; broccoli; ss.
Brassica oleracea.
                                         seq_documentation_block:
ID T33136 standard; DNA; 1384
    seq_name: N_Geneseq_36:T33136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9621027-A1
                                                                                                                                                                                                                                               primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       primer_bind
                                                                                                                                                                                                                                                                                                                                                                        intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                       intron
                                                                                                                                                                                                                                                                                                                                                                                                                  exon
                                                                                                                                                                                                                                                                                                               exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 exon
                                                             This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S. aureus DNA sequences allows putative functions to be assigned so that prictein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are industrial importance can be obtained. Specifically, sequences which are be used in a vaccine composition against S.aureus infection. The be used in a vaccine composition against S.aureus infection. The complexity to be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating computer; readable medium.
                                                                                                                                                                                                                                                                                                                                                                                                           Staphylicoccus aureus contig SEO ID #4228.
Compute: readable medium: vaccine; S.aureus infection; immunodetection; cellulitis; eyelld infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic slock syndrome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polynuc.ectide(s) and proteins derived from Staphylococcus aureus stored in computer readable medium and used in the production of anti-S. Hureus vaccines
                 Gaps: 0 Gaps: 0 Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JAN-(997; 100117,
25-JAN-(996; US-009861.
(HUMA-) HUMAN GENOWE SCI INC.
Barash (C, Choi GH, Dillon PJ, Fannon MR, Kunsch CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 10
Gaps: 0
Percent Identity: 60.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 G;
                                                                                                                                                                to: 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91 C;
                                                                                                                                                                                                                                241 TACAGACTAGCTCTGCGCATCACAGAG 267
                                                                                                                                                                                                        1 Tyr//rgLeuAlaIleArgLeuAsnGlu 9
                                                                                                                                                                Align seg 1,1 to: X51895 from: 1
                                                                                                                                                                                                                                                                                                                                                  itandard; DNA; 333 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90 A;
                                                                                                                                                                                                                                                                                                                                                                                        16-MAR-1999 (first entry)
                                         Ratio: 3.778
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                       seq_name: N_Geneseq_36:V78539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus
EP-7865:9-A2,
                                                                                                alignment_block:
US-08-653-204-9 x x51895
                                                                                                                                                                                                                                                                                                                            seq_document@tion_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1374922/35
                     ()uality:
Ratio:
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    (uality:
        Ratio:
        Percent Sim;larity:
alignment_scures
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MPI; 97
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NEW WENT WANTED BY THE PARTY OF 
/*tag= f 1352, 1382 /*tag= g /note= "primer RMM394"

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DNA encoding 1-amino:cyclo:propyl-1-carboxylic acid synthase of Brassica oleracea - used to regulate ethylene-dependent processes in plants, esp. to improve shelf life

Train 2: Figla.B: to prove shelf life
Claim 2: Figla.B: 50pp; English.

Brassica oleracea genomic clone ACCAl (733136) codes for 1-aminocyclopropyl-1-carboxylic acid synthase (ACC-synthase)
CR98598), an enzyme involved in ethylene blosynthesis. It was cold. by subjecting broccoli leaf total genomic DNA to PCR using primers (see also T33137-38) based on the Arabidopsis thaliana ACC synthase gene. The product was cloned into PCRII to obtain clone continues or antisense orientation, into an expression cassette and then transferred to a binary vector suitable for Agrobacterium-mediated plant transformation. The constructs permit control of the level of CRC synthase in a transgenic plant (esp. B. oleracea or cucumis melo) and hence a control of maturation, ageing and shelf-life. Sequence 1384 BP; 401 A; 290 C; 310 G; 383 T;
11-JUL-1996.
07-JUN-1995; UO7271.
30-DEC-1994; US-36692.
(ASGR-) ASGROW SEED CO.
WPI: 96-334002/33.
P-PSDB; R98598.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality: 33.00 Length: 10
Ratio: 3.300 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 50.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to reverse of: T33136 from: 1 to: 1384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             601 TATCGAATCTGTATTCAAATAAATAAACGT 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TyrArgLeuAlalleArgLeuAsnGluArg 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-9 x T33136/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
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seq_name: N_Geneseq_36:V20113

Align seg 1/1 to: V78539 from: 1 to: 333

alignment_block: US-08-653-294-9 x V78539

3.667

1 TyrirgLeuAlaIleArgLeuAsnGluArg 10

us-08-653-294-9.rng

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We of oligo:nuclectide primers and probes - for detection, identification and quantification of bacteria, fungi and bacterial antibiotic resistance gene(s)
antibiotic resistance gene(s)
Claim 19; Page 108: 167pp; English.
The present sequence represents an antibiotic resistance gene blaz
fresistant to beta-lactams), and was used to design PCR primers
V37050-51. The specification describes the use of probes and/or amplification primers which are specific, ubiquitous and sensitive for determining the presence and amount of nucleic acids from a bacterial antibiotic resistance gene and specific bacterial and fungal species in any sample suspected of containing the bacterial or fungal nucleic acids where each of the nucleic acid or variant or part comprises a selected target region hybridisable with the probes or primers. The method of
                                                                                                                                                                                                                                                                                                     The AMAY 1995; UOR 108 208.

The AMAY 1995; UOS 551155.

The AMAY 1995; UOS 551155.

The Amaz 1995; UOS 1995; UOS 1995.

The Amaz 1995; UOS 1995; UOS 1995; UOS 1995.

The Amaz 1995; UOS 1995; UOS 1995.

The Amaz 1995; UOS 1995; UOS 1995.

The Amaz 1995; UOS 1995; UOS 1995.

The Ama
                                                                                                                      Probe (14) for microbial genes induced during host infection. Probe; identification; microbial gene; pathogenic microorganism; host infection; virulence gene; vaccine; antimicrobial agent; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibiotic resistance gene blaz for beta-lactams.
Detection; bacterial antibiotic resistance gene; bacteria;
fungal species; identification; beta-lactam; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.00 Length: 10
3.556 Gaps: 0
90.000 Percent Identity: 70.000
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04.NOV-1996; US-743637.
(IDIL-) IDI INPECTIO DIAGNOSTIC INC.
Bergeron MG, Ouellette M, Picard FJ, Roy PH;
WPI; 98-286967/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to: 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TyrArgLeuAlaIleArgLeuAsnGluArg 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 IICCGIIIGGCAAIACGACIAAAGAIGCGG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: V20113 from: 1
                          V20113 standard; DNA; 336 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: N_Geneseq_36:V37110
                                                                                                                                                                                                               Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-653-294-9 x V20113
seq_documentation_block
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Ratio:
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                                                                                         86-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-MAY-1998
                                                                                                                                                                                                                                                                                 27-NOV-1997
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claim 1; Page 1712; 3271pp; English.

This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable conditum, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, oxicomyelitis, syndrome, etc. Organisms transforamed with the DNA sequences can be used to the polypeptides. The now DNA sequences can be used to the polypeptides. The now DNA sequences can be used to the polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus aureus contig SEQ ID #858.
Computer readable meds contig SEQ ID #858.
cellulitis; eyelld infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
Staphylococcus aureus.
EP-786519-A2.
use comprises contacting the sample with the probes or primers and detecting the presence of hybridised probes or amplified products as an indication of the presence of the specific bacterial or fungal species and bacterial antibiotic resistance genes. The methods and products can be used to detect and identify the bacterial and fungal species. Agenera and determine the bacterial resistance to antibiotics. Sequence 846 BP, 356 A, 99 C, 135 G, 256 T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (and their fragments) are useful as primers or probes for isolating nomologues of any of the S.aureus DNA sequences contained on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ė
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Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA,
                                                                                                                                                                                                                      9 2 2 5 5 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 10
Gaps: 0
Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                             to: 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            221 G;
                                                                                                                                                                                                                                                                  Percent Identity: 55.
                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                               from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TyrArgLeuAlalleArgLeuAsnGlu 9
                                                                                                                                                                                                                                                                                                                                                                             to reverse of: V37110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           V75169 standard; DNA; 1176 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          432 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                             alignment_block:
US-08-653-294-9 x V37110/rev
                                                                                                                                                                                                                    Quality: 32.00
Ratio: 3.556
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: N_Geneseq_36:V75169
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07-JAN-1997; 100117.
05-JAN-1996; US-009861.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 anti-S.aureus vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homologues of any of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 97-374922/35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
Ratio:
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                                                                                                                                                                                                    alignment_scores;
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                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosen CA;
  8888888
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Donován WP;
194523682,36.
P-PSDB; P91462.
Bacillus thuringiensis var israelansis cry D toxin gene and proteins
- used for producing insecticide compsns.active against Dipteran species.
Claim 1; fig 2; 58pp; English.
cryb gene is inserted into plasmid and used to transform a microorganism.
                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; R97735.

Wew DNA construct for expressing cryIV D protein in cyanobacteria under control of a phycocyanin beta promoter, useful for control of a thycocyanin beta promoter, useful for control of a dipteran larvae in water under control of a phycocyanin beta promoter, useful for control of a dipteran larvae in water models the B. thuringiensis ssp. israelensis cryIVD toxic protein, which was used in the prep. of a claimed DNA construct for the expression of CryIVD in cyanobacteria, comprising the present sequence under the control of phycocyanin beta (cpcB) promoter. Cyanobacteria (which may be adapted for growth in fresh to promoter. Cyanobacteria (which may be adapted for growth in fresh cas insecticides for controlling dipteran larvae, esp. those of as insecticides for controlling dipteran larvae, esp. those of consquitoes and blackfiles, that live in water. The percentage of collex pipens (mosquito) larvae surviving after 4 days with cyanobacteria transformed with the claimed DNA construct as their only food source was 51 %, compared to 94 % for those fed with cyanobacteria, CryIVD is efficiently expressed under the control of the strong cpcB promoter, even though the CryIVD gene contains 19 contains 19 may their and the changereria in the strong cpcB promoter, even though the CryIVD gene contains 19 contains 19 contains 19 in contains 19 contains 10 con
       transformed cyanobacteria; phycocyanin beta; cpcB; promoter;
insecticide; dipteran larvae; mosquito; blackfly; ss.
accilius thuringlensis.
Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: 2040
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Ratio: 4.000 Gaps: 0
Percent Similarity: 88.889 Percent Identity: 66.667
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cryD protein; Bacillus thuringlensis; biopesticide.
Bacillus thuringlensis var.israelesis.
WO8907605-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    373 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       315 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TyrargleualaileargleuasnGlu 9
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ID N90712 standard; DNA; 2100 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       716 A;
                                                                                                                                                                                                                             21-MAY-1996.
04-MAY-1992; 877876.
04-MAY-1992; US-877876.
28-JAN-1994; US-188581.
UYMB-) UNIV MEMPHIS STATE.
MUZPMY RC. Steevens SE;
                                                                                                                              41. .1972
/*tag= a
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09-JAN-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-08-653-294-9 x T29774/rev
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17-FEB-1989; U00663.
19-FEB-1988; US-158176.
(ECOG) Ecogen Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2040 BP;
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Sequence 204
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                                                                                                                                                                                                     US5518897-A
          NAMES OF THE PROPERTY OF THE P
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The present sequence encodes a protein disulphide isomerase (PDI) derived form a methylotrophic yeast, Candida boldinii strain S2. PDI is a major protein present in the lumen of the endoplasmic reticulum. PDI is a major protein protein must stay in the national proteins of secretory proteins. As the protein must stay in the endoplasmic reticulum, it has a sequence known as the endoplasmic reticulum retention signal sequence at the carboxy terminus (W56317). The PDI protein is useful in gene therapy and genetic engineering. The PDI gene may be coexpressed with a gene of interest to ensure the production of a correctly folded biologically active protein.

Sequence 2030 BP; 678 A; 351 C; 304 G; 697 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-JUL-1998 (first entry)

Protein disulphide isomerase gene derived from Candida boidinii.

Protein disulphide isomerase. PDI; methylotrophic yeast;

Candida boidinii strain S2; endoplasmic reticulum; stable conformation;

candida boidinii strain S2; endoplasmic reticulum; stable conformation;

endoplasmic reticulum retention signal sequence; genetic engineering; ds.

Candida boidinii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-NOV-1996 (first entry)
Bacillus thuringiensis ssp. israelensis CryIVD protein DNA.
CryIVD: toxic protein; crystal toxin; expression construct;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to reverse of: V22800 from: 1 to: 2030
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Percent Identity: 87.500
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                                                                                               Align seg 1/1 to: V75169 from: 1 to: 1176
                                                                                                                                                                                                     1 TyrkrgLeuAlaileArgLeuAsnGluArg 10
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367. .1962
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/product= PDI
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ID T29774 standard; DNA; 2040 BP.
AC T29774;
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04-SEP-1997; 306871.
04-SEP-1996; JP-234287.
(SUNR) SUNTONY LTD.
RATO N, SARAI Y, Shibano Y;
WPI; 98-161102/15.
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US-08-653-254-9 x V22800/rev
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alignment_blcck:
US-08-653-254-9 x V75169
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**%** E E E S E

The 67kD protein encoded by the gene has insecticidal activity against dipteran larvae. Sequence 2100 BP; 746 A; 316 C; 378 G; 660 T; ខ្លួ

alignment_scores:
Quality: 32.00 Length: 9
Ratio: 4.000 Gaps: 0
Percent Similarity: 88.889 Percent Identity: 66.667

alignment_block: US-08-653-294-9 x N90712/rev

Align seg 1/1 to reverse of: N90712 from: 1 to: 2100

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AQ912901 nbeb0038P10r CUGI R
AI001920 ov23a05.s1 Soares_t
B80514 CIT-HSP-2050B15.TF CI
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 455)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Meller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
LOCUS AW156527 342 bp mRNA EST 04-NOV-1999
DEFINITION se28c06.yl Gm-c1015 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1015-2531 5', mRNA sequence.
ACCESSION AW156527
VERSION AW156527.1 GI:6227999
KEYWORDS EST.
                                                                                                                                                                                                   seq_documentation_block:
LOCUS AQ146935 455 bp DNA GSS 08-OCT-1998
DEFINITION HS_2248_A2_B10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2248 Col=20 Row=C, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db.xef="texton:9606"
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/clone="Plate=2248 Col=20 Row=C"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Col1 DH10B"
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Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3867
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2248 row: C column: 20
Class: BAC ends
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Ratio: 4.556 Gaps: 0
Percent Similarity: 90.000 Percent Identity: 80.000
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Location/Qualifiers
1. 455
/organism="Homo sapiens"
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AQ146935.1 GI:3537588
GSS.
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                                                                                                                                                 gb_gss9:AQ146935
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gb_gss7:AQ912901
gb_est22:A1001920
gb_gss3:B80514
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tc76f07.x1 Soares_NhHM
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-LOTALIGN-200 -THR_SCORE-PCT -ALIGN-15 -MODE-LOCAL
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-NCPU-6 -ICPU-3 -NO_XLPXY -NAIT -THREADS-1
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AL176387 B
AL383239 t
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Query length: 10
Database: EST:*
Database sequences: 4538634
Database length: 1887831982
Search time (sec): 8553.360000
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gb_est40:AW147713
gb_gss3:B3379
gb_gss3:B63467
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9b_gss15:AQ591361

9b_est27:A1463881

9b_est32:A1728666

9b_gss13:B12156

9b_est40:AV242923

9b_est6:W04025
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gb_est14: AA1243290
gb_est12: AA101730
gb_est12: AA522632
gb_est12: AA522632
gb_est15: AA489711
gb_est15: AA489711
gb_est15: AA639302
gb_est15: AA639302
gb_est21: CA889368
gb_est21: CA889368
gb_est20: AA884239
gb_gss1: CAS00666
gb_est24: AA1176387
gb_est24: AA1176387
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9b_gss10:AQ178284
9b_gss4:AQ685122
9b_gss15:AQ636347
9b_gss10:AQ157379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_gss10:AQ157379
gb_gss6:AQ856431
gb_est22:AI071976
gb_est22:AI018355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gb_gss14:AQ543638
gb_gss4:AQ705201
gb_est11:AA270757
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gb_est3:R38349
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gb_gss9:AQ146935
gb_est40:AW156527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       score_list:
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30-NOV-1999

SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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Le Johnson, S.L., Blumberg, B., Song, J., Clifton, S., Hillier, L., Pohnson, S.L., Blumberg, B., Song, J., Clifton, S., Hillier, L., Pohnson, S.L., Blumberg, B., Song, J., Clifton, S., Hillier, L., Pohnson, S.L., Martin, J., Wylle, T., Underwood, K., Theising, B., Bowers, Y., Person, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R., Waterston, R. and Wilson, R. Inopublished (1999)

On Dec 20, 1995 this sequence version replaced gi:ll35577.

Other ESTs: dal6c03.y1

Contact: Stephen L. Johnson/WashU Xenopus EST project, 1999

WashU Xenopus EST project, 1999

WashIngton University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: purecript SK-; site_1: ECORI; site_2:
XhOI: CDNA was prepared from 2ug of poly A+ RNA (equal
parts from stage 10.5 and stage 11.5 gastrulae).
ECORI-XhOI cut CDNA was then ligated into UniZap-XR
(Stratagene) with ECORI at the 5' end and XhOI at the 3'
end. SS-library phagemids were prepared by mass excision
from the original library and normalized by hybridization
to biotinylated driver (prepared from the same library by
PCR) to Cot-omega of 11. After removal of hybrids and
excess driver by streptavidin sepharose chromatography,
the ss-phagemids were made double stranded and
electroporated into Top-10 F'. Original library
contruction by Bruce Blumberg (Cho et al. 1991 Cell 67,
1111-1120). Normalized by Jihwan Song (Song, Cho and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: estewatson.wustl.edu
Library constructed by Bruce Blumberg
Library normalized by Jihwan Song
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clone distribution information for
Anna library can be found through Research Genetics, visit their
web page at: http://www.resgen.com/
Seq primer: -400p from Gibco.
                     dal6c03.x1 normalized Xenopus laevis gastrula Xenopus laevis cDNA clone XENOPUS_SOURCE_ID:xlnga001n05 3', mRNA sequence.
                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="norm_lized Xenopus laevis gastrula"
/tisone_lib="gastrula (stages 10.5, 11.5 mixed)"
/lab_host="Top-10 F'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .235
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XENOPUS_SOURCE_ID:xlnga001n05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235
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Gaps: 0
Percent Identity: 77.778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blumberg, unpublished).
  mRNA
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235 bp
                                                                                                                                                         African clawed frog.
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Percent Similarity: 100.000
                                                                                                                                                                                      Xenopus laevis
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                                                                                                                                                                                                                                                                    Xenopus.
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  LOCUS
                                                                                                                                                                                 ORGANISM
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ORIGIN
                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
COMMENT
                                                                              ACCESSION
                                                                                                   VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hiller, L., Kucaba, T., Martin, J., Brck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Mitter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCan, R., Watterston, R. and Wilson, R.

I unpublished (1999)

L unpublished (1999)

L on Dec 20, 1995 this sequence version replaced gi:1134478.

Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest park Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800

Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
arkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     info@genomesystems.com web site: www.genomesystems.com
Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: 342
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Gaps: 0
Percent Identity: 77.778
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US-08-653-294-9 x AW156527/rev
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Ratio: 4.22
Percent Similarity: 100.000
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source

FEATURES

BASE COUNT

246

SOURCE ORGANISM ACCESSION VERSION KEYWORDS

TITLE JOURNAL COMMENT

AUTHORS REFERENCE

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

Ei (bases 1 to 428)

KS Mahalras, G.G., Zackrone, K.D., Smith, T., Tipton, S., Schmidt, S., Traicoff, R., Abajian, C., Blanchard, A., West, A. and Hood, L.E.

Construction of a Characterized Clone Resource for Genomic Sequencing: Generation and Preliminary Analysis of 20,000 Sequence Tagged Connectors

Unpublished (1997)

Contact: Mahalras GG, Zackrone KD, Hood L
University of Washington
Seattle, WA 98195, USA

Tel: (206) 616-8144

Fax: (206) 668-7301

Email: Kzackronêu. Washington.edu
Sequence Tagged Connector

Plate: CT 792 row: K column: 24

Class: BAC ends

High quality sequence stop: 428.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH108"
                                                                                                                                                                                                                                                                                                                        B33379 428 bp DNA GSS 17-OCT-1997 HS-1017-A2-F12-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 792 Col=24 Row=K, genomic survey
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/organism="taxon:9606"
/db_xref="taxon:9606"
/clone="plate=CT 792 Col=24 Row=K"
/clone_lib="CIT Human Genomic Sperm Library C"
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Gaps: 0
Percent Identity: 77.778
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B63467.1 GI:2637457
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US-08-653-294-9 x B33379/rev
                              Align seg 1/1 to: AW147713
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Percent Similarity: 100.000
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Locus B33379
DEFINITION HS-1017-A2-F1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: gb_gss3:B63467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E Johnson, S. L., Blumberg, B., Song, J., Clifton, S., Hillier, L., Pape, D., Martin, J., Wylle, T., Underwood, K., Theising, B., Bowers, Y., Parson, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R., Wash U Kanopus Esr project, 1999

L. Mash U Kanopus Esr project, 1999

On May 1, 1997 this sequence version replaced gi:2059622.

Other_Esrs: ad16c03.x1

Contact: Stephen L. Johnson/Wash U Kanopus Esr project, 1999

Washington University School of Medicine

4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .246

/organism="Xenopus laevis"
//do.ref="txenopus laevis"
//do.ref="txenopus laevis"
//do.ref="txenopus laevis"
//do.ref="txenopus laevis gastrula"
//do.ref="txenopus_source_pus_gastrula"
//do.ref="txenopus_source_pus_gastrula"
//do.ref="txenopus_gastrula"
//do.ref="txeno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eax: 14 286 1810
Email: est@watson.wustl.edu
Library constructed by Bruce Blumberg
Library normalized by Jihwan Song
Library normalized by Jihwan Song
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Renopus clone distribution information for
this library can be found through Research Genetics, visit their
web page at: http://www.resgen.com/
Seq primer: -40RP from Gibco.
Location/Qualifiers
                                                                                                                 seq_documentation_block:
LOCUS
LOCUS
AW147713
246 bp mRNA EST 30-NOV-1999
DEFINITION da16c03.y1 normalized Xenopus laevis gastrula Xenopus laevis cDNA
clone XENOPUS_SOURCE_ID:x1nga001n05 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps: 0 Gaps: 0 Percent Identity: 77.778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blumberg, unpublished)."
52 c 59 g 72 t
205 TACAGATTGGCCATACGTGTGAACAAG 179
                                                                                                                                                                                                                                                             AW147713
AW147713.1 GI:6195609
                                                                                                                                                                                                                                                                                                                                                                    African clawed frog.
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Percent Similarity: 100.000
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US-08-653-294-9 x AW147713
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FEATURES

to: 428

alignment_scores:

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37.00.
4.625
88.889
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Ratio:
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                  COMMENT
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                                                                                                                                                                                                                                                                                                                                                                        library availability, please contact Pieter de Jong
(pieterédejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
                                                                                                                                        and
                                                                                                                                                                                                                                                                                                                                                                                                                               Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: T?
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo saplens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 707)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
Venter,J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="vector: pBAce3.6; Site_1: EcoRI; Site_2: EcoRI; RPCIII Human Male BAC Library" 120 c 126 g 164 t
                                                                                                                                                                                                           Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
                                                                                 1 (bases I to 666)
Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. Venter, J.C.
Use of BAC End Sequences for Sequence-Ready Map Building Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
LOCUS
LOCUS
DEFINITION RPCI-11-346H13, genomic survey sequence.
                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1. 666
Corganism="Homo sapiens"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="RPCI-11"
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/cell_type="Lymphocytes"
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AQ543638.1 GI:4873922
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Ratio: 4.625
Percent Similarity: 100.000
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                                          Homo sapiens
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  GSS.
human.
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                    SOURCE
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Unpublished (1997)
Other_GSSs: RPCI-11.346H13.TJ
Other_GSSs: RPCI-11.346H13.TJ
Cother_GSSs: RPCI-11.346H13.TJ
Cother_GSSs: RPCI-11.346H13.TJ
Contect: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0208
Email: bbeetigr.cog
Email: bbeetigr.cog
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
Research Genet cs (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (http://bacpac.med.bac.end_search/bac.end_search.html.
Seg primer: T7
Class: BAC ends.
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Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 453)
Mahaliras, G.G.; Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"
125 c 123 g 237 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block: 453 bp DNA GSS 07-JUL-1999 LACUS AQ705201 453 bp DNA BAC Library Homo sapiens DEFINITION HS_5522_806_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1098 Col=12 Row=D, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence-tagged connectors: A sequence approach to mapping and
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Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
TEI: (206) 616-3818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: 707
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Gaps: 0
Percent Identity: 77.778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. 707
Acganism="Homo sapiens"
/db_xref="GDB:7632660"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="RPCI-11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to reverse of: AQ543638
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AQ705201.1 GI:5414627
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US-08-653-294-9 x AQ543638/rev
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source

FEATURES

BASE COUNT ORIGIN

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 578)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS A0715952 578 bp DNA GSS 15-JUL-1999
DEFINITION HS_2261_A1_F09_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2261 Col=17 Row=K, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
High Throughput Sequencing Center
101 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Blate: 2261 row: K column: 17
Seq primer: T7
Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 10
Gaps: 0
Percent Identity: 60.000
                                             /db_xref="texon:10090"
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/clone_lib="Soares mouse 3NME12 5"
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/strain="C57BL/6J"
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Location/Qualifiers
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                                                                                                                         /sex-"unknown"
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AQ735952.1 GI:5507504
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US-08-653-294-9 x AA270757/rev
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Ratio: 3.600
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Muss. Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 55) Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                        library availability, please contact Platter of Jones Resources (http://bacpac.med.buffalo.edu). Clones may be purchased from Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
latte: 1098 row: D column: 12
Seq primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pBACe3.6; Genomic sequence of BAC ends" 71 c 66 g 143 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
LOCUS AA270757 555 bp mRNA EST 26-MAR-1997
DEFINITION va67-906.rl Soares muuse 3NME12 5 Mus musculus cDNA clone
IMAGE:736450 5', mRNA sequence.
ACCESSION AA270757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1398092.
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=1098 Col=12 Row-D"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 10
Gaps: 0
Percent Identity: 60.000
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High quality sequence stop: 494.
Location/Qualifiers
1. .555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to reverse of: AQ705201 from: 1
                                                                                                                                                                                                                                     High quality sequence stop: 453.
Location/Qualiflers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-08-653-294-9 x AQ705201/rev
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4.000
90.000
                                                                                                                                                                                                                                                                                          .453
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Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
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Align seg 1/1

ORGANISM

VERSION KEYWORDS

REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

source

FEATURES

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seq_documentation_block:
LOCUS AI463881
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Mus musculus
   ಥ
                                                                                                                                                                                                                         Percent Similarity:
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   147
                                                                                                                                   alignment_scores
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BASE COUNT
ORIGIN
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ORGANISM
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JOURNAL
COMMENT
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AUTHORS
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KEYWORDS
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401 Queen Anne Avenue North, Seattle, WA 98109, USA
71e1: (206) 616-3618
Fax: (206) 616-3618
Fax: (206) 616-3818
Fax: (20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 584)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
1.578
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=2261 Col=17 Row=K"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
                                                                                                                                                           /sex="male"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BAC ends"
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Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A0591361 584 bp DNA GSS 08-JUN-1999 HS_5410_B2_E01_T7A RPCI-11 Human Male BAC Library Homo sapien: genomic clone Plate=986 Col=2 Row=J, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence-tagged connectors: A sequence approach to mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On Sep 10, 1998 this sequence version replaced gi:3556571.
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/clone="Plate=986 Col=2 Row=J"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                                                                   4 others
                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 10
Gaps: 0
Percent Identity: 60.000
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High quality sequence stop: 584.
Location/Qualifiers
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                                                                                                                                                                                                                                                               90 9
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AQ591361.1 GI:5023013
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US-08-653-294-9 x AQ735952
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                               207
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      source
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                                                                                                                                                                                                                                                               BASE COUNT
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AUTHORS
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KEYWORDS
SOURCE
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TITLE

COMMENT

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This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1:to SB5)

Marra, M.; Hiller, L.; Kucaba, T.; Martin, J.; Beck, C.; Wylie, T.; Underwood, K.; Steptoe, M.; Theising, B.; Allen, M.; Bowers, Y.; Viderwood, K.; Steptoe, M.; Theising, B.; Allen, M.; Bowers, Y.; Ritter, E.; Kohn, S.; Shin, T.; Jackson, Y.; Cardenas, M.; McCann, R.; Waterston, R. and Wilson, R.

The WashJ-NCI Mouse EST Project 1999
Unpublished (1999)
On Apr 7, 1998 this sequence version replaced g1:3034529.

Contact: Marra M/WashJ-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@lmage.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTACOGE TO SOURCE STATES AND SOUR MUSICALUS CONA CLONE IMAGE: 736450 5', MRNA sequence.
13 others
                                                                                                                                                                                                                                                                                        to: 584
                                                                                                               Length: 10
Gaps: 0
Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
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/dev_stage="12.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                      from: 1
189

    585
    /organism="Mus musculus"
    /strain="C57BL/6J"

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Location/Qualifiers
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Seq primer: -40RP from Gibco
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  Б
103
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132 c
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4.000
90.000
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and was

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409 TACGAAGTCGCAATCCGCATAAACGAGAAA 438
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US-08-653-294-9 x B12156
                                         seq_name: gb_gss3:B12156
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KEYWORDS
SOURCE
ORGANISM
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JOURNAL
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ORIGIN
                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                             REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
LOCUS A1728666 626 bp mRNA EST 11-JUN-1999
DEFINITION BNLGH111358 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (AR032448) ethylene receptor [Malus domestica], mRNA sequence.
ACCESSION A1728666.1 GI:5047518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gossyptum hirsutum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossyptum.
I chases I to 6256
Blewitt,M., Matz,E.C., Davy,D.F. and Burr,B.
ESTS from developing cotton fiber
Onpublished (1999)
On Jun 5, 1998 this sequence version replaced gi:3187861.
Library went through one round of normalization, an constructed by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Gossyplum hirsutum"
/cultivar=/Acala Maxxa"
/db_xref="taxon:3635"
/clone_lib="six-day Cotton fiber"
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/lab_host="XLI-Blue"
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                                                                                                                                         Length: 10
Gaps: 0
Percent Identity: 60.000
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Percent Identity: 60.000
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112 c 163 g 174 t
                                                                                                                                                                                                                                                                                   from: 1
                                                                                                                                                                                                                                                                                                                      1 TyrargLeualaileargLeuasnGluarg 10 :::|||:::|||:::||| 290 TICCGAGTGGCTCTAAGACTGAATAAAGG 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biology Department
Brookhaven National Laboratory
Upton, NY 11973, USA
Tel: 516-344-3396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TyrArgLeuAlalleArgLeuAsnGluArg 10
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1. .626
                                                                                                                                                                                                                                                                                   Align seg 1/1 to reverse of: AI463881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 516-344-3407
Email: burr@bnlux1.bnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: AI728666 from: 1
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                                                                                                                                                                                                                        alignment_block:
US-08-653-294-9 x AI463881/rev
                                                                                                                                         Quality: 36.00
Ratio: 3.600
Percent Similarity: 100.000
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Ratio: 3.600
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: gb_est32:AI728666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-653-294-9 x AI728666
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                                                                                                                      alignment_scores
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                                       BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEYWORDS
SOURCE
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seg_documentation_block:
LOCUS AV242923 LIKEN full-length enriched, 0 day neonate head Mus
DEFINITION AV242923 RIKEN full-length enriched, 0 day neonate head Mus
musculus cDNA clone 4831414015 3' similar to NM_004576 Homo saplens
protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52),
beta isoform (PPP2R2B) mRNA, mRNA, mRNA sequence.
AV242923.1 GI:6230332
                                                                                                                                                                               thale cress.

Arabidopsis thaliana
Eukaryophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
Arabidopsis.

1 (Dases 1 to 1224)
Feng,J., Dewar,K., Buehler,E., Kim,C., Li,Y., Shinn,P., Sun,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: BeloBACII; Site_1: EcoRI; Site_2: EcoRI; Produced by Thomas Altmann" 9 others
seq_documentation_block:
LOCUS B12156 1224 bp DNA GSS 14-MAY-1997
DEFINITION F5L16-Sp6 IGF Arabidopsis thaliana genomic clone F5L16, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Ecker J.
Arabidopsis Thaliana Genome Center
University of Pennsylvania
Dept. of Biology, University of Pennsylvania, Philadelphia, PA
19104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leuyin: 10 Gaps: 0 Percent Identity: 60.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. 1224 "Arabidopsis thaliana" /organism="Arabidopsis thaliana" /strain="Columbia" /db_xref="taxon:3702" /clone="FSI16" /clone="Ib="16F" /sex="hermaphrodite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rel: 215-898-9384
Fax: 215-889-8780
Email: jecker@atgenome.bio.upenn.edu
Seq primer: Sp6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: B12156 from: 1 to: 1224
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High quality sequence start: 80
High quality sequence stop: 762.
Location/Qualifiers
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Unpublished (1997)
Other_GSSs: F5L16-T7
                                                                           survey sequence.
B12156
B12156.1 GI:2093276
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Ratio: 3.600
Percent Similarity: 100.000
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alignment_scores
                                                                                                                                                    E 1 (Dases 1 to 246)

S Konno, H., Alzawa K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukuda, J., Carninci, P., Endo, T., Fukuda, S., Fukuda, M., Hayatsu, N., Hiozane, T., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Shipata, K., Shipata, K., Shipata, K., Shipata, K., Shibata, Y., Shipata, K., Shibata, Y., Shipata, K., Shibata, Y., Shipata, K., Tarenoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yoshiki, M., Watanabe, S., Yamamura, T., Yasunishi, A., Yoshiba, M., Muramatsu, M. and Hayashizki, Yokota, T., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, J. Honbulished (1999)

On May 18, 1998 this sequence version replaced gi:3137751.

Genome Exploration Research Group, Life Science Tsukuba Center, Genome Science Laboratory

The Institute of Physical and Chemical Research (RIKEN), Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: genome-resertc.riken.go.jp,
URL:http://genome-rec.riken.go.jp,
Sasaki,w. zawa,m. watahiki,M. Ozawa,K., Tanaka,T., Yoneda,Y.,
Sasaki,w. zawa,m. watahiki,M. Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
Hayashizaki,Y.
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase. Proc. Nati. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
Okazaki,Y. and Hayashizaki,Y., Ozawa,Y., Muramatsu,M.,
Okazaki,Y. and Hayashizaki,Y., 465-470 (1999)
System. Genome Res. 9 (5), 465-470 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Ist strand cDNA was GAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
                                                                                                   Mammalia;
                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                             Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3-1-1 Koyadal, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'tissue_type="head"
'dev_stage="0 day neonate"
'lab_host="DH10B"

    .246
    /organism="Mus musculus"

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/clone="4831414015"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "sex="mixed"
                                                                     Mus musculus
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AUTHORS
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66
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37
39 C
71 a
BASE COUNT
ORIGIN
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Length: 9
Gaps: 0
Percent Identity: 77.778 4.375 Quality: Ratio: Percent Similarity:

alignment_block: US-08-653-294-9 x AV242923

to: 246 Align seg 1/1 to: AV242923 from: 1

1 TyrArgLeuAlaIleArgLeuAsnGlu 9

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

February 7, 2000, 11:54:22; Search time 117.7 Seconds (without alignments) 4.008 Million cell updates/sec Run on:

US-08-653-294-10 49 1 RENLRILLRY 10 Perfect score: Sedneuce:

142080 seqs, 47169319 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

142080 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

PIR_62:* Database :

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

		ď			SUMMARIES		
Result		Ouerv					
No.	Score	Match	Length	DB	QI	Description	1
-	44	6	137	7	180174	class I hist	histocompa
7	44	φ.	273	~	I38509	class I	histoc
က	44	89.8	274	7	I54463	MHC HLA-B38	chain
4	44	σ.	354	N	593	class I hist	histocompa
2		σ.	354	7	180168	class I hist	histocompa
9		σ.	354	~	180167	Н	histocompa
7	44	φ.	355	~	180169	H	histocompa
œ		σ.	355	~	180171	class I hist	histocompa
Φ		σ.	359	Н	HLHU12	Н	histoc
10	44	σ.	362	-	HLHUB8	ass I	histoc
11		6	362	7	B30345	MHC class I	histoc
12	44	6	362	7	JH0541	н	histocompa
13	44	σ.	362	7	JH0539	H	histocompa
14	44	φ,	362	7	JH0540	ЯIР	histocompa
15	44	φ.	362	7	A45834	MHC class I	I histoc
16	44	δ.	362	7	I84486	transmembrane glyc	e glyc
17	44	σ.	362	7	I62045	gene HLA B-1	517 pr
18	44	ó	362	~	184490	lymphocyte a	antigen
19	44	6	362	~	137521	Bw57.	antigen
20	44	6	362	~	A30345		I histoc
21	44	6	362	7	159633	MHC HLA-B tr	transmem
22	44	φ.	362	~	S24434	class I hist	histocompa
23	44	σ.	362	~	I37120	class	I histoc
24	44	σ,	363	~	807113	class I hist	histocompa
25	44	6	363	7	803537	class I hist	stocompa
26	44	9	364	7	D35997	class I	histoc
27	44	6	365	7	S77963	class I	histoc
28	44	σ,	365	~	5441	-AW24 pro	protein -
29	44	م	365	~	I54493	SS I	histoc
30	39	σ.	274	Н	HLHU32	MHC class I	histoc

79.6 338 2 156116 79.6 352 2 137516 79.6 362 2 C35997 79.6 362 2 C35997 79.6 362 2 A45850 79.6 362 2 16861 79.6 362 2 161861 79.6 362 2 137485 79.6 362 2 137515 79.6 362 2 137515 79.6 362 2 137515 79.6 362 2 15447 77.6 362 2 15447 77.6 362 2 154457 77.5 362 2 15489	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
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ALIGNMENTS

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RESULT 1 1180174 class I histocompatibility antigen - chimpanzee (fragment) class I histocompatibility antigen - chimpanzee) C:Species: Pan troglodytes (chimpanzee) C:Accession: 180174 C:Accession: 180174 R:McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994 A:Title: A uniquely high level of recombination at the HLA-B locus.	A. Status: preliminary; translated from GB/EMBL/DDBJ A. Molecule type: DNA A. Mossidus: 1-137 CRES: A. Corser references: EMBS: UD5885; NID:9454787; PIDN:AAA50188.1; PID:9454788 A. Cross references: EMBS: UD5885; NID:9454787; PIDN:AAA50188.1; PID:9454788	89.8%; Score 44; DB 2; Length 137; 90.0%; Pred. No. 0.074; ive 0; Mismatches 1; Indels 0; Gaps
RESULT 1 180174 class I histocompatibility antigen - ch C;Species: Pan troglodytes (chimpanzee) C;Date: 24-May-1996 #sequence_revision C;Accession: 180174 R;McAdam, S.N.; Boyson, J.E.; Liu, X.; Proc. Natl. Acad. Sci. U.S.A. 91, 5893-A;Title: A uniquely high level of recompany R; Recenter number: 159308; MUID:942865	A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-137 CRES> A; Cross-references: EMBL:U05585; NID:9454787; PIDN:: C; Superfamily: class I histocompatibility antigen;	Query Match 89.8%; Best Local Similarity 90.0%; Matches 9; Conservative

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MHC class I histocompatibility antigen - human (fragment)

Cispecies: Homo sapiens (man)
Cispecies: No. Chol, J.W.; Rlu, K.2.; Yang, S.Y.
Tissue Antigens 44, 271-273, 1994
A; Title: HLA-B*5105, a newly identified B51 IEF variant.
A; Reference number: 138509; MuID: 95176331
A; Accession: I38509
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-273 <RES>
A; Cross-references: EMBL: U06697; NID: 9469544; PIDN: AAA92997.1; PID: 9469545
C; Genetics:
A; Gene: GDB: HLA-B
A; Cross-references: GDB: 120048; OMIM: 142830
A; Man position: 6p21.3-6p21.3
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology

ö Gaps ; 0 Query Match 89.8%; Score 44; DB 2; Length 273; Best Local Similarity 90.0%; Pred. No. 0.15; Matches 9; Conservative 0; Mismatches 1; Indels

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Gaps

; 0

Indels

Length 354;

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class I histocompatibility antigen - pygmy chimpanzee (fragment)
C:Species: Pan paniscus (pygmy chimpanzee, bonobo)
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999
C:Accession: 180167
R:WcAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Wat Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A;Title: A uniquely high level of recombination at the HLA-B locus.
A;Reference number: 159308; MUID:94286544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R,McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Wat Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A;Title: A uniquely high level of recombination at the HLA-B locus.
A;Reference number: I59308; MUID:94286544
A;Accession: I80169
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C;Species: Pan troglodytes (chimpanzee)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999
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C;Species: Pan troglodytes (chimpanzee)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999
C;Accession: I80171
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A;Cross-references: EMBL:U05579; NID:q454775; PIDN:AAA50182.1; PID:q454776
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:U05578; NID:9454773; PIDN:AAA50181.1; PID:9454774 C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
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Pred. No. 0.2;
0; Mismatches
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Pred. No. 0.2;
0; Mismatches
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                                                                                                      Pred. No. 0.2;
); Mismatches
                                                                                   Score 44;
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90.0%;
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Matches 9; Conservative
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Best Local Similarity 90.0%;
Matches 9; Conservative
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Matches 9; Conservative
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91 RENLRIALRY 100
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                                                                                                                                                              class I histocompatibility antigen - chimpanzee (fragment)
C:Species: Pan troglodytes (chimpanzee)
C:Species: Pan troglodytes (chimpanzee)
C:Species: Pan troglodytes (chimpanzee)
C:Date: 24 May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999
C:Accession: 180168
R:McAdam, S.N.: Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Watkin R:McAdam, S.N.: Boyson, J.S.A. 91, 5803-5897, 1994
A:Title: A uniquely high level of recombination at the HLA-B locus.
A:Reference number: 159308; MUID:94286544
A:Accession: 180168
A:Accession: preliminary; translated from GB/EMBL/DDBJ
A;Accelle type: mRNA
A;Residues: 1-354 <RES>
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Pred. No. 0.15;
0; Mismatches
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90.0%;
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Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
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                       1 RENLRILLRY 10
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Length 355;

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J. Exp. Med. 174, Marren, E.; Taylor, P.; Parham, P.

J. Exp. Med. 174, 1491-1509, 1991
A; Title: Gorilla class I major histocompatibility complex alleles: comparison to huma A; Reference number: JH0534; MUID:92078860
A; Rocession: JH054
A; Molecule type: DNA
A; Residues: 1-362 CLAMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUCCLass I histocompatibility antigen HLA-Bw52 precursor - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: B30349
R;Hayashi, H.; Ennis, P.D.; Ariga, H.; Salter, R.D.; Parham, P.; Kano, K.; Takiguchi, J. Immuol. 142, 306-311, 1989
A;Title: HLA-B51 and HLA-B52 differ by only two amino acids which are in the helical A;Reference number: A30345; MUID:89080265
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-362 <HAY>
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F;220-285/Domain: immunoglobulin homology <IMM>
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F;210-285/Domain: immunoglobulin homology <IMM>
F;220-285/Domain: immunoglobulin homology <IMM>
F;320-285/Domain: irransmembrane #status predicted <IVM>
F;323-362/Domain: intracellular #status predicted <INT>
F;310/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Pred. No. 0.21;
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90.0%;
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Matches 9; Conservative
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99 RENLRIALRY 108
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Best Local Similarity
Matches 9; Conserv
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R;McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Watkin Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A;Title: A uniquely high level of recombination at the HLA-B locus.
A;Reference number: 159308; MUID:94286544
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C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
C; Superfamily: class I histocompatibility antigen; irransmembrane protein; transplantat
E; Newyords: duplication; glycoprotein; heterodimer; transmembrane protein; transplantat
E; 1-21/Domain: signal sequence #status predicted <SIG>
E; 22-359/Product: class I histocompatibility antigen HLA alpha chain #status predicted
E; 22-304/Domain: extracellular #status predicted <EXT>
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the domain structure of this
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C;Date: 05-Apr-1983 #sequence_revision 05-Apr-1983 #text_change 22-Jun-1999
C;Accession: A02189
R;Malissen, M.: Malissen, B.; Jordan, B.R.
Proc. Natl. Acad. Sci. U.S.A. 79, 893-897, 1982
A;Title: Exox/intron organization and complete nucleotide sequence of an HLA gene. A;Reference number: A02189; MUID:82151002
A;Reference number: A02189; MUID:82151002
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C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 05-Sep-1997
C;Accession: A23895
                                                                                                    A;Accession: 180171
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: mr.
A;Residues: 1-355 <RES>
A;Residues: 1-355 <RES>
A;Residues: 1-355 <RES>
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
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A; Cross-references: GB:J00191; GB:V00526; NID:g187600; C; Comment: The seven exons correspond approximately to
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J. Biol. Chem. 260, 11924-11933, 1985
A:Title: The complete primary structure of HLA-Bw58.
A:Reference number: A23895; MUID:86008247
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Pred. No. 0.2;
0; Mismatches
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Pred. No. 0.2;
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F;112-203/Domain: alpha-2 <EX2>
F;217-282/Domain: immunoglobulin homology <IMM>
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90.0%;
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RENLRIALRY 105
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R;Hayashi, H.; Ooba, T.; Nakayama, S.; Sekimata, M.; Kano, K.; Takiguchi, M. Immunogenetics 32, 195-199, 1990
A;Title: Allospecificities between HLA-Bw53 and HLA-B35 are generated by substitution A;Reference number: A45834; WUID:91033941
                                                                                                                                Aintrons: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
C; Reywords: transmembrane protein
C; Reywords: transmembrane
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A;Residues: 1-362 <HAX>
A;Cross-references: GB:M58636; NID:q187756; PIDN:AAA36228.1; PID:q187757; GB:M33574
A;Note: this allele is designated B*5301
C;Genetics:
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C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 23-Jul-1999
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A;Map position: 6p21.3-6p21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology C;Superfamily: class I histocompatibility antigen; immunoglobulin homology C;Keywords: glycoprotein; heterodimer; transmembrane protein F;1-24/Domain: signal sequence #status predicted <SIG>F;220-285/Domain: immunoglobulin homology <IMM>F;210-285/Domain: immunoglobulin homology <IMM>F;210/Binding site: carbohydrate (Asn) (covalent) #status predicted
A;Cross-references: EMBL:X60693; NID:922867; PIDN:CAA43101.1; PID:922868
A;Experimental source: EBV-transformed B cell
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Best Local Similarity 90.05
الموافقة 9, Conservative
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99 RENLRIALRY 108
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                                                                                  A;Introns: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Seywords: transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-362/Product: class I histocompatibility antigen heavy chain, Gogo-B0103 #status pre
F;25-114/Domain: alpha-1 <ALI>
F;25-114/Domain: alpha-2 <ALI>
F;206/Domain: alpha-3 <ALI>
F;207-288/Domain: alpha-3 <ALI>
F;209-362/Domain: immunoglobulin homology <IMM>
F;299-362/Domain: intracellular #status predicted <INT>
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A.Residues: 1-362 < LAWD
A.Residues: 1-362 < LAWD
A.Residues: 1-362 < LAWD
A.Cross-references: EMBL:X60255; NID:922865; PIDN:CAA42807.1; PID:922866
A.Cross-references: EBV-transformed B cell
C.Genetics:
A.Introns: 25/1: 115/1: 207/1: 299/1: 338/1: 349/1
C.Superfamily: class I histocompatibility antigen; immunoglobulin homology
C.Keywords: transmembrane protein
F:1-24/Domain: signal sequence #status predicted < SIG>
F:25-362/Product: class I histocompatibility antigen heavy chain, Gogo-B0101 #status pre
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C; Species: Gorilla gorilla gorilla (lowland gorilla)
C; Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C; Accession: JH0540
R; Lawlor, D.A.; Warren, E; Taylor, P.; Parham, P.
A; Title: Gorilla class I major histocompatibility complex alleles: comparison to human A; Reference number: JH0534; MUID:92078860
A; Accession: JH05540
A; Residues: 1-362 <LAW>A; Residues: 1-362 <LAW
A; Residues: 1
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J. Exp. Med. 174, 1491-1509, 1991
A;Title: Gorilla class I major histocompatibility complex alleles: comparison to human A;Reference number: JH0534; MUID:92078860
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Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
Accession: JH0539
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Pred. No. 0.21;
0; Mismatches 1; Indels
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:299-362/Domain: intracellular #status predicted <INT>
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Best Local Similarity 90.C
Matches 9; Conservative
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HLA-B2702 84-75-84
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Peptide B2702.60-8
Sequence of HLA-BW
Sequence of HLA-BW
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HLA-B2702 CTL modu
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Immunomodulatory p
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HLA-B2702.75-84(L)
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1.933 Million cell updates/sec
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T-cell modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                           ; Search time 122.56 Seconds
                              Compugen Ltd
                                                                                                                                                                                                                                                                                                           hits satisfying chosen parameters:
              GenCore version 4.5 Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                188963 segs, 23686106 residues
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                                                                                                         8, 2000, 01:29:37
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                                                                            sw model
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Gapop 10.0 , Gapext 0.5
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W47267
W33789
R41208
R83062
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R95427
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W07514
W47265
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W33795
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W33791
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R83095
                                                                            using
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Listing first 45
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                                                                                                           February
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Maximum DB seq
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HLA-B2705.75-84. C
HLA-B2702.75-84(D)
HLA-B2702.75-84(T)
T-cell modulating
R95423
R95425
R95426
W07513
W47269
W33785
W33788
R71442
R71443
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Immunomodulatory p
Peptide B2705.75-8
Peptide B2702.75-8
Human HLA-B27-(62-
Human [Phe-Y4]-HLA-
HLA-B2702 CTL modu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 14; Page 34; 80pp; English.

R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 75-84 of the alpha-1 domain of the class I MHC acceptance by a recipient of a transplant from an MHC unmatched of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs) of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R83096;
HIA-B3702 CTL modulating peptide (B2702.75-84(L)).
Gytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HLA-B2702.
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12-OCT-1995: U04349.

05-APR-1994; US-222851.

(STRD ) UNIV LELAND STANFORD JUNIOR.

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WPI: 95-35880446.

Extension of acceptance period of transplants from MHC unmatched

Extension of acceptance period of transplants from MHC unmatched

Extension of acceptance period of transplants from MHC unmatched

Extension of acceptance period of transplants from MHC unmatched

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Extension of acceptance period of transplants from MHC unmatched
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1. .10
/note= "at least one of the amino acids is the
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Immunomodulator; Class I HLA-B alpha-1 domain; inhibition;
transplant rejection; treatment; autoimmune disease.
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W47267;
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10 AA;
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 Sequence
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alpha-1 domain, used for preventing rejection of transplants or
treating autoimmune diseases
Example 1: Page 19: 41pp; English.

Peptides W33784-98 and W33778-9 were assayed for their immunomodulating
activity. A peptide-type compound or variant is claimed which has
activity. A peptide-type compound or variant is claimed which has
creaminal amidated or esterified forms of up to 60 amino acids, where
the peptide-type compound comprises the formula: A-B, where A, B
the peptide-type compound comprises the formula: A-B, where A, B
c Ranafb-71b, (aa79-84) or (aa84-79) (Laa77-76R); aa76 - E or V; aa77 -
D, S or N; aa79 - R or G; aa80 - I or N; aa81, aa84 - a hydrophobic or
small amino acid; aa82 - R or L; aa83 - G or R; and aa represents amino
c cid. The sequence in the brackets may optionally be absent or truncated
at any peptide type bond within the brackets. The compounds comprise
amino acid sequences related to a Class I HLA-B alphal domain (positions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the prolliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosis. The products can also be
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                Novel immunomodulatory peptide-type compound - useful for inhibiting
                                                                                                                                             transplant rejection
Claim 10: Page 36: 41pp: English.
The present sequence is an immunomodulatory peptide, which
The present sequence is an immunomodulatory peptide, which
Comprises a Class I HLA-B alpha-1 domain sequence. It can be used
in a pharmaceutical composition together with a subtherapeutic dose
of an immunosuppressant, to extend the period of acceptance of a
transplant from a major histocompatibility complex (MHC) unmatched
donor, i.e. to inhibit transplant rejection. It can also be used in
the treatment of autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JUN-1998 (first entry)
Peptide B2702.75-84LB1 tested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CTL activation; transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                  Length 10;
                                                                                                                                                                                                                                                                                                Peptides using the D-form amino acids are more effective immunomodulators than their diastereomers or enantiomers
                                                                                                                                                                                                                                                                                                                                                                                                                 0: Indels
                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 49; DB 1; 1
100.0%; Pred. No. 0.00049;
ive 0; Mismatches 0;
                                            23-APR-1997; U06705.
22-MAY-1996; US-651650.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beulow R, Clayberger C, Krensky AM;
WPI; 98-086530/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W33789 standard; peptide; 10 AA.
                                                                                                   Krensky AM;
                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-MAY-1996; US-653294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-MAY-1997; U08689
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                                                                                                              WPI; 98-018220/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
WO9744351-A1.
             WO9744052-A1.
                                                                                                 Clayberger C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W33789;
19-JUN-1998
                                27 - NOV - 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 - NOV - 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rejection.
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                                                                                                                                                                                                                                                                                                                               Sequence
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16-MAY-1996 (first entry)
HLA-B2702 CTL modulating peptide (B2702.75-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; fimunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 15; Page 9; 80pp; English.
R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of
                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wey peptide(s) based on class I HLA antigen domains - used for modulating cytotoxic T-lymphocyte activity towards targets claim 1; Page 34; flpp; English.

The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL activity in parasitic diseases and neoplasia and in studies on viral infection. The peptide can also be used for identifying CTLs which bind to it and removing subsets of CTLs from a T-cell composition. This peptide sequence is more commonly found within larger peptide compounds of not more than 30 amino acids in length.
                                                                                                                                                                                                                                                                                                                                                                                                   15-MAR-1994 (first entry)
peptide fragment of Class I HLA peptide.
Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
parasitic disease; cytotoxic I lymphocyte; modulation.
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   100.0%; Score 49; DB 1; Length 10; 100.0%; Pred. No. 0.00049;
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90.0%; Pred. No. 0.0048;
                                                                  Mismatches
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05-APR-1995; U04349.
05-APR-1994; US-222851.
(STAD ) UNIV LELAND STANFORD JUNIOR.
CLAYDerGer C, Krensky AM, Parham P;
WPI; 95-358582/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-FEB-1993; U01758.
02-MAR-1992; US-844716.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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                                                                                                                                                                                                                                                                                                                                             R41208 standard; peptide; 10 AA.
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Best Local Similarity 90.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clayberger CA, Krensky AM;
WPI; 93-303134/38.
Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                           1 RENLRILLRY 10
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12-NOV-1996 (first entry)
HIA-B2702.75-84(L).
HIA-B2702.75-84(L).
HIA- P74: alphal-helix; human-leucocyte-associated antigen; inhibitor;
HIA- P74: alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calclum influx; cytotoxic T lymphocyte; CTL; differentiation;
cytolysis; antigen presenting cell.

R95427 standard; peptide; 10 AA. R95427;

/note- "A7L mutation"

.... Location/Qualifiers misc_difference 7

10-NOV-1994; U12985. 10-NOV-1993; US-150493. (STRD) UNIV LELAND STANFORD JUNIOR. CLRYDETGER C, Krensky AM; WPI; 95-194027/25.

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Example: Mage 11: 24pp; inglish.

This sequence represents the alphal-helix of the human-leucocyte-associated antigen B2702 (HLA-B2702). This sequence, epitopes, and palindromes of it (such as R95428) can be used to isolate the protein p74 from a T-cell lysate. P74 is a T-cell surface membrane protein associated with T-cell lysate. P74 is a T-cells, and is a limited number of cell types, but is particularly expressed on B and T cells. P74 can be isolated by lysis of a suitable cell with an amphoteric detergent, and then passed through an affinity expressed on B and T cells. P74 can be isolated by lysis of a suitable cell with an amphoteric detergent, and then passed through an affinity compositions comprising the extracellular fragment of P74 combined with HA-B2702.60-84 (see R95416), induces calcium influx, and inhibits compositions comprising the extracellular fragment of P74 combined with HA-B2702.by combining the amount of binding between the candidate compound and P74. T-cells, by combining them with the extracellular portion of P74 and determining the amount of binding between the candidate compound and p74. Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCS), by adding to the mix the extracellular portion of P74, in an amount sufficient to compete containing the binding of the P74 ligand.
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class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 75-84 of the alpha-1 domain of the class I MHC HLA-82702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.NOV-1996 (first entry)
Alphal-helix of HLA-B2702.
HLA: p74; alphal-helix; human-leucocyte-associated antigen; inhibitor;
HLA: p74; alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic I lymphocyte; CTL; differentiation;
cytolysis; antigen presenting cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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WPI: 95-194027/25.
Compsns. comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLs.
Example: Page 11: 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 44; DB 1; Length 10;
Pred. No. 0.0048;
0; Mismatches 1; Indels
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10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R95413 standard; peptide; 10 AA.
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Best Local Similarity 90.۰.
امری 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                       the patient
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WO9513288-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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While of the part of the proteins of the proteins of the part inhibit cytolytic activity and differentiation of CTLS.

Example: Page 12, 20pp: English.

Example: Page 22, 20pp:
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04-AUG-1997 (first entry)
T-cell modulating peptide #1.
T-cell modulator; autoimmune disease; tissue destruction; alphal-domain;
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90.08;
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Best Local Similarity
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WO9635443-A1.
14-NOV-1996.
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Gaps

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1; Indels

0; Mismatches

Score 44; DB 1; Length 10; Pred. No. 0.0048;

89.8%;

Ouery Match
Best Local Similarity 90.v.
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Sequence
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ID W4
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                                                                                 Treatment of auto-immune disease by admin. of peptide(s) corresp. to major histocompatibility complex antigens - esp. for delaying onset of cilifical symptoms of insulin dependent diabetes by modulating T cell madiated attack on target cells

Treatment of the constant of the cells claim 7: Page 20; 24pp; English.

W07512-W07518 represent T-cell modulating peptides that can be used in the method of the invention. These sequences are based on a portion of the major histocompatability complex (MFO) class I antigen (see W07510). The method is for affecting the course of an autoimmune disease involving T-cell mediated destruction of tissue in mammals. These peptides are used especially to treat insulin-dependent diabetes mellitus, preferably being administered during the pre-clinical stage to delay onset of the disease. Other diseases that can be treated are multius, preferably being administered during the pre-clinical stage to delay onset of the disease. Other diseases that can be treated are multius, at disease, thyroid disease, Hashimoto's thyroiditis, myasthenia gravis, etc. The peptides modulate T-cell mediated attack on autologous transfer cells, and may also reduce inflammation, swelling, and release of cytokines, perforins, granzymes etc. associated with T cell activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treatment of auto-immune disease by admin. of peptide(s) corresp. to major histocompatibility complex antigens - esp. for delaying onset of clinical symptoms of insulin dependent diabetes by modulating T coll mediated attack on target cells.

The page 20: 24pp; English.

The page 20: 24pp; English.

WO7512-W07518 represent T-cell modulating peptides that can be used in the method of the invention. These sequences are based on a portion of the generic peptide corresponding to residues 70-91 of the alphal-domain of the major histocompatability complex (MHC) class I antigen (see W07510). The method is for affecting the course of an autofimmune disease peptides are used especially to treat insulin-dependent diabetes mellitus, preferably being administered during the pre-clinical stage to delay onset of the disease. Other diseases that can be treated are multiple scierosis, rheumatoid arthritis, psoriasis, pemphygus vulgaris, Sjogren's disease, thyroid disease, Hashimoto's thyroiditis, myasthenia gravis, etc. The peptides modulate T-cell mediated attack on autologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-AUG-1997 (first entry)
T-cell modulating peptide #3.
T-cell modulator; autoimmune disease; tissue destruction; alphal-domain;
T-cell modulator; autoimmune disease; tissue destruction; alphal-domain;
mammal; major histocompatability complex; MHC class I; antigen; perforin;
insulin-dependent diabetes mellitus; multiple sclerosis; inflammation;
insulin-dependent diabetes mellitus; multiple sclerosis; inflammation;
thuroid arthritis; psoriasis; pemphigus vulgaris; Sjogren's disease;
thyroid disease; Hashimoto's thyroiditis; myasthenia gravis; granzyme;
autologous target cell; cytokine release; T cell activation; therapy.
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Pred. No. 0.0048;
0; Mismatches 1; Indels
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12-MAY-1996; U3-440504.
(SANG-) SANGSTAT MEDICAL CORP.
Buelow R;
                 12-MAY-1995; US-440504.
(SANG-) SANGSTAT MEDICAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89.8%;
90.0%;
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05-APR-1996; U04710
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Best Local Similarity
Matches 9; Conserv
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| RENLRIALRY 10
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                                                                         WPI; 96-518410/51.
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  swelling, and release o with T cell activation.
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The present sequence is an immunomodulatory peptide, which comprises a Class I HiA-B alpha-1 domain sequence. It can be used in a pharmaceutical composition together with a subtherapeutic dose of an immunosuppressant, to extend the period of acceptance of a transplant from a major histocompatibility complex (MHC) unmatched donor, i.e. to inhibit transplant rejection. It can also be used in the treatment of autoimmune diseases.

Peptides using the D-form anno acids are more effective immunomodulators than their disastereomers or enantiomers.
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/note= "at least one of the amino acids is the
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunomodulatory peptide.
Immunomodulator; Class I HLA-B alpha-1 domain; inhibition;
transplant rejection; treatment; autoimmune disease.
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Immunomodulator; Class I HLA-B alpha-1 domain; inhibition;
transplant rejection; treatment; autoimmune disease.
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                                                                                                                Length 10;
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target cells, and may also reduce inflammation, cytokines, perforins, granzymes etc. associated Sequence 10 AA;
                                                                                                              Score 44; DB 1;
Pred. No. 0.0048;
); Mismatches 1
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                                                                                                              89.8%;
90.0%;
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Best Local Similarity 90.v
                                                                                                                                                             Conservative
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WPI; 98-018220/02.
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23-APR-1997; U06705.
23-APR-1996; US-651650.
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Best Local Similarity
Matches 9; Conserv
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Misc_difference 1.
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patient
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WO9744351-A1.
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19-JUN-1998
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                             Query Match
Best Local S
Matches 9
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R92912
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W33795
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Example 1: Page 19: 41pp: English.

Peptides Wa374-98 and Wa3778-9 were assayed for their immunomodulating cerivity. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or crivity.

Crieminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula: A-B, where A, B = (Crieminal amidated comprises the formula: A-B, where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a class I HLA-B alphal domain (positions or a class of a complex comprises and combination with antiqenic peptides or proteins of interest to activate CTLS. They can also inhibit the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treathing autoimmune diseases, e.g. diabetee, rheumatoid arthritis and lupus srythematosis. The products can also be used for detection and diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                         Novel immunomodulatory peptide-type compound - useful for inhibiting
                                                                                                                   transplant rejection
Claim 10: Page 36: 41pp; English.
The present sequence is an immunomodulatory peptide, which
The present sequence is an immunomodulatory peptide, which
Comprises a Class I HLAH a lipha-1 domain sequence. It can be used
in a pharmaceutical composition together with a subtherapeutic dose
of an immunosuppressant, to extend the period of acceptance of a
transplant from a major histocompatibility complex (MHC) unmatched
donor, i.e. to inhibit transplant rejection. It can also be used in
the treatment of autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-JUN-1998 (first entry)

Peptide Ba702.75-84 tested for immunomodulating activity.

Immunomodulating dimer: immunosuppressant drug; CTL activation; transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or
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Pred. No. 0.0048;
1; Mismatches 0; Indels
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24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Bellow R. Clayberger C, Krensky AM;
WPI; 98-086530/08.
                                          22-MAY-1996; US-651650.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W33784 standard; peptide; 10 AA.
W33784;
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90.0%;
                                                                          Clayberger C, Krensky AM; WPI; 98-018220/02.
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Best Local Similarity 90.0
Matches 9; Conservative
             27-NOV-1997.
23-APR-1997; U06705
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EXAMPLE 15; Page 36; 80pp; English.
R83061-R83085, R83090-R83096 and R9297-R92913 represent fragments of class I major histocompetability complex (MHC) antigens. This sequence corresponds to residues 70-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of The peptides are administered to a patient from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLS)
                                                                                                                                                                                                                                                                                                                                                                                                   16-MAY-1996 (first entry)
HLA-B2702 CTL modulating peptide (B2702.70-84).
HLA-B2702 CTL modulating peptide (B2702.70-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy;
                                                                    Gaps
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Peptide B2702.70-84 tested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CTL activation; transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clank ) variety of transky AW, rainsman clayberger C, Krensky AW, rainsman c, 85-35882/46.
WPI; 95-35882/46.
Extension of acceptance period of transplants from MHC unmatched Annor hosts - using Class I B75-84 MHC antigen of the recipient
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Score 44; DB 1; Length 10;
Pred. No. 0.0048;
0; Mismatches 1; Indels
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05-APR:1995.
05-APR:1994; US-22285.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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22-MAY-1997; U08689.
24-MAY-1996; US-653294.
(STRD ) UNIY LELAND STANFORD JUNIOR.
Beulow R, Clayberger C, Krensky AM:
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      89.8%;
                             Similarity 90.09; Conservative
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treating autoimmune diseases.

Example 1: page 19: 41pp: English.

Example 1: page 19: 41pp: 41p
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R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75.84 of the alpha-1 domain of the class I MHC HLA B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Yytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC, immunosuppressant; graft versus host disorder; transplantation; the class I MHC; HLA-B2702.
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Extension of acceptance period of transplants from MHC unmatched Annor hosts - using Class I B75-84 MHC antigen of the recipient
New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or
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05-APR-1995; U04349.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          used for detection and diagnosis
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89.8%; Score 44; DB 1; Length 20; 90.0%; Pred. No. 0.01; ive 0; Mismatches 1; Indels

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                                             (without alignments)
4.688 Million cell updates/sec
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                                        Search time 63.71 Seconds
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           Compugen Ltd.
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     GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                     82229 segs, 29864866 residues
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                                        8, 2000, 00:59:50
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1801_GORGO
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1803_GORGO
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Perfect score:
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                                     haemophius
felis silve
felis silve
felis silve
bos taurus
mus musculu
                                                                                                                                                                 ustilago ho
mus musculu
mus musculu
                     rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLEIN J.;
"Nucleotide sequences of chimpanzee MHC class I alleles: evidence for
trans-species mode of evolution.";
EMBO J. 7:2765-2774(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
B-1 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-1 ALPHA CHAIN PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (FEB-1989) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                              P33688
P21664
P15695
P14428
O14438
P14426
Q62120
Q62689
P44082
P33687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pan troglódytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 89030641.
MAYER W.E., JONKER M., KLEIN D., IVANYI P., VAN SEVENTER G.,
KLEIN J.;
                                                                                                                                                                                                                                                                                                                                                                               359 AA
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PFAM; PF00129; MHC_I; 1.
MHC_I; Transmembrane; Glycoprotein; Signal.
SIGNAL < 1 20
                                                                                                                                                                                                                                                                        ALIGNMENTS
                   JAK2_RAT
Y941_HAEIN
LACB_FELCA
LACA_FELCA
LACA_FELCA
TP12_BOVIN
TP12_BOVIN
HA10_MOUSE
HA113_MOUSE
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11129
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1101
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CYTOPLASMIC TAIL SIMILARITY.
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                                                                                                                                                                                                                                                                              LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
"GOTHIA class I major histocompatibility complex alleles: comparison
"GOTHIA class I major histocompatibility complex alleles: comparison
to human and chimpanzee class I.";
J. Exp. Med. 174:1491-1509(1991).
-!- FUNCTION: INVOLYED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMONE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                       01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-ARR-1993 (Rel. 25, Last annotation update)
CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0102 ALPHA CHAIN PRECURSOR.
GOVILLA GOVILLA GOVILLA (Lowland GOVILLA).
ELWATYOTA: Metazoa: Chordata: Craniata: Vertebrata; Mammalia:
Eutheria: Primates; Catarrhini: Hominidae: Gorilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AR-1993 (Rel. 25, Last sequence update)
01-AR-1993 (Rel. 25, Last annotation update)
CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0103 ALPHA CHAIN PRECURSOR.
GOAILLA gorilla gorilla (Lowland gorilla).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R PROSITE; PSUVALY.

R PRAM; PF00047; 1g; 1.

R PFAM; PF00129; MHC_L; 1.

RW MHC I; Transmenbrane; Glycoprotein; Signal.

FT SIGNAL 25 362 CLASS I HISTOCOPATIBLLITY ANTIGEN, GOGO-BOILO ALPHA CHAIN.

FT CHAIN 25 114 EXTRACELLULAR ALPHA-1.

FT DOMAIN 115 206 EXTRACELLULAR ALPHA-1.

FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.

AND CONNECTING PEPTIDE.
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0.077;
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 3CF119AD CRC32;
                                                      362 AA
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Pred. No. 0.077
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40204
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                                                      STANDARD;
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MICROGLOBULIN).
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                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE; 92078860.
                                                1B02_GORGO
P30380;
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P30381;
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DISULFID
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
"Gorilla class I major histocompatibility complex alleles: comparison to human and chimpanzee class I.";
J. Exp. Med. 174:1491-1509(1991).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
                                                                                                                                                                                                                                                                                                01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CLASS I HISTOCOMPATIBLITY ANTIGEN, GOGO-B0101 ALPHA CHAIN PRECURSOR.
GOTILLA GOTILLA (Lowland GOTILLA).
Eukaryota, Metacza; Chordata; Cranita; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
                                                                                           Gaps
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CLASS I HISTOCOMPATIBILITY ANTIGEN,
GOGO-BOIO1 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
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Pred. No. 0.077;
0; Mismatches 1; Indels
                                                  Score 44; DB 1; Length 359;
Pred. No. 0.077;
                                                                                           1; Indels
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2E33E2B8 CRC32;
5395FFC9 CRC32;
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                                                                                           Mismatches
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PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
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40173 MW;
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90.0%;
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90.0%;
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                                                    Query Match 89.8
Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                STANDARD;
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HSSP; P03989; 1HSA.
PROSITE; PS00290; IC
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95 RENLRIALRY 104
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110
362 AA;
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                                                                                                                                1 RENLRILLRY 10
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1B01_GORGO
ID 1B01_GORGO
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DOMAIN DOMAIN TRANSMEM

SIGNAL

DOMAIN DOMAIN DISULFID CARBOHYD

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DOMAIN

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SEQUENCE FROM N.A.
PARHAM P., ARNETI K.L., ADAMS E.J.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; B25092; HLHUBK.
HSSP; P03989; 1HSA.
MIM; 142830; -
PROSITE; PS00290; IG_MHC; 1.
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99 RENLRIALRY 108
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309
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125
227
362 AA;
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Best Local Similarity
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ID 1847_HUMAN
ID 1847_HUMAN
AC P30487;
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                                                                                              LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.,
"Gorilla class I major histocompatibility complex alleles: comparison
"Gorilla class I major histocompatibility complex alleles: comparison
to human and chimpanzee class I.";
J. Exp. Med. 174:1491-1509(1991).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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SEEMANN G.H.A., REIN R.S., BROWN C.S., PLOEGH H.L.;
"Gene conversion-like mechanisms may generate polymorphism in human
class I genes.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-MAR-1993 (Rel. 10, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B+2702 ALPHA CHAIN
PRECURSOR (B-27K) (B27.2).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                   THE IMMUNE SYSTEM.
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CLASS I HISTOCOMPATIBILITY AN
GOGO-BOILO3 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
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  Eutheria; Primates; Catarrhini; Hominidae; Gorilla
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Pred. No. 0.077;
0; Mismatches
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HSSP; P03989; 1HSA.

PROSITE: P500290; IG_MHC; 1.

PFAM; PF00047; Ig; 1.

PFAM; PF00129; MHC_I; 1.

PFAM; PF00129; MG_I; 1.

PFAM; PF00129; MG_I; 1.

PFAM; PF00129; MHC_I; 1.
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EMBO J. 5:547-552(1986).
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Best Local Similarity
9; Conserve
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                                                      FROM N.A. 92078860.
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P10317;
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DOMAIN
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                                                                                                                          "Structural analysis of an HLA-B27 functional variant: identification of residues that contribute to the specificity of recognition by cytolytic T lymphocytes.";
Proc. Natl. Acad. Sci. U.S.A. 82:7394-7398(1985).
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01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-49(B-21) B*4901 ALPHA CHAIN
PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                       THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89.8%; Score 44; DB 1; Length 362; 90.0%; Pred. No. 0.077; 1: Indels ive 0; Mismatches 1; Indels
                              MEDLINE; 86042671.
VEGA M.A., EZQUERRA A., ROJO S., APARICIO P., BRAGADO
LOPEZ DE CASTRO J.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONNECTING PEPTIDE
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PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
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EMBL; X03667; CAA27301.1; JOINED.
EMBL; L38504; AAA69724.1; -.
SEQUENCE OF 86-107 AND 171-181
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                                                                              SECUENCE FROM N.A.
MEDILINE; 89080265.
HAYSAIT H., ENNIS P.D., ARIGA H., SALTER R.D., PARHAM P., KANO K.,
TAKIGUCHI M.;
"HLA-B51 and HLA-Bw52 differ by only two amino acids which are in the
helical region of the alpha 1 domain.";
J. Immunol. 142:306-311(1989).
             ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
"Rapid cloning of HLA-A,B cDN by using the polymerase chain
reaction: frequency and nature of errors produced in amplification.";
Proc. Natl. Acad. Sci. U.S.A. 87:2833-2837(1990).
                                                                                                                                                                                                                      POHLA H., KUON W., TABACZEWSKI P., DOERNER C., WEISS E.H.;
thallelic variation in HLA-B and HLA-C sequences and the evolution
the HLA-B alleles.";
Immunogenetics 29:297-307(1989).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
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PFAM: PF00129; MHC_I; 1.
PFAM: PF00129; MHC_I; 1.
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AAA59620.1; JOINED.
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AAA59620.1; JOINED.
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AAA64513.1;
AAA64513.1;
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EMBL; M22788; AAA59620.1;
EMBL; M22789; AAA59620.1;
EMBL; M22790; AAA59620.1;
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EMBL; L41087; AAA6451
EMBL; L41086; AAA6451
PIR; A30345; A30345
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HSSP; P30491; 1A1M.
MIM; 142830; -.
PROSITE; PS00290; IG.
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Best Local Similarity
Matches 9; Conserv
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TRANSMEM
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01-NOV-1990 (Rel. 16, Last sequence update)
01-FB-1996 (Rel. 33, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-51(B-5) B*5101 ALPHA CHAIN
PRECURSOR.
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                                                                               REVISION TO 78.
MEDLINE; 3056529.
MILLIAMS R.C., PARHAM P., BELICH M.P., ZEMMOUR J., WARD F.E., WILLIAMS R.C., PARHAM P., SECTOPIC Cross-reactivities poorly reflect allelic relationships the HLA-B12 and HLA-B21 groups. Dominant epitopes of the alpha 2 helix.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASS I HISTOCOMPATIBILITY ANTIGEN
                                                                                                                                                                                         -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
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Pred. No. 0.077;
0; Mismatches 1; Indels
                        PARHAM P., LAWLOR D.A., LOMEN C.E., ENNIS P.D.;
Diversity and diversification of HLA-A,B,C alleles.";
J. Immunol. 142:3937-3950(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONNECTING PEPTIDE
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; E996F82F CRC32;
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PROSITE: PS00290; IG_MHC; 1.
PFAM; PF00047; ig; 1.
PFAM; PF00129; MHC_I; 1.
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Best Local Similarity 90.0
The Gonservative
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362
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227
362 AA;
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FROM N.A.
89235215.
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P18464;
SEQUENCE | MEDLINE; {
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         BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

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                                                                     Score 44; DB 1;
Pred. No. 0.077;
); Mismatches
CYTOPLASMIC TAIL.
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                                        40566 MW;
                                                                      89.8%;
90.0%;
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RENLRIALRY 108
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HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-51(B-5) B*5101 ALPHA CHAIN. EXTRACELLULAR ALPHA-1. EXTRACELLULAR ALPHA-2. EXTRACELLULAR ALPHA-3.

CONNECTING PEPTIDE

LB52_HUMAN

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                                                                                                                                                              "HLA-B51 and HLA-Bw52 differ by only two amino acids which are in the helical region of the alpha 1 domain.";
J. Immunol. 142:306-311(1989).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-52(B-5) B*5201 ALPHA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-52(B-5) B*5201 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                       MEDLINE; 89080265.
HAYASHI H., ENNIS P.D., ARIGA H., SALTER R.D., PARHAM P., KANO K.,
TAKIGUCHI M.;
                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 362;
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Pred. No. 0.077;
0; Mismatches
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Last sequence update)
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BY SIMILARITY.
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PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
SIGNAL
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90.0%;
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99 RENLRIALRY 108
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                                                                                                           SEQUENCE FROM N.A.
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                                HLA-B OR HLAB
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01-APR-1993
15-JUL-1998
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P30491;
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Best Local S
Matches 9
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TRANSMEM
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SEQUENCE
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1B54_HUMAN
ID 1B54_HU
AC P30491;
DT 01-APR-
DT 15-JUL-
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                                                                                         01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-51(B-5) B*5104 ALPHA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                MEDLINE; 92269955.

BELICH M.P., MADRIGAL J.A., HILDEBRAND W.H., ZEMMOUR J.,

WILLIAMS R.C., LUZ R., PETZL-ERLER M.L., PARHAM P.;

"Unusual HLA-B alleles in two tribes of Brazilian Indians.";

Nature 357:326-329(1992).

-i- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                            THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 44; DB 1; Length 362;
Pred. No. 0.077;
0; Mismatches 1; Indels
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Last sequence update)
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                                                             362 AA
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PROSITE; PS00290; IG_MHC; 1.
PFAM; PF00047; ig; 1.
MHC_I; Transmembrane; Glycoprotein; Signal.
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90.0%;
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                                                             STANDARD;
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                                                                                                                                                                                        Homo sapiens (Human).
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227
362 AA;
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Best Local Similarity
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01-APR-1993 (
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P30489;
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P30490;
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RESULT 9 1B53_HUMAN

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                                                                                                                                                                                                                          ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
"Rapid cloning of Han-A,B cDNA by using the polymerase chain
reaction: frequency and nature of errors produced in amplification.";
Proc. Natl. Acad. Sci. U.S.A. 87:2833-2837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                                                                                                                                MEDLINE; 91067476.
ISAMAT M., GIRDLESTONE J., MILSTEIN C.;
Nuclectide sequence of an HLA-Bw57 gene.";
Nuclectide sequence of an HLA-Bw57 gene.";
Nucleic Acids Res. 18:6702-6702(1990).
-i- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-i- SUBUNIT: DIMMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-57(B-17) B*5701 ALPHA
HLA-B OR HLAB.
                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 0.077;
0; Mismatches 1; Indels
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90.0%;
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MIM; 142830; -.
PROSITE; PS00290; IG_MHC; 1.
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PFAM; PF00129; MHC_I; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane;
                                                                                                               Homo sapiens (Human)
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99 RENLRIALRY 108
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                                                                                                                                                                                                        MEDLINE; 90207291
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DISULFID
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SIGNAL
CHAIN
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1B61_HUMAN
ID 1B61_HU
AC P30497;
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                                                                                                                                                                                                                                                                                                                                                                          "Bound water structure and polymorphic amino acids act together to
allow the binding of different peptides to MHC class I HLA-B53.";
                                                                                                                                                                                                                                                                                                                                                                                                                 Immunity 4:215-228(1996).
 CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-53 B*5301 ALPHA CHAIN
                                                                                                                                                                                                      "Allospecificities between HLA-Bw53 and HLA-B35 are generated by substitution of the residues associated with HLA-Bw4/Bw6 public
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                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 25-302.
MEDLINE; 96209672.
SMITH K.J., REID S.W., HARLOS K., MCMICHAEL A.J., STUART D.I.,
BELL J.I., JONES E.Y.;
                                                      Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    THE IMMUNE SYSTEM.
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PRAM: PF00047; ig: 1.
PFAM: PF00129; MHC_I; 1.
MHC_I; Transmembrane_ Glycoprotein; Signal; 3D-structure.
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                                                                                                                                                          HAYASHI H., OOBA T., NAKAYAMA S., SEKIMATA M., KANO K., TAKIGUCHI M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BW-53 B*5301 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY
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                                                                                                                                                                                                                                                             .mmunogenetics 32:195-199(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M58636; AAA36228.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24
362
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PDB; 1A1M; 08-APR-98.
PDB; 1A1O; 08-APR-98.
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227
362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||||| |||
99 RENLRIALRY 108
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MICROGLOBULIN
                                                                                                                                                    91033941
                                       HLA-B OR HLAB.
                                                                                                                                SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM; 142830;
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1B60_HUMAN
ID 1B60_HUMAN
AC P18465;
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                     PRECURSOR
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DOMAIN
TRANSMEM
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DISULFID
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DOMAIN
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Gaps

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362 AA.

PRT;

STANDARD;

1B61_HUMAN P30497;

362 AA

PRT;

STANDARD:

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DOMAIN

SIGNAL CHAIN FOREIGN ANTIGENS TO

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-58(B-17) B*5801 ALPHA CHAIN. EXTRACELLULAR ALPHA-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-DEC-1999 (Rel. 39, annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN H PRECURSOR
   Homo sapiens (Human).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhin; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                               THE IMMUNE SYSTEM.
SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 44; DB 1; Length 362;
Pred. No. 0.077;
                                                                                                                                                                              TISSUE-BLOOD;
INOUE T., OGAWA A.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR ALPHA-2. EXTRACELLULAR ALPHA-3.
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Y SIMILARITY.

Y SIMILARITY.

3E5E7534 CRC32;
                                                                                                                HLA-Bw58.";
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PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
SIGNAL
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BY SIMILARITY
BY SIMILARITY
BY SIMILARITY
                                                               SEQUENCE FROM N.A.
MEDLINE; 86008247.
WAYS J.P., COPPIN H.L., PARHAM P.;
"The complete primary structure of HI
J. Biol. Chem. 260:11924-11933(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M11799; AAA59628.1; -.
EMBL; AA008102; BAA22916.1; -.
PIR; A23895; HIMUB8.
HSSP; P30491; 1A1M.
MIM; 142830; ..
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MW;
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90.0%;
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188
283
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9; Conservative
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HLA-H OR HLAH.
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207
209
309
333
110
125
362 AA;
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                                                                                                                                                               SEQUENCE FROM N.A.
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P01893;
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DISULFID
SEQUENCE
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DOMAIN
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Best Local
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01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-57(B-17) B*5702 ALPHA CHAIN
PRECURSOR (BW57.2).
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                                                                                                                                                                           MEDLINE, 93056508.

MEDLINE, 93056508.

LITTLE A.-M., ZEMMOUR J., ENIS P.D., WARD F.E., PETZL-ERLER M.L., MARTELL R.W., DU TOIT E.D., PARRAM P., "Distinctive HLA-A,B antigens of black populations formed by interallelic conversion.", J. Immunol. 149:3411-3415(1992).

-I. FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
11-JUL-1998 (Rel. 36, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-58(B-17) B*5801 ALPHA
HLA-B OR HLAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                              Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                           THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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Pred. No. 0.077;
); Mismatches
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628C2156 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00047; ig; 1.
PFAM; PF00129; MHC_1; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
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90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, X61707; CAA43876.1; -. PIR; S16774; S16774. HSSP; P30491; IAIM. MIM; 142830; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24
362
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2206
2298
3308
332
362
110
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Best Local Similarity
Lac 9; Conserv?
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309
333
110
125
227
362 AA;
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99 RENLRIALRY 108
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                                                                                   HLA-B OR HLAB
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P10319;
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Search completed: February 8, 2000, 00:59:51
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"Molecular definition of an elusive third HLA-A9 molecule: HLA-A9.3.";
Immunogenetics 35:41-45(1992)
-i- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                    MALISSEN M., MALISSEN B., JORDAN B.R.; "Exon/intron organization and complete nucleotide sequence of an HLA
                                                                                                                                                                                                                                                                                                                                                         HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
ALPHA CHAIN H.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
CONNECTING PEPTIDE.
                                                                     PIOC. Natl. Acad. Sci. U.S.A. 79:893-897(1982).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS
-!- SUBUNIT: DIMEN OF A PSEUDOGENE.
-!- SUBUNIT: DIMEN OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-23(A-9) ALPHA CHAIN
PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89.8%; Score 44; DB 1; Length 362; 90.0%; Pred. No. 0.077;
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BY SIMILARITY.
BY SIMILARITY.
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PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
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PIR; A02189; HLHU12.
MSSP. P032989; 1HSA.
MIM; 142800; -.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40850 MW;
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Best Local Similarity 90.0
اتام 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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362 AA;
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99 RENLRIALRY 108
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                                                                                                                          MICROGLOBULIN)
[1]
SEQUENCE FROM N.A.
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P30447;
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1A23_HUMAN
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99 RENLRIALRY 108

1 RENLRILLRY 10

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EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
               POLYMORPHISM: THE ONLY ALLELE OF A-23 KNOWN IS A*2301 WHICH IS
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BY SIMILARITY.
BY SIMILARITY.
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Pred. No. 0.078;
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                                                                                                                                                                                                                                                                                                                            PFAM; PF00047; 1g; 1.
PFAM; PF00129; MHC_I: 1.
MHC_I; Transmembrane; Glycoprotein; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40732
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Best Local Similarity
MICROGLOBULIN)
                                                                                                                                                                                                                                                                                                                                                                                                                          25
                                       SHOWN HERE.
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TRANSMEM
DOMAIN
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i AF030927 Homo sapiens MHC cl
AF030929 Homo sapiens MHC cl
U59699 Human MHC class I (HL
                                                                                                                                                                                                                                              Homo sapiens
Eukaryota, Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 250)
Rojas-Munoz,A., Mendez,I. and Yunis,I.
Molecular evolution of HIA-B locus in a small population amerindian Gommunity: The Nukak-Maku
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (07-0CT-1996) A. Rojas-Munoz, National Institute Of
Health, Immunogenetics, Avenida El Dorado, Carrera 50, Santafe De
Bogota / Zona 6, COLOMBIA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-OCT-1996
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/db_xref="texon:9606"

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Gaps: 0
Percent Identity: 90.000
                                                                                                                                 HSHLABHBA 250 bp DNA PRI
H.sapiens HLA-B gene, exon 2, HB(a) allele.
Y08692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSHLABHBB 250 bp DNA HSaplens HLA-B gene, exon 2, HB(b) allele. Y08693 TV08693 Gene; human leukocyte antigen.
270
270
270
                                                                                                                                                                                                             Y08692.1 GI:1619287
HLA-B gene; human leukocyte antigen.
human.
0.5259
0.5259
0.5259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="blood"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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162.09
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/note="allel H1
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  2 (bases 1 to 250)
Rojas-Munoz, A.
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US-08-653-294-10 x HSHLABHBA
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4.889
90.000
                                                                                       seq_name: gb_pr1:HSHLABHBA
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                                                                                                                          seq_documentation_block:
LOCUS HSHLABHBA
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Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
  gb_pr3:HS611HLA1
gb_pr3:HS639HLA1
gb_pr4:HSKM315S1
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DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                             VERSION
KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                       DEFINITION
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ORIGIN
                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AJ011699 Homo sapiens HLA-A gen AJ133780 Homo sapiens HLA-B gen AJ133780 Homo sapiens HLA-B gen AJ133780 Homo sapiens HLA-B gen AJ238071 Homo sapiens HLA-B gen U37110 Human HLA-A24 gene, alle U37114 Human HLA-B gene, alle U18987 Human HLA-B gene, alle U1830 Homo sapiens MHC class AF030921 Homo sapiens MHC class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y08692 H. sapiens HLA-B gene, ex Y08693 H. sapiens HLA-B gene, ex Y08694 H. sapiens HLA-B gene, ex Y08694 H. sapiens HLA-B gene, ex Y08694 H. sapiens HLA-B gene, ex Y0861 Human cell line THAI DCH U90615 Human cell line THAI DCH U90422 Human cell line THAI DCH U90424 Human cell line THAI DCH U90424 Human cell line THAI DCH U90418 Human cell line THAI DCH AF022159 Homo sapiens isolate CAFC22160 Homo sapiens isolate CAFC2160 Homo sapiens isolate CAFC22160 Homo sapiens isolate CAFC2160 Homo sapiens isolate CAFC22160 Homo sapi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114590 Sequence 67 from patent 114591 Sequence 68 from patent 114592 Sequence 69 from patent 114593 Sequence 70 from patent 114594 Human MHC class I HLA-B5 M22794 Human MHC class I HLA-B5 U65395 Human MHC class I antige
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U52813 Human MHC class I antige
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AF030925 Homo sapiens MHC
AF030911 Homo sapiens MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U52815 Homo sapiens class
                                                                                                                                          Command line parameters:
-MODEL=frame+_p2n.model -DEV=x1p
-MODEL=frame+_0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -GAPEXT=4.000
-GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -EGAPOP=6.000
-GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -BELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX-blosum62 -TRANS-human40.cd1
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -ALIGN=15 -MODE=LOCAL
-OUTFNT=pfs -NORM=ext -MINEN=0 -MAXEN=1000000 -USER=US08653294
-NCPU=6 -ICPU=3 -NO_XLPXY -WAIT -THREADS=1
                                                                                    About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
  out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OM of: US-08-653-294-10 to: GenEmbl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database: GenEmbl:*
Database sequences: 821193
batabase length: -1518192014
Search time (sec): 11370.480000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search information block:
Query: US-08-653-294-10
Query length: 10
                                          Date: Feb 8, 2000 4:38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9b_pr1:HUMMHBW2
9b_pr2:HMHCHLA1
9b_pr2:HSA133780
9b_pr2:HSA133780
9b_pr2:HSA238971
9b_pr2:HSHL24501
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9b_pr2:HSHLA2451
9b_pr2:HSHLABEXN1
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9b_pr3:HS507HLA1
9b_pr3:HS507HLA1
9b_pr3:HS507HLA1
9b_pr3:HS507HLA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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gb_pri: HSHLABHBB
gb_pri: HSHLABHBB
gb_pri: HSHLABBI
gb_pri: HSHLABBI
gb_pri: HSHLABFI
gb_pri: HSHLABFI
gb_pri: HSHLABFI
gb_pri: HSHLABFI
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9b pr2: HSHLABJI
9b pr4: AF002159
9b pr4: AF002160
9b pr4: 114590
9b pr4: 114591
9b pr4: 114593
9b pr1: HSBJERZ
9b pr1: HSBJERZ
9b pr1: HSBJERZ
9b pr1: HSBJERZ
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us-08-653-294-10.rge

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Submitted (23-FEB-1997) Transfusion Medicine, Faculty of Medicine, Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
Submitted (07-00T-1996) A. Rojas-Munoz, National Institute Of Health, Immunogenetics, Avenida El Dorado, Carrera 50, Santafe De Bogota / Zona 6, COLOMBIA
Location/Qualifiers
1. 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSHLABB1 250 bp DNA PRI 22-MAR-1997 HUMAN cell line THAI DCH010 MHC class I HLA-B gene (allele HLA-B*1513), exon 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 250)
Chandanayingyong, D., Sirikong, M., Longta, K., Srinak, D., Rungroung, E., Belfochandra, S., Juji, T. and Tokunaga, K.
B15 alleles (B*1513)
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2 (bases 1 to 250)

Chandanayingyong, D., Sirikong, M., Longta, K., Srinak, D., Rungroung, E., Bejchandra, S., Juji, T. and Tokunaga, K. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 10
Gaps: 0
Percent Identity: 90.000
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2
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U90420.1 GI:1905830
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US-08-653-294-10 x HSHLABHBD
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Ratio: 4.889
Percent Similarity: 90.000
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AUTHORS
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JOURNAL
REFERENCE
AUTHORS
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JOURNAL
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             JOURNAL
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KEYWORDS
SEGMENT
                                                                                         FEATURES
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          human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;

Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;

Eine (Experiment)

Englas (Experiment)

Englas Munoz, A., Mendez, I. and Yunis, I.

Molecular evolution of HIA-B locus in a small population amerindian (Enpublished (Experiment))

Englas (Experiment)

Englas (Experimen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa: Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarhini; Hominidae; Homo.
1 (bases 1 to 250)
Rojas-Munoz,A., Mendez,I. and Yunis,I.
Molecular evolution of HLA-B locus in a small population amerindian community: The Nukak-Maku
                                                                                                                                                                                                                                           (bases 1 to 250)

Sojas-Munoz, A.

Birect Submission

Submitted (07-007-1996) A. Rojas-Munoz, National Institute Of

Health, Immunogenetics, Avenida El Dorado, Carrera 50, Santafe De

Bogota / Zona 6, COLOMBIA

Location/Qualifiers

1. 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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/cell_type="white"
/cell_type="white"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSHLABHBD 250 bp DNA PRI
H.sapiens HLA-B gene, exon 2, HB(d) allele.
Y08694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 10
Gaps: 0
Percent Identity: 90.000
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HLA-B gene; human leukocyte antigen.
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/clone="cHBC4(b)"
14. .250
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/note="allel HB(b)"
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Rojas-Munoz, A.
Direct Submission
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78 c
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US-08-653-294-10 x HSHLABHBB
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LOCUS HSHLABHBD
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Percent Similarity:
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US-08-653-294-10 x HSHLABD1
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LOCUS HSHLABF1
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Chandanayingyong, D., Sirikong, M., Longta, K., Srinak, D.,

Siriboonrit, U., Rungroung, E. and Bejchandra, S.

Direct Submission

Submitted (25-FEB-1997) Transfusion Medicine, Faculty of Medicine,

Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,

Thailand
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/db_xref="taxon:9606"
/chromosome="6"
/map="6p21"
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B51V,Cw14,DR12(DR52),DQ1"
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/note="Allele: HLA-B*51V; similar to exon 2 of B*5105"
                                                                                                                                                                                                                                                                                                                                                   HSHLABDI 250 bp DNA PRI 22-MAR-1997
Human cell line THAI DCH010 MHC class I HLA-B gene (allele
HLA-B*51V), exon 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 250)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chandanayingyong, D., Sirikong, M., Longta, K., Srinak, D., Siriboonit, U., Rungroung, E. and Bejchandra, S.
                                                                                                                                     Length: 10
Gaps: 0
Percent Identity: 90.000
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Percent Identity: 90.000
                                             class I HLA-B"
80 q 32 t
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1. .250
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/number=2
/product="MHC c
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Unpublished
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Ratio:
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                                                              BASE COUNT
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Chandanayingyong, D., Sirikong, M., Longta, K., Srinak, D.,
Siriboonrit, U., Rungroung, E. and Bejchandra, S.
Direct Submission
Submitted (25-FEB-1997) Transfusion Medicine, Faculty of Medicine,
Siriral Hospital, Mahidol University, Prannok Road, Bangkok 10700,
Thailand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /map="6p21"
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/note="Allele: HLA-B*51V; similar to exon 2 of B*5105"
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                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Chandanayingyong,D., Sirikong,M., Longta,K., Srinak,D.,
Siriboonrit,U., Rungroung,E. and Bejchandra,S.
B*Slv alleles
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Gaps: 0
Percent Identity: 90.000
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1. 250
Organism-"Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
to: 250
                                                                  202 CGAGAGAACCIGCGGAICGCGCICCGCIAC 231
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from: 1
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82 c
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US-08-653-294-10 x HSHLABF1
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                                                                                                                                                                                     Chandanayingyong, D., Sirikong, M., Longta, K., Srinak, D., Siriboonrit, U., Rungroung, E. and Bejchandra, S. Direct Submission Submitted (25-FEB-1997) Transfusion Medicine, Faculty of Medicine, Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700, Thailand
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/cell_line="THAI DCH011"
| . .250
/gene="HLA-B"
/note="Allele: HLA-B*51V; similar to exon 2 of B*5105"
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HUMBU Cell line THAI DCH011 MHC class I HLA-B gene (allele
HLA-B*1513), exon 2.
                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 250)
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1 (bases 1 to 20)
Chandanayingyong, D., Sirikong, M., Longta, K., Srinak, D., Rungroung, E., Bejchandra, S., Blasczyk, R. and Grosse-Wilde, H. Unpublished

2 (bases 1 to 20)
Chandanayingyong, D., Sirikong, M., Longta, K., Srinak, D., Rungroung, E., Bejchandra, S., Blasczyk, R. and Grosse-Wilde, H.
                                                                                                                               Chandanayingyong, D., Sirikong, M., Longta, K., Srinak, D., Siriboonit, U., Rungroung, E. and Bejchandra, S. Brill alleles
Unpublished
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Percent Identity: 90.000
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                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
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 GI:1906037
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US-08-653-294-10 x HSHLABG1
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LOCUS HSHLABI1
                                                                 Homo sapiens
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Ratio:
090615.1
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Direct Submission
Submitted (23-FEB-1997) Transfusion Medicine, Faculty of Medicine,
Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
Thailand
Direct Submission
Submitted (23-FFB-1997) Transfusion Medicine, Faculty of Medicine,
Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
Thailand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 250)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSHLABJI 250 bp DNA PRI 22-MAR-15
Ruman cell line THAI DCH028 MHC class I HLA-B gene (allele
HLA-B#1513), exon 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 250)
Chandanayingyong,D., Sirikong,M., Longta,K., Srinak,D.,
Rungroung,E. and Bejchandra,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chandanayingyong, D., Sirikong, M., Longta, K., Srinak, D., Rungroung, E. and Belchandra, S.
Bls alleles (B*1513)
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 10
Gaps: 0
Percent Identity: 90.000
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1. .250
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/note="Allele: HLA-B*1513"
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83 c 80 g 32 t
                                                                      Location/Qualifiers
1. 250
Organism="Homo sapiens"
Ab_xref="taxon:9606"
/chromosome="VI"
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/db_xref="taxon:9606"
/chromosome="VI"
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US-08-653-294-10 x HSHLABI1
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202 CGAGAGAACCTGCGGATCGCGCTCCGCTAC 231
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US-08-653-294-10 x AF022159
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                                         seq_name: gb_pr4:AF022159
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Locus AF022160
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Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
LOCUS HSHLMABI1 250 bp DNA PRI 22-MAR-1997
DEFINITION Human cell line THAI DCH009 MHC class I HLA-B gene (allele
HLA-B*1513), exon 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 250,
Chandanayingyong, D., Sirikong, M., Longta, K., Srinak, D.,
Rungroung, E., Bejchandra, S., Juji, T. and Tokunaga, K.
B15 alleles (B*1513)
                                                                                        Length: 10
Gaps: 0
Percent Identity: 90.000
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Gaps: 0
Percent Identity: 90.000
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55 a 83 c 80 g 32 t
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83 c 80 g 32 t
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/cell_line="THAI DCH009"
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/number=2
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="VI"
                                                                                                                                                                                                                                                  202 CGAGAGAACCTGCGGATCGCGCTCCGCTAC 231
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US-08-653-294-10 x HSHLABJ1
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US-08-653-294-10 x HSHLABT1
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Ratio:
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                             ORIGIN
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Chases 1 to 255)
Grimsley,C., Mather,K.A. and Ober,C.
Direct Submission
Submitted (03-SEP-1997) Fred Hutchinson Cancer Research Center,
1100 Fairview Ave. N., M374, Seattle, WA 98109, USA
                                                                                                                                     Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 255)
Grimsley,C., Mather,R.A. and Ober,C.
HLA-H: a pseudogene with increased variation due to balancing selection at neighboring loci
Mol. Biol. Evol. 15 (12), 1581-1588 (1998)
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Homo sapiens isolate 034 MHC class I antigen HLA-H (HLA-H)
pseudogene, partial sequence.
AF022160 GI:2655063
seq_documentation_block:
LOCUS AF022159 255 bp DNA PRI 05-JAN-1999
DEFINITION Homo sapiens isolate 026 MHC class I antigen HLA-H (HLA-H)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note-"African-American individual"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 10
Gaps: 0
Percent Identity: 90.000
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carea "Ha.H"
/note="MHC class I antigen HLA.H"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223 CGAGAGAACCTGCGGGATCGCGCTCCGCTAC 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ArgGluAsnLeuArgIleLeuLeuArgTyr 10
                                                            pseudogene, partial sequence.
AF022159
AF022159.1 GI:2655062
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/gene="HLA-H"
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1 ArgGluAsnLeuArgIleLeuLeuArgTyr 10

KEYWORDS

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I14591.1 GI:997074
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US-08-653-294-10 x 114590
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US-08-653-294-10 x I14591
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LOCUS I14591
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LOCUS 114592
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Ratio:
Percent Similarity:
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AUTHORS
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                                                                                                                             Chases 1 to 259)

2 (bases 1 to 259)

2 (chasely,C., Mather,K.A. and Ober,C.)

Direct Submission

Submitted (03-SEP-1997) Fred Hutchinson Cancer Research Center,

1100 Fairview Ave. N., M374, Seattle, WA 98109, USA

Location/Qualifiers
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukheria; Frimates; Catarrhin; Hominidae; Homo.
( Loase 1 to 25)
Grimsley, C., Mather, K.A. and Ober, C.,
HLA-H: a pseudogene with increased variation due to balancing selection at neighboring loci
Mol. Biol.
99083426
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Apple, R. J., Bugawan, T. L. and Erlich, H. A.
Methods and reagents for HLA class I A locus DNA typing
Patent: US 5451512-A 67 19-SEP-1995;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   others
                                                                                                                                                                                                                                                                                          /note="African-American individual"
1. .259
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Gaps: 0
Percent Identity: 90.000
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114590
114590.1 GI:997073
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                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
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US-08-653-294-10 x AF022160
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LOCUS I14590
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26-SEP-1995
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Unclassified.
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Unclassified.
Unclassified.
Apple, N.J., Bugawan, T.L. and Erlich, H.A.
Methols and reagents for HLA class I A locus DNA typing
Methot: US 5451512-A 69 19-SEP-1995;
Patent: US 5451512-A 69 19-SEP-1995;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                         Unclassified.

1 (bases 1 to 270)
Apple,R.J., Bugawan,T.L. and Erlich,H.A.
Methods and reagents for HLA class I A locus DNA typing
Patent: US 5451512-A 68 19-SEP-1995;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                   PAT
Length: 10
Gaps: 0
Percent Identity: 90.000
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4.889 Gaps: 0
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Sequence 68 from patent US 5451512.
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84 c 95 g
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alignment_scores:
Quality: 44.00 Length: 10
Ratio: 4.889 Gaps: 0
Percent Similarity: 90.000 Percent Identity: 90.000

alignment_block: US-08-653-294-10 x I14592

Align seg 1/1 to: I14592 from: 1 to: 270

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P79559 Q29679 O19521 O19597 Q29909

Q29701 Q29841 O19354

062892 062892 062922 062922 062923 019623 019623 029769 029769 029724

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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Gorilla gorilla gorilla (Lowland gorilla).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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Pred. No. 0.12;
0; Mismatches 1; Indels
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CAO K., BURDETT L., ZHANG G., FERNANDEZ-VINA M.;
Submitted (40G-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AF017320; AAB70286.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998 (TrEMBLrel. 05, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
HLA-E. CLASS I ANTIGEN (FRAGMENT).
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046697;
01-JUN-1998 (Tremelrel. 06, Created)
01-JUN-1998 (Tremelrel. 06, Last sequence update)
01-MAY-1999 (Tremelrel. 10, Last annotation update)
MHC CLASS I ANTIGEN HLA-H ORTHOLOG (FRAGMENT).
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Best Local Similarity 90.0
Matches 9; Conservative
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3.317 Million cell updates/sec
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                                                                                                                                                                        8, 2000, 13:17:37; Search time 209.03 Seconds
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                       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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sp_unclassified:*
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sp_phage:*
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sp_rodent:*
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Match Length

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Result

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us-08-653-294-10.rspt

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Query Match 89.E
Best Local Similarity 90.C
Matches 9; Conservative
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99 RENLRIALRY 108
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40 RENLRILLRY 49
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1999 (TrEMBLrel. 12, Last annotation update)
MHC CLASS I HISTOCOMPATIBILITY ANTIGEN-B (HLA-B-27KSH) (FRAGMENT).
HLA-B.
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred, No. 0.18;
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Pred. No. 0.12;
0; Mismatches 1; Indels
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                                                        STRAIN=SHAMBA;
GRIMSLEY C., MATHER K.A., OBER C.;
SUBmitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AF022172; AAC99794.1; -.
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PETERSDORF E.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
EMBL: U18659; AAB60357.1; MIN: 142830;
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-FCB-1998 (TrEMBLrel. 08, Last annotation update)
CLASS I HISTOCOMPATIBLLITY ANTIGEN (FRAGMENT).
Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
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133 133
133 AA; 15491 MW; 3A3BC802 CRC32;
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90 90
90 AA; 10689 MW; 5E5F2495 CRC32;
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Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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27 RENLRIALRY 36
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75 RENLRIALRY 84
                                      SEQUENCE FROM N.A.
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"An introdic mutation responsible for a low level of expression of an HLA-A*24 allele.";
Tissue Antigens 50:340-346(1997).
EMBL: Z72423; CA945533.1; -.
PFAM: PF00129; MHC_I; 1.
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LAFORET M., FROELICH N., PARISSIADIS A., BAUSINGER H., PFEIFFER TONGIO M.M.;
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MEDLINE; 94286544.

MCADAM S.N., BOYSON J.E., LIU X., GARBER T.L., HUGHES A.L.,
BONTROP R.E., WATKINS D.I.;
"A uniquely high level of recombination at the HLA-B locus.";
Proc. Natl. Acad. Sci. U.S.A. 91:5893-5897(1994).

EMBL; U05585; AAA50188.1; -.

PFAM; PF00129; MHC_I; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 0.19;
0; Mismatches 1; Indels
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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-INOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I HLA-B (FRAGMENT).
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01-NOV-1998 (TIEMBLIEL. 08, Last sequence update)
01-NAY-1999 (TIEMBLIEL. 10, Last annotation update)
HUMAN LEUKOCYIE ANTIGEN PRECURSOR (FRAGMENT)
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137
137 AA; 15922 MW; B316D3BC CRC32;
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138 AA; 15610 MW; B8417FAO CRC32;
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Best Local Similarity 90.0%;
Matches 9; Conservative
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EMBL; U90425; AAB50146.1; -.
EMBL; U90424; AAB50146.1; JOINED
PFAM; PF00129; MHC_I; 1.
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68 RENLRIALRY 77
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CHANDANAYINGYONG D., SIRIKONG M., LONGTA K., SRINAK D., RUNGROUNG E., BEJCHANDRA S., JUJI T., TOKUNAGA K.; Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases. EMBL; U90421; ABSD144-1; -. EMBL; U90421; ABSD144-1; -. PEMBL; U90429; AREC_1; 1.
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CHANDARINGYONG D., SIRIKONG M., LONGTA K., SRINAK D., RUNGROUNG E.,
CHANDARAYINGYONG D., SIRIKONG M., LONGTE, H.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL. 190422; AABSO145.1; -
EMBL. 190422; AABSO145.1; -
EMBL. 190422; AABSO145.1; -
PERML; PF00129; MHC_I; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; HomInidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 0.24;
0; Mismatches 1; Indels
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Pred. No. 0.24;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I HLA-B (FRAGMENT).
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CHANDARINGYONG D., SIRIKONG M., LONGTA K., SRINAK D., RUNGROUNG E.,
CHANDRA S., JULI I., TOKUNAGA K.;
SUDMILTCHG (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: U90419; AAB50143.1;
EMBL; U90418; AAB50143.1;
PEMBL; U90418; AAB50143.1;
PEMBL; U90418; AAB50143.1;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 0.24;
0; Mismatches 1; Indels
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BLASCZYK R.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; X96473; ZA46527.1; -.
PFAM; PF00129; MHC_I: 1.
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC HLA-B*51 PROTEIN (FRAGMENT).
HLA-B*51FA.
                                                                                                              Score 44; DB 7;
Pred. No. 0.24;
0; Mismatches
                                             CAAE5641 CRC32;
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172 172
172 AA; 19909 MW;
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19909 MW;
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Best Local Similarity 90.0%;
Matches 9; Conservative
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90.0%;
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Matches 9; Conservative
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Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                 Score 44; DB 7; Length 172;
Pred. No. 0.24;
0; Mismatches 1; Indels
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Pred. No. 0.24;
0; Mismatches 1; Indels
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PETERSDORF E.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
EMBL, 1028793, ABB60367.1; -.
HSSP; P10318; 1ROG.
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
CHANDANAYINGYONG D., SIRIKONG M., LONGTA K., SRINAK D.,
SIRIBOONRIT U., RUNGROUNG E., BEJCHANDRA S.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U90616; AAB50245.1; -.
EMBL; U90615, AAB50245.1; JOINED.
                                                                                                                                                                                                                                                                                                                                        Ul-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01.NOV-1998 (TrEMBLrel. 08, Last annotation update)
HLA-B.
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01.NOV-1996 (TrEMBLrel. 01, Last sequence update)
01.NOV-1999 (TrEMBLrel. 12, Last annotation update)
MHC CLASS I HLA-B ANTIGEN (FRAGMENT).
HLA-B.
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73 I -> T.
175 20332 MW, 83A0C5C3 ČRC32;
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172 AA; 20052 MW; F6214671 CRC32;
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90.0%;
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Matches 9; Conservative
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                       Query Match
Best Local Similarity
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68 RENLRIALRY 77
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68 RENLRIALRY 77
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SEQUENCE FROM N.A.
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029694
AC 029694
DT 01-NOV
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DT 01-NOV
DE MHC CL
GN HLA-B.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                        Score 44; DB 7; Length 172;
Pred. No. 0.24;
0; Mismatches 1; Indels
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CHANDANAYINGYONG D., SIRIKONG M., LONGTA K., SRINAK D.,
SIRIBOONRIT U., RUNGROUNG E., BEJCHANDRA S.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, U90611; AAB50151.1;
EMBL, U90611; AAB50151.1;
PPFAM; PF00129; MHC_I; 1.
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CHANDRAYINGYOG D., SIRIKONG M., LONGTA K., SRINAK D.,
SIRIBONARINGYOG D., SIRIKONG E., BEJCHANDRA S.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, 1906614, AAB50244.1;
EMBL, 1906613, AAB50244.1;
JOINED.
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01-JAN-1998 (TIEMBLrel. 05, Last sequence update)
01-NOV-1998 (TIEMBLrel. 08, Last annotation update)
MHC CLASS I HLA-B (FRAGMENT).
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I HLA-B (FRAGMENT).
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172 172
172 Aa; 20026 MW; 4D9A1043 CRC32;
172 172
172 AA; 19942 MW; 1A73E47D CRC32;
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172 172
172 AA; 20026 MW; 4D9A1043 CRC32;
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Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 0.24;
0; Mismatches 1; Indels
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MHC CLASS I HLA-A (FRAGMENT).
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180 180
180 AA; 20811 MW; CECC3537 CRC32;
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Pred. No. 0.25;
0; Mismatches
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Best Local Similarity 90.0%;
Matches 9; Conservative (
Query Match
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68 RENLRIALRY 77
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SEQUENCE
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019607
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Search completed: February 8, 2000, 13:17:37 Job time: 32486 sec

97 DP THIS PAGE BLANK (USPTO)

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473 | JAK2 encoding DNA. Novel pr
629 | Murine JAK2 Kinase coding s
557 | Staphylococcus aureus conti
110000 | Methanococcus jannaschi
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33-AUG-1990; 207329.
83-AUG-1990; JP-207329.
83-AUG-1990; JP-207329.
83-AUG-1990; JP-207329.
84 (OLYU) OLYMPUS OPTICAL CO.
84 PI; 92-342893/42.
87 Transgenic non-human mammalian HiA-Bw 52 gene - useful for mouse model of human disease
85 Transgenic non-human disease
85 Disclosure; Fig 1: 8pp; Japanese.
86 The sequence shows the exon 2 alpha-1-domain of the human leukocyte
87 The sequence shows the exon 2 alpha-1-domain of the human leukocyte
88 The sequence shows the exon 2 alpha-1-domain of the human leukocyte
88 The sequence in Port of mouse, or their ancestors at the primary developmental biological step via transplantation into the zygote or developmental transgenic non-human mammals incorporating the HiA-Bw 52 gene in both their germ cells and somatic cells. Transgenic non-human mammals conty, HiA-Bw 52 are useful for the analysis of expression of the gene, His structure, and prodn. of mouse models of human disease.
80 Sequence 270 BP; 59 A; 88 C; 86 G; 37 T;
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Homo sapiens.

Homo sapiens.

Homo sapiens.

Homo sapiens.

Homo 14-FEB-1990.

Homo 10 1989; JP-200758.

Homo 10 1989; JP-200758.

Homo Nor Takiguchi.

MPI; 90-046289/07.

MPV DNA for class 1 human leucocyte antigens and derived probes and transformed cells, useful for DNA typing, as immunogens etc.

Claim 1; Page 11; 23pp; English.

Claim 2; Page 11; 23pp; English.

Claim 3; Page 11; 23pp; English.

Claim 4; Page 11; 23pp; English.

Claim 5; Page 11; 23pp; English.

Claim 1; Page 11; 24pp; English.

Claim 1; Page 11; 24pp; English.

Claim 1; Page 11; 24pp; Engli
                                                                                                                                                                                                      seq_documentation_block:

ID 029167 standard; DNA; 270 BP.

AC 029167;

DT 09-MAR-1993 (first entry)

DE HLA-Bw 52 exon 2 alpha-1 domain.

KW Human leukocyte antigen; transgenic; germ cells; somatic cells;

PN 04091731-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.00 Length: 10
4.889 Gaps: 0
90.000 Percent Identity: 90.000
   1.1e+03
1.2e+03
1.5e+03
1.5e+03
33 5.2e+04
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Sequence encoding HLA-B51 antigen.
Probe; HLA class I DNA; immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 001834 standard; DNA; 1086 BP. 001834;
   N_Geneseq_36:025307 + 33.00
N_Geneseq_36:085412 + 33.00
N_Geneseq_36:074652 + 33.00
N_Geneseq_36:v21209_00 + 33.00
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US-08-653-294-10 x Q29167
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Ratio:
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Carcinoembryonic antigen CEA-b
CEA protein encoding cDNA. Clc
Carcinoembryonic antigen gene.
Human carcinoembryonic antigen
EST clone DX298. New polynucle
Sequence encoding bovine tropho
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Tumour rejection antigen prec

Enterococcus faecalis genome

Enterococcus faecalis genome

Aspartokinase II gene. DNA end

Enterocin-900 operon. Bacterial

Bacteriocin enterocin 900 forw
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CDNA clone of sequence encodin
Borrelia burgdorferi polynucle
Type II topoisomerase database
Rat choline kinase gene. Rat c
                                                                                                                                                                                                                                                 -MODEL=frame+p2n model -DEV=xlp
-Q=/cgn1_1/USPTO_spool/US08653294/runat_04022000_160701_15807/app_query.fasta.1
-DB=N_Geneseq_36 -OFMT=fastap -SUFFIX=rpg -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-GAPOP=4.500 -GCAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -PELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-ALIGN=15 -MODE-LOCAL -OUTFWT-Pfs -NORM-ext -MINLEN=0
-MAXLEN=1000000 -USER=US08653294 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
                                                                                                                                software, version 4.5,
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OM of: US-08-653-294-10 to: N_Geneseq_36:*
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Database sequences: 311585
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Search time (sec): 590.520000
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Query length: 10
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N_Geneseq_36:T46062
N_Geneseq_36:V70153
N_Geneseq_36:N81611
N_Geneseq_36:T75431
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N_Geneseq_36:012114
N_Geneseq_36:N70935
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N_Geneseq_36:T36495
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N_Geneseq_36:N81584
N_Geneseq_36:N92780
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N_Geneseq_36:V11704
N_Geneseq_36:X17728
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N_Geneseq_36:001822
N_Geneseq_36:005693
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N_Geneseq_36:069946
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N_Geneseq_36:067869
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N_Geneseq_36:Q04288
N_Geneseq_36:Q04286
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N_Geneseq_36:004285
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N_Geneseq_36:T85000
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N_Geneseq_36:T11549
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us-08-653-294-10.rng

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Allotype specific monoclonal anti- HLA antibodies prodn. - using hybridomas derived from transgenic animals carrying HLA gene and I mimulised with HLA antigen of different allotype Disclosure; Fig 1 A-G; 20pp; English.

C The human HLA-B51 gene was injected into fertilised mouse eggs and then these introduced into the uterus of a pseudo pregnant mouse. The young were tested to ensure incorporation of the gene into the chromosome, and one of them mated 3 times with a normal male to produce 16 young, seven of which carried the HLA-B51 gene. The transgeneic offspring were immunised with HLA-B51 gene. The spleen lymphocytes were fused with myeloma cells. Hybridomas producing antibodies were selected.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:

ID Q05701 standard; DNA; 1089 BP.

AC Q05701;
DT 03-3AN-1991 (first entry)
DE HA-BW52 gene for production of monoclonal antibodies.

KW Alloptype specific monoclonal anti-HLA antibodies; hybridomas;

KW transgenic animals; HLA-BW52 gene; ss.

FH Key Location/Qualifiers

FT exon /*tag= a /*tag= a /*tag= b

FT exon /*tag= b

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Gaps: 0
Percent Identity: 90.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               335 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                295 CGAGAGGAACCTGCGGATCGCGCTCCGCTAC 324
                  /note="alpha 1-domain"
344. .619
                                                                                                           2-domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ArgGluAsnLeuArgIleLeuLeuArgTyr 10
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                                                                                                         note="alpha;20. .895
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1013. .1042
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22-AUG-1990.
07-FEB-1990, 102424.
08-FEB-1989; JP-029313.
(OLYU ) OLYMPUS OPTICAL KK.
Takiguchi M;
                                                                                                                                                                                                                                                                                                                              /number=6
1043. .1089
/*tag= 9
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US-08-653-294-10 x Q05693
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WPI; 90-046289/07.
P-PSDB; R03142.
P-PSDB; R03142.

New DAM for class 1 human leucocyte antigens and derived probes and transformed cells, useful for DNA typing, as immunogens etc.
Claim 2: ppl1-12; 23pp; English.
The HLA class I DNA can be used a source of probes for use in DNA typing. Transformed cells, which are useful as immunogens, can be obtained by introducing these DNAs into eucaryotic cells.
Sequence 1086 BP; 223 A; 335 C; 358 G; 170 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-JAN-1991 (first entry)
HJA-B51 gene for production of monoclonal antibodies.
HJA-B51 gene for production of monoclonal antibodies; hybridomas; transgenic animals; HJA-B51 gene; Ss.
Key
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exon
74. 343
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Gaps: 0
Percent Identity: 90.000
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Gaps: 0
Percent Identity: 90.000
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                                                                                                                                                                                                                                                                  294 CGAGAGAACCTGCGGATCGCGTCCGCTAC 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          294 CGAGAGAACCTGCGGATCGCGCTCCGCTAC 323
                                                                                                                                                                                                                                                                                                                                                                                                                                            19-MAY-1991 (first entry)
Sequence encoding HLA-Bw52 antigen.
Probe; HLA class I DNA; immunogen; ss.
                                                                                                                                                                                                                                            1 ArgGluAsnLeuArgIleLeuLeuArgTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ArgGluAsnLeuArgileLeuLeuArgTyr 10
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1. .1086
/*tag= a
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110-AUG-1989.
11-AUG-1989. JP-200758.
(OLXU) Olympus Optical Co., Ltd.
                                                                                                                                                                                              Align seg 1/1 to: Q01834 from: 1
                                                                                                                                                                                                                                                                                                                                                                            _documentation_block:
Q01822 standard; DNA; 1086 BP
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ID Q05693 standard; DNA; 1089 BP.
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                                                                                                                              alignment_block:
US-08-653-294-10 x Q01834
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US-08-653-294-10 x Q01822
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Quality:
Ratio:
                                                             Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                    alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                          001822;
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Key

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28-NOV-1985; 542024.
28-NOV-1985; 542024.
28-NOV-1985; DE-545576.
28-NOV-1985; DE-545576.
28-NOV-1985; DE-545576.
38 21-DEC-1985; DE-545576.
39 REHWILLER G, Meo T, Weiss E, Szots H;
Rethmuller G, Meo T, Weiss E, Szots H;
RPI: 81-157893/23.
30 P-PSDB; P70590.
31 P-PSDB; P70590.
32 P-PSDB; P70590.
33 P-PSDB; P70590.
34 Rethmuller G, Meo T antibody
35 Claim 2; Page 4; 5pp; German.
36 Claim 2; Page 4; 5pp; German.
37 Claim 2; Page 4; 5pp; German.
38 A hybridisation probe for detecting the HLA B27 gene, e.g. for assessing susceptibility to rheumatic disorders such as ankylosis spondylitis, or may be used to transform cells corp produce mono- or polyclonal HLA B27 antiboddes for use in immunoassay.
39 C Gequence 1026 BP; 213 A; 307 C; 344 G; 162 T;
Claim 1; Page 1; 11pp; Japanese.

Probes comprising part of the sequence can be used to identify class I genes. The DNA can be expressed for immunisation of animals and prodn. of monoclonal antibodies specific for the HLA-BW53 antigen. See also J03112485 and J03112486.

Sequence 1089 BP; 222 A; 337 C; 356 G; 174 T;
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence encoding the human histocompatibility antigen HLA B27. Rheumatic disorder; genetic screening; diagnosis; ankylosing spondylitis; ss. Homo sapiens.
                                                                                                                                    Length: 10
Gaps: 0
Percent Identity: 90.000
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4.333 Gaps: 0
90.000 Percent Identity: 80.000
                                                                                                                                                                                                                                              Align seg 1/1 to: Q12114 from: 1 to: 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from: 1 to: 1026
                                                                                                                                                                                                                                                                             223 CGAGAGGACCTGCGGACCCTGCTCCGCTAC 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ArgGluAsnLeuArgIleLeuLeuArgTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1. .1026
                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
ID N70935 standard; DNA; 1026 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
ID N70225 standard; DNA; 3874 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                 10-APR-1991 (first entry)
                                                                                                                                      44.00
4.889
90.000
                                                                                                                                                                                                                                                                                                                                        seq_name: N_Geneseq_36:N70935
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                                                                                                                                                                                                   alignment_block:
US-08-653-294-10 x Q12114
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US-08-653-294-10 x N70935
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Ratio:
                                                                                                                    alignment_scores:
Quality:
Ratio:
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                                                                                                                                                                    Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cds
DE3542024-A.
    8000000
8000000
                                                                                                                                                                                                                                                                                                                                                                                         The spleen lymphocytes were fused with myeloma cells (P3x63-Ag8.653). Hybridomas producing antibodies were selected. Sequence 1089 BP; 223 A; 336 C; 359 G; 171 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HLA-Bw53 exon. Haman leukocyte antigen; probe; major histocompatibility complex; MHC; class I; ss. Homo saplens.
                                                                                                                                                                                                                                                                                                                                                                                Allotype specific monoclonal anti- HLA antibodies prodn. - using hybridomas derived from transgenic animals carrying HLA gene and immunised with HLA antigen of different allotype Disclosure; Fig 1 A-G; 20pp; English.

The human HLA-BW52 gene was introduced into mouse L cells and then these cells used to immunise one of the transgenic mice (see 005693).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; R12463.
HLA-Bw53 gene, DNA probe and transformant cells - used for
immunisation, identifying specificity of antiserum etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.00 Length: 10
4.889 Gaps: 0
90.000 Percent Identity: 90.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: Q05701 from: 1 to: 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             295 CGAGAGAACCTGCGGATCGCGCTCCGCTAC 324
    /note≕"alpha 1-domain"
344. .619
                                                                                                                    /note="alpha 3-domain"
896. .1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ArgGluAsnLeuArgIleLeuLeuArgTyr 10
                                                              note="alpha 2-domain"
520. .895
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1. .1089
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ID Q12114 standard; DNA; 1089 BP.
                                                                                                                                                                                                                   /number=6
1043. .1089
/*tag= g
/number=7
                                                                                                                                                                                    1013. .1042
/*tag= f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-SEP-1989; JP-247697.
(OLXU ) OLYMPUS OPTICAL KK.
WPI; 91-182991/25.
                                                                                                                                                                                                                                                                                             22-AUG-1990.
07-FEB-1990; 102424.
08-FEB-1989; JP-029313.
(OLYU ) OLYMPUS OPTICAL KK
                                                                                                                                                      /*tag= e
/number=5
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                                                /number=3
                                                                                                           /number=4
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US-08-653-294-10 x Q05701
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                                                                                                                                                                                                                                                                                                                                                         Takiguchi M;
WPI; 90-255479/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio:
Percent Similarity:
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                                                                                intron
                                                                                                                                            exon
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                      exon
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us-08-653-294-10.rng

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(USSH
                  mrna
 DNA coding for human histocompatibility antigen HLA-B 27 - useful for diagnosis and antigen and antibody prodn.

Claim 1: p6: 13pp: German.

THE DNA may be used to detect the HLA-B 27 gene (opt. mutated) in human genetic material. The HLA-B 27 may be used to detect anti-HLA-B 27 antibodies in human serum. The antibodies may be used to determine HLA-B 27 levels in human serum, e.g. for diagnosis of rheumatic disorders, esp. ankylosing spondylitis.

Sequence 3874 BP; 751 A; 1094 C; 1171 G; 858 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /"tag=" a hah.b27 3' flanking region, downstream of 3' untranslated region" 4112. .4556
 03-APR-1991 (first entry)
Sequence of genomic DNA encoding human histocompatibility antigen
HLA-B 27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLA B27 consensus sequence.
HLA B27; seronegative spondylarthropathy; ankylosing spondylitis;
Reiter's syndrome; arthritis; acute anterior uveitis; diagnosis;
                                                                                                                                                                                                                                  Szots H, Weiss E, Dorner C, Lang M, Meo T, Riethmuller G; WPI; 87-171469/25.
                                 Ankylosing spondylitis; rheumatic disorder; diagnosis;
                                                                                                                                                                                                                                                                                                                                                               Length: 10
Gaps: 0
Percent Identity: 80.000
                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: N70225 from: 1 to: 3874
                                                                                                                                                                                                                                                                                                                                                                                                                                                            941 CGAGAGGACCTGCGGACCCTGCTCCGCTAC 970
                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                       /*tag= e
3009. ?
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ID T61639 standard; DNA; 6553 BP.
                                                                                                                                   /*tag* f
3148. /*tr
                                                                                ,40. .1506
/*tag= c
/32.
                                                          518. .590
/*tag= a
720. .989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                               39.00
4.333
90.000
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                                                                                                                      /*tag=
2450.
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                                                                                                                                                                       /*tag=
                                                                                                                                                                                               21-NOV-1986; 116139.
01-JAN-1985; DE-542024.
21-DEC-1985; DE-545576.
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US-08-653-294-10 x N70225
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Ratio:
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                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                               EP-226069-A
                                                                                                                                                                                        24-JUN-1987
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N70225;
                                                           intron
                                                                            intron
                                                                                                             intron
                                                                                                                              Intron
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                                                                                                                                              intron
                                                                                                                                                              intron
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Detecting pre-disposition to seronegative spondylarthropathies - Trom the absence of a C residue at a specific position in the 3'-flanking region of the HLA B77 allele

Claim 1; Page 52-56; 68pp; Bnglish.

Genetic predisposition to seronegative spondyloarthropathies (SNSA) is detected by determining the absence of a cytosine nuclectide in the 3' flanking region (see also T61647-48) of an HLA-B gene at a position corresponding to nuclectide 4495 of the HLA-B27 consensus sequence given in T61639. Probes and primers (see also T61640-46) chased on this region can be used in diagnostic assays to detect the genetic predisposition to SNSA, and permit the distinction of B27+ individuals who are resistant to SNSA from B27+ normal individuals who are resistant to SNSA from B27+ normal individuals sequence 6553 Bp; 1443 %; 1619 C; 2017 G; 1474 T;
/note= "3' flanking region diagnostic for genetic predisposition to SNSA" 4270. .4556
                                                                                               /*tag= b
/note="3' flanking region diagnostic for genetic
predisposition to SNSA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Delivering agents to target cells - where monospecific binding proteins are administered to a host and bind to target cells, followed by admin. of multivalent antibodies to direct the agents to the target cells
Example, Page 29; 80pp; Explish.

The sequence is that of a PCR primer used to isolate the U7.6 variable region gene by PCR from murine mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-1995 (first entry)
U7.6 L3' PCR primer for U7.6 variable regions.
Marker; antibody; single chain Fv fusion protein; sFv; ss;
amplification.
                                                                                                                                                                                                            /*tag- d
/note- "absence of cytosine at this site
indicative of a predisposition to SNSA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 10
Gaps: 0
Percent Identity: 80.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: T61639 from: 1 to: 6553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1102 CGAGAGGACCTGCGGACCCTGCTCCGCTAC 1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ArgGluAsnLeuArgIleLeuLeuArgTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CREA-) CREATIVE BIOMOLECULES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Segal DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                  (CEDA-) CEDARS SINAI MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US DEPT HEALTH & HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
ID 069946 standard; DNA; 59 BP.
AC 069946;
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4.333
90.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09415642-A.
21-JUL-1994,
07-JAN-1994; U00261.
08-JAN-1993; US-002324.
                                                                                                                                                                                                                                                                                                                                                                                                      01-SEP-1995; US-522942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-08-653-294-10 x T61639
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                                                                                                                                                                                      misc_difference
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Ratio:
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                                                                                                                                                                                                                                                                                                            WO9709450-A1
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misc_feature
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                                                    Synthetic.
WO9415642-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP-343946-A
                                                                                                                                                                                               George AJT,
                                                                                                                                                                               SERVICES.
 Example 1: Page 27; 65pp; English.

PCR primer 5 (T12618) was designed to introduce a BamHI site print of cDNA coding for the VL region of anti-mouse CD3-epsilon chain scFv 2C11. It was used with antisense primer 6 (T12619), which introduces a (G4S)3 linker and NotI site, for the PCR amplification of 2C11 VL DNA. VH CDNA was amplified using primers 7 and 8 (T12620-21). The PCR products were subcloned into pcDNA/AMP and expressed in GOS-7 transfectants. Blologically sective ScFv 2C11 was secreted into the cell culture medium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Single-chain Fv molecules with additional glycosylation sites increased rates of secretion, decreased antigenicity, modified ligand binding affinity and are protected from proteolytic
                                                                                                                                                                                                                                                                                                                                                                                                                  20-JUL-1996 (first entry)
2C11 SCFV VL PCR primer 6.
Single-chain Fy: sCFV; glycosylation; protein secretion; endoplasmic reticulum; antibody engineering; primer; PCR;
                 12 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ratio: 3.700 Gaps: 0 Gaps: 0 Incomment Similarity: 100.000 Percent Identity: 60.000
                                                                                      Length: 10
Gaps: 0
Percent Identity: 60.000
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                 11
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14-AUG-1995: U10348.
17-AUG-1994: US-292124.
(CREA-) CREATIVE BIOMOLECULES INC.
(USSH) US DEPT HEALTH & HUMAN SERVICES.
HUSCON JS, JOST CR, Segal DM;
                                                                                                                                                                                                                 to: 59
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                                                                                                                                                                                                                                                       1 ArgGluAsnLeuArgIleLeuLeuArgTyr 10
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                 ij
                 29
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                  Il2619 standard; DNA; 80 BP
                  Ä
                                                                                      Quality: 37.00
Ratio: 3.700
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                             seq_name: N_Geneseq_36:T12619
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                                                                                                                                                            alignment_block:
US-08-653-294-10 x Q69946
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US-08-653-294-10 x T12619
See also Q69933-49.
Sequence 59 BP;
                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9605228-A1.
                                                                     alignment_scores:
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carcinoembryonic antigen fragments - used in assays to determine the presence and amt. of the antigen in samples also contg. related antigens. Disclosure; page 4; 15pp; English. CEA fragments can be used in assays to determine the presence and amt. of CEA in samples which also may contain related antigens including its normal cross-reacting antigen or the 128 kD antigen. sequence 534 BP; 137 A; 172 C; 110 G; 115 T;
                                                                                                                                                                                                            WPI; 94-248905/30.
Delivering agents to target cells - where monospecific binding proteins are administered to a host and bind to target cells, followed by admin. of multivalent antibodies to direct the agents to the target cells.
Example; Page 29; 80pp; English.
The sequence is that of a PCR primer used to isolate the U7.6 variable region gene by PCR from murine mRNN.
See also 069933-49.
Vk3'AL2 PCR primer for U7.6 variable regions.
Marker; antibody; single chain Fv fusion protein; sFv; ss;
amplification.
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08-MAY-1990 (first entry)
Sequence of carcinoembryonic antigen domain III.
Carcinoembryonic antigen; domain III; domain A; domain
Key
1. .534
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity: 100.000 Percent Identity: 60.000
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07-JAN-1994; U00261.
07-JAN-1993; US-002324.
(CREA-) CREATIVE BIOMOLECULES INC.
(USSH ) US DEPT HEALTH & HUMAN.
                                                                                                                                                                                                 Huston JS, Segal DM;
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/note="domain P
268. .534
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/note="domain
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ID N92449 standard; DNA; 534 BP.
AC N92449;
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24-MAY-1989; 305232.
25-MAY-1988; US-198289.
(CITY) City of Hope.
Shively JE;
WPI: 89-349991/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: N_Geneseq_36:N92449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-08-653-294-10·x Q69941
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alignment_scores:

069941 standard; DNA; 83 BP. 069941; 26-MAR-1995 (first entry)

SAF

seq_documentation_block:

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signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; R98519
 misc_feature
                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                     primer_bind
                                                                                                                                                                                                                                                                                                                             primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                            terminator
                                                                       cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carcinoembryonic antigen (CEA) derivs - useful as reagents in immunoassy for diagnosis of neoplastic diseases Claim 4; Page 18; 30pp; English.

Q71567 is the DNA sequence which encodes carcinoembryonic antigen (CEA) R60619. CEA is free from cross-reactive CEA-like antigens, it is antigenically indistinguishable from the solution form of CEA shed from tumour cells, and it is devoid of ethanolamine. R66619 can be used in a reagent composition for detecting neoplastic diseases in biological samples, or in an immunoassay process where it can specifically detect the presence of tumour cells in a biological sample e.g. blood. Sequence 2031 BP; 551 A; 642 C; 417 G; 421 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-NOV-1996 (first entry)
Immunogenic carcinoembryonic antigen cDNA.
Carcinoembryonic antigen; immunogen; breast cancer; lung cancer;
carcinoembryonic antigen; immunogen; breast cancer; lung cancer;
colon cancer; therapy; immunotherapy; vaccine; baculovirus; vector;
Spodoptera frugiperda; insect; pA9000 ACNPV-CEA; ss.
Chimeric Autographa californica nuclear polyhedrosis virus;
Chimeric Homo sapiens.
                                                                                                                                                                                                                                                                                                                         11-MAY-1995 (first entry)
Carcinoembryonic antigen DNA.
Carcinoembryonic antigen; CEA; neoplastic diseases; ds.
Length: 10
Gaps: 0
Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 10
Gaps: 0
Percent Identity: 70.000
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                                                                                                                            to: 534
                                                                                                                          Align seg 1/1 to reverse of: N92449 .from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to reverse of: Q71567 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ArgGluAsnLeuArgIleLeuLeuArgTyr 10 :::||||||||| :::|||||||||||| 1923 AAAGAGAACTTGTGTGTGTTGCTGCGGTAT 1894
                                                                                                                                                            05-OCT-1994.
15-MAR-1994.
15-MAR-1994.
16-MAR-1993. EP-810214.
(HOFF ) HOFFMANN LA ROCHE & CO AG F. Mach J. Pelegrin A. Terskikh A; PP-PSDB; R60619.
                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
103. .2028
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
ID T36495 standard; cDNA; 2059 BP.
AC T36495;
                                                                                                                                                                                                                                                                        seq_documentation_block:
ID Q71567 standard; DNA; 2031 BP
                                                                   alignment_block:
US-08-653-294-10 x N92449/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-08-653-294-10 x Q71567/rev
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4.111
90.000
Quality: 37.00
Ratio: 4.111
Percent Similarity: 90.000
                                                                                                                                                                                                                                    seq_name: N_Geneseq_36:Q71567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: N_Geneseq_36:T36495
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Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                     mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                        Key
                                                                                                                                                                                                                                                                                             HA KAM KAM COS OS COS
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Timmunogenic carcinoembryonic antigen produced using insect cell
bacilovirus expression system - useful in cancer therapy
bacilovirus expression system - useful in cancer therapy
bisclosure; Page 47-49; Edpp; English.

A portion (136494) of pA9080 ACNPV-CEA vector codes for recombinant,
soluble, immunogenic carcinoembryonic antigen (rCEA) (R98519). The
chuman CEA gene was cloned from colon adenocarcinoma LSI14T (ATCC
CL 188) cells by PCR (see also T36493-94) and modified for
cxpression in insect cells by replacement of the signal sequence
with a 61 kDa baculovirus signal sequence, and deletion of DNA
encoding the hydrophobic C-terminal region. The construct was
concoding the hydrophobic C-terminal region. The construct was
inserted into baculovirus vector pW6S12 contg. a polyhedrin promoter,
giving plasmid pA9080 AcNPV-CEA. rCEA was produced at high levels
con in SF90+ insect cells grown in serum-free media and isolated to a
purity of over 95%. It can be used as an immunogen in humans to
protect against breast, lung or colon cancer.
Sequence 2059 BP; 572 A; 623 C; 425 G; 439 T;
                                                                                                                                                                                                                                                                                                                                                               /function= 3 N-terminal residues of the baculovirus (MGS12) not present in human CEA 81. .2006
1. .7
/*tag= a
/function= 7-adenine motif in the polyhedrin mRNA
                                                                                                                                   /*tag- b
18. 71
/*tag- c
/function- AcNPV 61k protein signal sequence
/*tag- d
/*tag- d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /function- universal translation termination signal contg. stop codons in all 3 reading frames in vector MGS12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= g
/note= "5' primer for CEA amplification"
1985. . 2006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= g
/note= "3' primer for CEA amplification"
2030. .2040
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Gaps: 0
Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to reverse of: T36495 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30.NOV-1995; U06373.
20-MAY-1995; U06373.
20-MAY-1994; US-246981.
(MLCR-) MICROGENESYS INC.
Hackett C, Smith G, Volvovitz F;
WPI; 96-020581/02.
                                                                               leader
18. .2009
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4.111
90.000
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US-08-653-294-10 x T36495/rev
                                                                                                                                                                                                                                                                                                       72. .80
                                                                                                                                                                                                                                                                                   *tag=
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Quality:
Ratio:
Percent Similarity:
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I AL058765 Drosophila melanog
I AA298855 EST11529 Uterus Hom
I AV337956 AV337956 RIKEN full
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Fax: 81-3-5449-5433
Email: yusuke@ims.u-tokyo.ac.jp.
Location/Qualifiers
1. .232
/organism="Homo sapiens"
//dxxef="texon:9606"
//clone="3NHC2444"
//clone="3NHC2444"
//clone="3NHC2444"
//dx-stage="adult"
//dx-stage="adult"
//oct=="0rgan: heart; normalized directionally cloned cDNA from adult heart; from adult heart; normalized directionally cloned cDNA from adult heart?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Construction of a normalized directionally cloned cDNA library from adult heart and analysis of 3040 clones by partial sequencing Genomics 35 (1), 231-235 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block: 10-DEC-1996 LOCUS AA151891 255 bp mRNA EST 10-DEC-1996 DEFINITION zoolf06.r1 Stratagene colon (#937204) Homo sapiens CDNA clone IMAGE:566435 5' similar to 9b:M15497_cds1 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-24(A-9) A*2401 (HUMAN); mRNA
                                                                                                                                               seq_documentation_block: 232 bp mRNA EST 30-JUL-1996 LOCUS C03945 Haman heart cDNA (YNakamura) Homo sapiens cDNA clone 3NHC2454, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 232)
1 (bases 1 to 232)
1 Tanaka,T., Ogiwara,A., Uchiyama,I., Takagi,T., Yazaki,Y. and Nakamura,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96299762
On Oct 24, 1995 this sequence version replaced gi:1040105
Contact: Yusuke Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 10
Gaps: 0
Percent Identity: 90.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shirokanedai, Minato-ku, Tokyo 108,
316.90
128.43
136.09
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University of Tokyo
4-6-1, Shirokanedal, Minato-k
125.52
132.56
132.11
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AA151891.1 GI:1720754
                                                                                                                                                                                                                                               C03945
C03945.1 GI:1467196
36.00
35.00
35.00
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Percent Similarity: 100.000
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US-08-653-294-12 x C03945
                                                                                                seq_name: gb_est8:C03945
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Ratio:
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                                                                                                                                                                                                                                                                                                                                human.
gb_gss1:CNS00CE8
gb_est12:AA298855
gb_est43:AV337956
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
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ORIGIN
                                                                                                                                                                                                                                               ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D82169 HUMHBC4524 Human panceed AQ204294 HS_3113 B2_CQ2_MR CIT AQ317259 FCIL1-105A4 TJ RRCIT AQ517559 HS_3102_A2_A05_TJA_RCIT AQ512530 HS_5104_B1B02_SP6E_RF AQ512233 HS_504_B1B02_SP6E_RF AQ51233 HS_504_B1B02_SP6E_RF AQ301014 HS_3105_A2_E01_MR CIT R13004 F6203.Tl Scares infant AQ440876 HS_509_B12_B04_TJA_RPC W07747 zb03401.rl Scares_fetal_AQ57033 HS_553_B1G08_TJA_RPC AQ892680 TENS1864_T. CITZI epin AQ5164169 HS_503_B1_G09_TJA_RPC AQ892680 TENS186_TT. CITZI epin AQ101532 HS_255_A1_E04_MF CIT AQ101532 HS_255_A1_E04_MF CIT AQ101532 HS_526_A1_E04_MF CIT AQ101534 HS_552_A1_E04_MF CIT AQ101547 HS_506_A2_F07_SP6E_RF AQ16595 HS_3006_B2_A07_T7 CIT AQ10557 HS_3006_B2_A07_T7 CIT AQ16596 HS_3006_B2_A07_T7 CIT AD81224 Wj63a07_X1 NI_CGAP_LU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Documentation | ... | Documentation | ... | Documentation | ... | C03945 | C03945 | Human heart cDNA | AA151891 2001166 r1 | Stratagene | AA263158 | PMY0534 | KG1 a Lambda Z | D8221 | HUMHBC4626 | Human pancrea | A135926 | Q12707 x1 | NCI_CGAP_B1 | A135966 | Q12707 x1 | NCI_CGAP_B1 | A1696864 | W074h11 x1 | NCI_CGAP_B1 | A1036690 | DKEZP564D2463 x1 | 564 | | T24384 | Crs1519 | lambdaZAPST | Rich | A1124815 | An56606 x1 | Ohnston | E1 | AW090252 | xc85906 x1 | NCI_CGAP_B1 | AM090252 | xc85906 x1 | NCI_CGAP_B1 | AM090252 | xc85906 x1 | NCI_CGAP_B1 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A1124815 | A11248815 | A1124885 | A1124885 | A1124885 | A1124885 | A112485 | A112485 | A11248
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HS_5118_A1_F09_T7A RPC
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CITBI-E1-2657B1.TF CIT
coau0004K01 Cotton Bol
AU056838 Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaste
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                                                                                                                                                                 Command line parameters:
-MODEL=frame+_p2n.model_DEV=x1p
-Q=/cgn1_1/USPTO_SPOOl_VS08653294/runat_04022000_160700_15770/app_query.fasta.1
-Q=/cgn1_1/USPTO_SPOOl_VS08653294/runat_04.000 -GAPEXT=4.000
-DB=EST -OPMT=fastap -SUFFTX=rst -GAPOP=12.000 -GAPEXT=4.000
-MINAATCH=0.100 -LOOPET=0.000 -KGAPEXT=0.000 -GAPOP=4.500
-GAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -EGAPOP=6.000
-DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.000
-LST=45 -DOCALIGN=200 -THE_SCORE-pct -ALIGN=15 -MODE-LOCAL
-OUTPHT=Pfs -NORM=ext -MINLEN=0 -MAXLEN=1000000 -USER=US08653294
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                                                                                                  About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           out_format : pfs
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  EST:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query: US-08-653-294-12
Query length: 10
Database: EST:*
Database sequences: 4538634
Database length: 1887811982
Search time (sec): 8553.360000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of: US-08-653-294-12 to:
                                                 Date: Feb 8, 2000 4:02 AM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search information block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gb_est10:AA151891
gb_est11:AA263158
gb_est6:D82221
gb_est26:A1359260
gb_est31:A1696864
gb_est10:AA147151
gb_est13:AA136390
gb_est13:AA13481
gb_est23:A124815
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95-5513.843904

95-6516.807747

95-95514.80570343

95-95517.80896303

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95-5571.80896303

95-5571.80896303

95-5521.80896933
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gb_est6:D82189
gb_gss10:AQ204294
gb_gss11:AQ317269
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gb_gss14:AQ517553
gb_gss14:AQ512233
gb_gss11:AQ301014
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gb_gss9:AQ165275
gb_gss9:AQ164696
gb_est35:AI831224
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gb_gss4:AQ704919
gb_est37:AI967800
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gb_est30:AU056838
gb_gss1:CNS00L2E
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gb_gss15:AQ625443
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gb_gss7:AQ899472
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gb_est8:C03945
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expressed within the human hematopoietic hierarchy Genomics 50 (1), 44-52 (1998)
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Percent Similarity: 100.000
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US-08-653-294-12 x AA263158
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//organism="Homo sapiens"
/db_xref="GDB:4590808"
/db_xref="Tabs=15008"
/db_xref="Tabs=15008"
/clone="InMags:566435"
/clone=lib="Stratagene colon (#937204)"
/lab_host="Sork cells (Kanamycin resistant)"
/lab_host="Sork cells (Kanamycin resi
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PMY0534 KG1-a Lambda Zap Express cDNA library Homo sapiens cDNA 5'
Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 255)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
Radiais,E., Moore,B., Moris,M., Parsons,J., Prange,C., Ni,Rikin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry Weg,J.,
Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butharyota: Metazoa; Charrhini; Hominidae; Homo.
1 (bases 1 to 283)
Claudio,J.O., Liew,C.C., Dempsey,A.A., Cukerman,E., Stewart,A.K.,
Na,E., Atkins,H.I., Iscove,N.N. and Hawley,R.G.
Identification of sequence-tagged transcripts differentially
                                                                                                                                                                                                                                                                                                                          Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -28M13 rev2 from Amersham
                                                                                                                                                                                                                                                                                                                                                                                               97044478
On May 8, 1995 this sequence version replaced gi:800234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 10
Gaps: 0
Percent Identity: 90.000
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Wilson RK
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US-08-653-294-12 x AA151891
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AA263158
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On May 5.

On May 5.

On May 5.

On May 6.

On May 7.

On May 7.

On May 7.

On May 8.

Tel: Hawley RG

On May 8.

Tel: 416 340384.

Fax: 416 340384.

Fax: 416 340384.

Fax: 416 340384.

Fax: 416 340384.

May 8.

May 9.

M
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Unpublished (1995)
On Apr 14, 1993 this sequence version replaced gi:785255.
Contact: Jun Takeda
Institute for Molecular and Cellular Regulation, Gunma University
3-39-15 Showa-machi, Maebashi Gunma 371, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D8221 375 bp mRNA EST 09-FEB-1996 HUMHBC4626 Human pancreatic islet Homo sapiens cDNA similar to HLA-B, mRNA sequence. B2221 GI:1183739
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
Takeda,J.
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Gaps: 0
Percent Identity: 90.000
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Location/Qualifiers
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ENCARAGORA: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria: Primates; Catarrhini; Hominidae; Homo.

Eutheria: Primates; Catarrhini; Hominidae; Homo.

Eutheria: Primates; Catarrhini; Hominidae; Homo.

String Stroke: Mational Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index

Unpublished (1998)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausbergenih.gov

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
/db_xref="taxon:9606"
/clone_llb="Human pancreatic islet"
/clone_llb="Human pancreatic islet"
/note="vector: Lambda ZAPII; Site_l: Eco RI; Site_2: Xho
I; mRNA was prepared from normal adult human islets. cDNA
was directionally synthesized from the Xho I in the vector
to the EcoRI site. cDNA was size fractionated to remove
sequences <look pin size." 3 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A1359260 618 bp mRNA EST 15-FEB-1999 qy27b07.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2013205 similar to gb:D32129 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, AW-66(A-10) A*6601 ALPHA (HUMAN);, mRNA sequence.
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Gaps: 0
Percent Identity: 90.000
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Seg primer: -40UP from Glbco
High quality sequence stop: 458.
1. Gl8
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AI359260.1 GI:4110881
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Ratio: 4.400
Percent Similarity: 100.000
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US-08-653-294-12 x D82221
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LOCUS A1359260
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Unpublished (1997)
Unpublished (1997)
Unpublished (1997)
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tal: (301) 496-1558.
Email: Robert_Strausberg(min.gov)
Email: Robert_Strausberg(min.gov)
Email: Robert_Strausberg(min.gov)
Email: Robert_Strausberg(min.gov)
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Email: Robe
T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into Libe Not I and Eco RI sites of the modified pr773 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
LOCUS AL696864 748 bp mRNA EST 03-JUN-1999
DEFINITION WC14111.X1 NCI_CGAP_Pan1 Homo sapiens CDNA clone IMAGE:2324421
Similar to gb:M28205 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
B-51(B-5) B*5101 ALPHA (HUMAN);, mRNA sequence.
ACCESSION AL696864 GI:4984764
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Gaps: 0
Percent Identity: 90.000
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Location/Qualifiers
1.748
/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           319 CGAGAGAACCTGCGGATCGCGCTCCGCTAC 290
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US-08-653-294-12 x AI359260/rev
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Ratio: 4.400
Percent Similarity: 100.000
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Align seg 1/1 to: AA147151
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US-08-653-294-12 x AL036690
                                                                                                                                 seq_name: gb_est38:AL036690
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LOCUS AL036690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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/db_xref="taxon:9606"
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EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. T-84 colonic epithalial cell line. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; -5 adaptor
sequence: 5 GAATTCGGCACGAG 3' -3' adaptor sequence: 5'
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 581)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Rucaba,T., Lacy,M., Le,M., Le,N., Le,N., Denno,B., Morris,M., Parange,C., Rifkin,L.,
Mardis,E., Moore,B., Morris,M., Pacons,J., Prange,C., Rifkin,L.,
Rohling,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,
Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -2BM13 rev2 from Amersham
High quality sequence stop: 272.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Sep 12, 1996 this sequence version replaced gi:1393699. Contact: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         others
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  Percent Similarity: 100.000
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US-08-653-294-12 x AA147151
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                                                                                                                                                                                                                                                                                              seq_documentation_block:
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
sequenced by Qiagen within the cDNA sequencing consortium of the
German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6, 14059
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DEFINITION crs1519 lambda2APST Ricinus communis cDNA clone pcrs1519, mRNA
                                                                                                                                                                                AL036690 171 bp mRNA EST 27-SEP-1999 DKFZp564D2463_r1 564 (synonym: hfbr2) Homo sapiens cDNA clone DKFZp564D2463 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 171)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="DKFZDSG4D2463"
/clone=lb="564 (synonym: hfbr2)"
/tissue_type="brain"
/dev_stage="feral"
/lab_host="%1.2blue"
/note="Vector: pAMP1; Site_1: Not1; Site_2: Sal1"
1 53 c 60 g 22 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wiemann,S.
EST (buesterhoeft, et al.)
Unpublished (1999)
On Jul 7, 1999 this sequence version replaced gi:5866258.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No s1 sequence available.
This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Am Klopferspitz 18a D-82152 Martinsried, Germany
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Gaps: 0
Percent Identity: 80.000
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/db_xref="taxon:9606"
                         1 ArgGluAspLeuArgIleAlaLeuArgTyr 10
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                                                                                                                                                                                                                                                                                     AL036690.3 GI:5927859
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seq_name: gb_est38:AW090252
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                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Malpighiales; Euphorbiaceae;
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1 (bases 1 to 414)

1 (lainer, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Wash Unix N. Unman EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      am56e06.x1 Johnston frontal cortex Homo sapiens cDNA clone INAGE:539586 3' similar to gb:MA4038 cds1 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-44(B-12) B*4402 (HUMAN); contains MRR22.t3 TAR1 repetitive element ;, mRNA sequence. A1124815 I GI:3593329
                                                                                                                                                         1 (bases 1 to 351)
vandeLoo,F.J., Turner,S. and Somerville,C.
bxpressed sequence tags from developing castor seeds
Plant Physiol. 108, 1141-1150 (1995)
Contact: Somerville CR
Carnegie Institution
Carnegie Institution, 290 Panama St, Stanford, CA 94305
Tel: 415325151
Email: crs@andrew.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 10
Gaps: 0
Percent Identity: 80.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Ricinus communis"
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1. .351
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US-08-653-294-12 x T24384/rev
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                     castor bean.
Ricinus communis
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AW090252 413 bp mRNA EST 15-OCT-1999 xC85g06.x1 NCI_CGAP_Brn35 Homo sapiens cDNA clone IMAGE:2591098 3', mRNA sequence.
AW090252 GI:6047596
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El (Dasea I to 413)

NCI/NINDS-CGAP Http://www.ncbi.nlm.nih.gov/ncicgap.

NAtional Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAPPERGAP), Tumor Gene Index

L Unpublished (1998)

On Jul 8, 1999 this sequence version replaced gi:5422650.

Tol: (301) 496-1550

Email: Robert_Strausberg*enih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.
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                                                                                                                                                              Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL : contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 frwd. Er from Amersham.
Location/Qualifiers
Unpublished (1997)
Onpublished (1997)
On Jan 17, 1998 this sequence version replaced gi:1899887.
Contact: Wilson RK
Washington University School of Medicine
Washington Tark Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
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Gaps: 0
Percent Identity: 80.000
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US-08-653-294-12 x AI124815
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                                                                                                                                                    Percent Similarity:
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                                                                                                                                                                                     /organism="Homo sapiens"
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/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Sal1;
Site_2: Not1: Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.33 kb. Tumor types include:
meningiona, oligodendroglioma, astrocytoma (grade II),
medulloblastoma, astrocytoma (grade IV). Life Technologies
catalog #: 11544-012"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human pancreatic islet"
/clone_lib="Human pancreatic silet"
/note="vector: Lambda ZAPII; Site_1: Eco RI; Site_2: Xho
I; mRNA was prepared from normal adult human islets. cDNA
was directionally synthesized from the Xho I in the vector
to the EcoRI site. cDNA was size fractionated to remove
sequences <1000 bp in size."
  Sequencing Center
information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human pancreatic islet ESTs
Unpublished (1995)
On Apr 14, 1993 this sequence version replaced gi:785206.
Contact: Jun Takeda
Institute for Molecular and Cellular Regulation, Gunma University
3-39-15 Showa-machi, Maebashi Gunma 371, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D82189 415 bp mRNA EST 09-FEB-1996
HUMHBC4524 Human pancreatic islet Homo sapiens CDNA similar to
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
DNA Sequencing by: Washington University Genome Clone distribution: NGT-CGAP Colone distribution found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
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Gaps: 0
Percent Identity: 77.778
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                                                                                                        Seq primer: -40UP from Gibco
High quality sequence stop: 401.
Location/Qualiflers
1. .413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: jtakeda@sb.gunma-u.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to reverse of: AW090252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HLA-B, mRNA sequence.
D82189
D82189.1 GI:1183662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-08-653-294-12 x AW090252/rev
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Takeda, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality: 38.00
Ratio: 4.222
Percent Similarity: 100.000
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Fax: 272-20-8896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
LOCUS D82189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: gb_est6:D82189
                                                                                                                                                                                                                                                                                                                                                                                                                                                    100
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ORGANISM
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VERSION
KEYWORDS
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ORIGIN
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JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
                                                                                                                                                  FEATURES
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Holzman, T.,
Adams, M.D. and
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/clone_lib-"CIT Approved Human Genomic Sperm Library D"
/sex-"male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B" 147 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 425)
Mahalras, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, Reller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS AQ204294 425 bp DNA GSS 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule 1/ Jule
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Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
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University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109,
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: 425
Length: 10
Gaps: 0
Percent Identity: 80.000
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Gaps: 0
Percent Identity: 77.778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to reverse of: AQ204294 from: 1
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                          to: 415
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Location/Qualifiers
1. 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         279 CGAGAGAACCTGNGGATCGCGCTCCGNTAC 308
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ArgGluAspLeuArgIleAlaLeuArgTyr 10
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US-08-653-294-12 x AQ204294/rev
38.00
4.222
90.000
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Ratio: 4.222
Percent Similarity: 100.000
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Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: gb_gss10:AQ204294
                                                                                                                                                                                   alignment_block:
US-08-653-294-12 x D82189
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Homo

VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL

COMMENT

REFERENCE AUTHORS

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High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3887

Fax: (206) 616-3887

Email: jwallacedu.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pleerefede)ong med.buffalo.edu). Clones may be purchased from RACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 968 row: A column: 10
                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 551)
Mahalras, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pBACe3.6; Genomic sequence of BAC ends" 114 c 93 g 218 t 6 others
                                                                                                                                                                                                                                           Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .551
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/db_xref="faxon:9606"
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/clone_lib="RPCI-11 Human Male BAC Library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 551
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Gaps: 0
Percent Identity: 60.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 551.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          190 AGAGAAGACATACAAATGGCCATCAGGTAT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ArgGluAspLeuArgIleAlaLeuArgTyr 10
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AQ725101
AQ725101.1 GI:5484770
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US-08-653-294-12 x AQ725101/rev
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Ratio: 3.800
Percent Similarity: 100.000
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                                                                                                  Homo sapiens
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                                                                         human.
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ORIGIN
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AUTHORS
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                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0208
Fax: 301 838 0208
Email: hoeftigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Piter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butharyota; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 427)
Adams, M. D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.
Use of human BAC End Sequences for Sequence-Ready Map Building
                                                                                                                                                          seq_documentation_block: 427 bp DNA GSS 04-MAY-1999
LOCUS AQ317269 11-105A4.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-105A4, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPCIII Human Male BAC Library"

126 c 92 q 95 t
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Gaps: 0
Percent Identity: 77.778
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1. 427
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Ab_xref="GDB:753939"
Ab_xref="taxon:9606"
Clone="RPCI-11-105A4"
/clone_lib="RPCI-11"
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/cell_type="Lymphocytes"
                    92 g
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AQ317269.1 GI:4048520
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US-08-653-294-12 x AQ317269/rev
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Percent Similarity: 100.000
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                                                                                                                       seq_name: gb_gss11:AQ317269
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                                                                                                                                                                                                                                                                                                                                                human.
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source

FEATURES

BASE COUNT ORIGIN

LOCUS A0725101 551 bp DNA GSS 14-JUL-1999
DEFINITION HS_5392_A2_A05_T7A RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=968 Col=10 Row=A, genomic survey sequence.

seq_name: gb_gss4:AQ725101 seq_documentation_block: THIS PAGE BLANK (USPTO)

1

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GenCore version 4.5
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 protein search, using sw model OM protein Search time 122.56 Seconds (without alignments)
1.933 Million cell updates/sec 8, 2000, 01:29:38 February Run on:

US-08-653-294-12 Title:

1 REDLRIALRY 10 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

188963 segs, 23686106 residues Searched:

188963 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

A_Geneseq_36:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description)2 CIL	LA-B2702.75-8	nodulat	` ^	~	Peptide fragment o	HLA-B2702 CTL modu	Alpha1-helix of HL	T-cell modulating	Immunomodulatory p	Immunomodulatory p	Peptide B2702.75-8	HLA-B2702 CTL modu	Peptide B2702.70-8	HLA-B2702 CTL modu	HLA-B2702 CTL modu	HLA-B2702 84-75-84	Immunomodulating d	B2702.84-	Peptide fragment o	44	2 CTL mod	н.	2.60-	HLAB38.6084. Comps	de B2702	Peptide Seg ID No:	nce of HLA-B		m	ide fr	702	-B2702 CTL	
SUMMARIES	ព	309	R95425	751	726	378	120	306	541	21	726	727	378	291	379	290	290	542	377	379	120	328	309	309	541	542	379	0680	0314	14	9	4121	8307	R83095	309
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HLA-B2705.75-84. C HLA-B2702.75-84(T) Immunomodulatory p Peptide B2705.75-8 Peptide B2702.75-8 Peptide B2702.75-8 Human [Phe74]-HLA- HLA-B2702.CTL modu HLA-B2702.CTL modu Peptide B2702.78-8	
R95423 R95426 W47267 W33788 W33788 W71442 R71443 R92910 W33792	
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ALIGNMENTS

RESULT

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Example 14; Page 34; 80pp; English.

Example 14; Page 34; 80pp; English.

Example 183085, R8309-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 75.84 of the alpha-1 domain of the class I MHC HLA-B2702.

These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly of the patient.
                             R83094;
116-MAY-1996 (first entry)
HIA-B2702 CTL modulating peptide (B2702.75-84(D)).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
Immunosuppressant; graft versus host disorder; transplantation; therapy;
Synthetic.
Synthetic.
W09526979-A1.
                                                                                                                                                                              R83094 standard; peptide; 10 AA.
                                                                                                                                                                 12-OCT-1995.
R83094
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Length 10; 100.0%; Score 49; DB 1; I 100.0%; Pred. No. 0.00038; Query Match 100. Best Local Similarity 100. Matches 10; Conservative 10 AA;

1 REDLRIALRY 10 ð 요

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Gaps

.. 0

0; Indels

0; Mismatches

R95425 standard; peptide; 10 AA.

R95425, 1956 (first entry) HLA-B-NOV-1996 (first entry) HLA-B-NOV-1996 (first entry) HLA-B-NOV-1996 (first entry) HLA-B-NOV-1996 (first entry) HLA: P74; alphal-helix; human-leucocyte-associated antigen; inhibitor; T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC; B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation; cytolysis; antigen presenting cell. Synthetic.

..., Location/Qualifiers misc_difference 3

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Example: Page 11: 29pp: English

Example: Page 11: 29pp: English

Composition of CTLS.

Example: Page 11: 29pp: English

Composition of CTLS.

Example: Page 11: 29pp: English

Composition of CTLS.

These sequences can be used to isolate the protein pot 4 is a T-cell system a T-cell system of the English of Sequences can be used to isolate the protein cassociated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein Hsc70. p74 is cound in a limited number of cell types, but is particularly expressed on English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of English of Engl
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r-cell modulator: autoimmune disease; tissue destruction; alphal-domain; mandlator: autoimmune disease; tissue destruction; antigen; perforin; insulin-dependent diabetes mellitus; multiple sclerosis; inflammation; insulin-dependent diabetes mellitus; multiple sclerosis; inflammation; thenmatoid arthritis; psoriasis; pemphigus vulgaris; sjogren's disease; thyroid disease; Hashimoto's thyroiditis; myasthenia gravis; granzyme; autologous target cell; cytokine release; T cell activation; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell mediated attack on target cells

Tage 20, 24pp; English.

W07512-W07518 represent T-cell modulating peptides that can be used in the method of the invention. These sequences are based on a portion of the generic peptide corresponding to residues 70-91 of the alphal-domain of the major histocompatability complex (MHC) class I antigen (see W07510). The method is for affecting the course of an autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treatment of auto-immune disease by admin. of peptide(s) corresp. to major histocompatibility complex antigens - esp. for delaying onset of clinical symptoms of insulin dependent diabetes by modulating T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                               Compsns. comprising lymphoid surface membrane proteins - which may
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100.0%; Pred. No. 0.00038;
Live 0; Mismatches 0; Indels
/note= "N3D mutation
                                                                                                  STRD ) UNIV LELAND STANFORD JUNIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W07513 standard; peptide; 10 AA.
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                                                                                                                        Krensky AM;
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                                                                               US-150493
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12-MAY-1995; US-4405
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                        Clayberger C, Kre
WPI; 95-194027/25.
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                                                                               10-NOV-1993;
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involving T-cell mediated destruction of tissue in mammals. These peptides are used especially to treat insulin-dependent diabetes mellitus, preferably being administered during the pre-clinical stage to delay onset of the disease. Other diseases that can be treated are multiple sclerosis, rheumatoid arthritis, psoriasis, pemphigus vulgaris, sjogren's disease, thyroid disease, Hashimoto's thyroiditis, myasthenia gravis, etc. The peptides modulate T-cell mediated attack on autologous target cells, and may also reduce inflammation, swelling, and release of cytokines, perforins, granzymes etc. associated with T cell activation. Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clayberger C, Krensky AM;
WPI; 98-018220/02.
Novel immunomodulatory peptide-type compound - useful for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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The present tequence is an immunomodulatory peptide, which
comprises a class I HiA-B alpha-1 domain sequence. It can be used
in a pharmaceutical composition together with a subtherapeutic dose
of an immunosuppressant, to extend the period of acceptance of a
transplant from a major histocompatibility complex (MHC) unmatched
donor, i.e. to inhibit transplant rejection. It can also be used in
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19-JUV198 (first entry)
Peptide B2702.75-84D77 tested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
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    /note= "at least one of the amino acids is the

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Immunomodulator; Class I HLA-B alpha-1 domain; inhibition;
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                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 49; DB 1; Length 10; 100.0%; Pred. No. 0.00038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transplant rejection; treatment; autoimmune disease.
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W47269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-MAY-1998 (first entry)
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23-APR-1997; U06705.
22-MAY-1996; US-651650.
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Best Local Similarity
Matches 10; Conserv
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10 AA;

Sequence

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22-MAY-1997; U08689.

24-MAY-1997; U08689.

PR 24-MAY-1997; US-53294.

PR (STRD) UNIV LELAND STANFORD JUNIOR.

CC (Terminal and STATA) English.

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The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL activity in parasitic diseases and neoplasia and in studies on viral infection. The peptide can also be used for identifying CTLs which bind to it and removing subsets of CTLs from a T-cell composition. This peptide sequence is more commonly found within larger peptide compounds of not more than 30 amino acids in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-MAR-1994 (first entry)
Peptide fragment of Class I HLA peptide.
Peptide fragment of Class I HLA peptide.
Patide: transplantation; neoplasia;
parasitic disease; cytotoxic I lymphocyte; modulation.
Synthetic.
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain; rejection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R41208 standard; peptide; 10 AA.
R41208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Krensky AM;
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Best Local Similarity 100.

Matches 10; Conservative
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                                                                              Homo sapiens.
WO9744351-A1.
                                                      Synthetic.
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R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs)
                                                                                                                                                                                                                                                                                                                                                                                                               R83062;
116-MAY-1996 (first entry)
HIA-B2702 CIL modulating peptide (B2702.75-84).
HIA-B2702 CIL modulating major histocompatibility complex; MHC;
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation; therapy;
Synthetic.
Synthetic.
M09526979-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R95413 standard; peptide; 10 AA.
R95413;
12-NOV-1996 (first entry)
Alphal-helix of HLA-B2702.
Alphal-helix inhibitor;
Ficel lysate; membrane protein; mammal; heat shock protein; Hsc70; AP
B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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05-APR-1995; U04349.

05-APR-1994; US-222851.

(STRD) UNIV LELAND STANFORD JUNIOR.

Clayberger C, Krensky AM, Parham P;

WPI: 95-38582/46.

Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
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                                    Length 10;
                                                                                                   0; Indels
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                                    Score 44; DB 1;
Pred. No. 0.004;
                                                                                                1; Mismatches
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10-NAY-1995.
10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
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                                                                                                                                                                                                                                                                                                                                                                                     R83062 standard; peptide; 10 AA.
                                    89.8%;
90.0%;
Ouery Match
Best Local Similarity 90.0.
--- 9; Conservative
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Matches 9; Conservative
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R83062
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Synthetic.
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W47271
AC W47271
BC W47271
DT 22-MAY
DE Immuno
KW transp
COS Homo S
OS Synthe
FH Key
FT Misc_d
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W47265
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                                                                                           the protein py4 from argument and sequence, epitopes, and palindromes of it (such as R95428) can be used to isolate the protein py4 from a T-cell lysate. py4 is a T-cell surface membrane to protein associated with T-cell activation in mammalian T-cells, and is a solation associated with T-cell activation in mammalian T-cells, and is a solation associated with T-cell activation in mammalian T-cells, and is a solated by inmunologically cross reactive with the heat shock protein HsC70. py4 is found in a limited number of cell types, but is particularly expressed on B and T cells. py4 can be isolated by lysis of a suitable cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HLA-B2702 palindromic peptide. Column containing a covalently bound HLA-B2702 palindromic peptide. Column containing a covalently bound HLA-B2702 palindromic peptide. Column containing a covalently bound HLA-B2702 palindromic peptide. Combined with HLA-B2702.60-84 (see R95416), indices calcium influx, and inhibits composition and by pytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate compounds can be screened for their effect on the cytolytic activity of T-cells, by combining them with the extracellular portion of py4 and determining T-cells and antigen presenting cells (APCS), by adding to the mix the extracellular portion of py4, in an amount sufficient to compete with py4 for the binding of the py4 ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T-cell modulating peptide #1.

T-cell modulator: autoimmune disease; tissue destruction; alphal-domain; mandulator: autoimmune disease; tissue destruction; antigen; perforin; insulin-dependent histocompatability complex; MHC class I; antigen; perforin; insulin-dependent diabetes mellitus; multiple sclerosis; inflammation; insulin-dependent diabetes mellitus; multiple sclerosis; inflammation; theumatoid arthritis; psoriasis; pemphigus vulgaris; sjoyerer's disease; thyroid disease; Hashimoto's thyroiditis; myasthenia gravis; granzyme; autologous target cell; cytokine release; T cell activation; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treatment of auto-immune disease by admin. of peptide(s) corresp. to major histocompatibility complex antigens - esp. for delaying onset of clinical symptoms of insulin dependent diabetes by modulating T cell mediated attack on target cells

Claim 7; Page 20; 24pp; English.

Claim 7; Page 20; 24pp; English.

Claim 7; Page 20; 24pp; English.

These sequences are based on a portion of the method of the invention. These sequences are based on a portion of the generic peptide corresponding to residues 70-91 of the alphal-domain of the major histocompatability complex (MHC) class I antigen (see W07510). The method is for affecting the course of an autoimmune disease involving T-cell mediated destruction of tissue in mammals. These peptides are used especially to treat insulin-dependent diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mellitus, preferably being administered during the pre-clinical stage to delay onset of the disease. Other diseases that can be treated are multiple sclerosis, rheumatoid arthritis, psoriasis, pemphigus augaris, sjooren's disease, thyroid disease, Hashimoto's thyroiditis, myasthenia gravis, etc. The peptides modulate T-cell mediated attack on autologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                   Compsns. comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLS. Example: Page 11: 29pp: English. This sequence represents the alphal-helix of the
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Pred. No. 0.004;
1; Mismatches 0; Indels
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(SANG-) SANGSTAT MEDICAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W07512 standard; peptide; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89.8%;
90.0%;
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05-APR-1996; U04710.
12-MAY-1995; US-4405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity
Matches 9; Conserv
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WPI; 95-194027/25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence
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    swelling, and release of with T cell activation.
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The present sequence is an immunomodulatory peptide, which comprises a Class I HiA-B alpha-1 domain sequence. It can be used in a pharmaceutical composition together with a subtherapeutic dose of an immunosuppressant, to extend the period of acceptance of a transplant from a major histocompatibility complex (MHC) unmatched donor, i.e. to inhibit transplant rejection. It can also be used in
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    /note= "at least one of the amino acids is the

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    /note= "at least one of the amino acids is the

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Immunomodulator; Class I HLA-B alpha-1 domain; inhibition; transplant rejection; treatment; autoimmune disease.
Homo sapiens.
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Immunomodulatory peptide.
Immunomodulator; Class I HLA-B alpha-1 domain; inhibition;
Irmnsplant rejection; treatment; autoimmune disease.
Homo sapiens.
Synthetic.
                                                                                                                        Length 10;
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                                                                                                                                                                       Indels
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target cells, and may also reduce inflammation, cytokines, perforins, granzymes etc. associated Sequence 10 AA;
                                                                                                                        Score 44; DB 1;
Pred. No. 0.004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 44; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 0.004;
1; Mismatches
                                                                                                                                                                       1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-NOV-1997.
23-ARR-1997; U06705.
22-MAY-1996; US-651650.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM;
WPI; 98-018220/02.
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                                                                                                                        89.8%;
90.0%;
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                                                                                                                        Query Match 89.8
Best Local Similarity 90.0
Matches 9; Conservative
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1 RENLRIALRY 10
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Best Local Similarity
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Misc_difference 1.
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27-NOV-1997.
22-MAY-1997; U08689.
24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Beulow R, Clayberger C, Krensky AM;
WPI; 98-086530/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
WO9744351-A1.
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                                    Query Match
Best Local S.
Matches 9
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W33795
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Example 1: Page 19; 41pp; English.

Example 1: Page 19; 41pp; English.

Peptides W33784-98 and W33778-9 were assayed for their immunomodulating activity, including the N-terminal acylated and/or crivity.

Immunomodulating activity, including the N-terminal acylated and/or creminal amidated or esterified forms of up to 60 amino acids, where cremonand comprises the formula; A-B, where A, B = (C-terminal amidated comproses the formula; A-B, where A, B = (C-terminal amino acids; aa80 - I or N, aa81, aa84 - a hydrophobic or small amino acid; aa82 - R or L; aa83 - G or R; and as represents amino acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a Class I HLA-B alphal domain (positions 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of Interest to activate CTLs. They can also inhibit the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, chematoid atthritis and lupus erythematosis. The products can also be considered to the component of transplants or for treating autoimmune diseases, e.g. diabetes, considered to the component of transplants or for treating autoimmune diseases, e.g. diabetes, considered to the component of transplants or for treating autoimmune diseases, e.g. diabetes, considered to the component of transplants or for treating autoimmune diseases, e.g. diabetes, considered to the component of transplants or for treating autoimmune diseases, e.g. diabetes, considered to the component of transplants or for treating autoimmune diseases, e.g. diabetes, considered to the component of transplants or proventing transplants or proventing transplants or treating autoimmune diseases, e.g. diabetes, cons
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                                                                                         Clayberger C, Krensky AM;
WPI; 98-018220/02.
Novel immunomodulatory peptide-type compound - useful for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                         Comprises a Class I HLA-B alpha-1 domain sequence. It can be used in a pharmaceutical an immunomodulatory peptide, which comprises a Class I HLA-B alpha-1 domain sequence. It can be used in a pharmaceutical composition together with a subtherapeutic dose of an immunosuppressant, to extend the period of acceptance of a transplant from amajor histocompatibility complex (MHC) unmatched donor, i.e. to inhibit transplant rejection. It can also be used in the treatment of autoimmune diseases.

Peptides using the D-form anino acids are more effective immunomodulators than their diastereomers or enantiomers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUN-1998 (first entry)
Peptide B2702.75-84 tested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CTL activation; transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 44; DB 1;
Pred. No. 0.004;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-NOV-1997.
22-MAY-1997; U08689.
24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Beulow R. Clayberger C, Krensky AM;
                                                                             (STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                        transplant rejection
Claim 10; Page 36; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W33784 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                   89.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                         US-651650.
                                    23-APR-1997; U06705.
22-MAY-1996; US-6516
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 9; Conserv
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WO9744351-A1.
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Rample 15; Re3090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 70-84 of the alpha-1 domain of the class I MHC HLA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLs) of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                         HIA-B2702 CTL modulating peptide (B2702.70-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HIA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                 Gaps
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Peptide B3702.70-84 tested for immunomodulating activity.

Immunomodulating dimer: immunosuppressant drug; CTL activation; transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clayberger C, Krensky AM, Fallow - Clayberger C, Krensky AM, Fallow - Clayberger C, WPI; 95-35882/46.

Extension of acceptance period of transplants from MHC unmatched Annor hosts - using Class I B75-84 MHC antigen of the recipient
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   Length 10;
                                                                 0; Indels
Score 44; DB 1;
Pred. No. 0.004;
L; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-OCT-1995.
05-APR-1995.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                  R92912 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W33795 standard; peptide; 15 AA.
   89.8%;
90.0%;
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Best Local Similarity 90.0
Matches 9; Conservative
                                Similarity 90.(
9, Conservative
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treating autolimume diseases

Example 1: Page 19: 41pp: English.

Peptides W33784-99 and W33778-9 were assayed for their immunomodulating activity. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or C-terminal amidated or esterilided forms of up to 60 amino acids, where the peptide-type compound comprises the formula A-B, where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or Small amino acid; aa82 = R or L; aa83 = G or R; and an represents amino acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise at any peptide type bond within the brackets alphal domain (positions 79-84). They can be used to inhibit cytotoxic T-laymphocytes (CTL) from undestrably attacking cells in a host or in vitro. They can also be cused in combination with antigenic peptides or proteins of interest to activate CTLS. They can also inhibit the proliferation of r calls in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, response to anti-tis and lupus erythematosis. The products can also be considered to see the underly attacking autoimmune diseases, e.g. diabetes, conserved the component of the conserved or treating autoimmune diseases.
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R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of
class I major histocompatibility complex (MHC) antigens. This sequence
is an inverted dimer of residues 75-84 of the alpha-1 domain of the class
I MHC HLA-B2702. These sequences can be used to extend the period of
acceptance by a recipient of a transplant from an MHC unmatched donor.
The peptides are administered to a patient in conjunction with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HLA-B2702 CTL modulating peptide (B2702.84-75/75-84). Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Subthergoetic amount of an immunosuppressant. This is administrated to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly administration for current treatments). The peptides particularly of the patient.
New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or
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89.8%; Score 44; DB 1; Length 15;
Best Local Similarity 90.0%; Pred. No. 0.0061;
Matches 9; Conservative 1; Mismatches 0; Indels
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05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R92907 standard; peptide; 20 AA.
R92907;
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WPI; 95-358582/46.
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R92907
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Gaps

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0; Indels

1; Mismatches

9; Conservative

Ouery Match Best Local Similarity Matches 9; Conserva

Score 44; DB 1; Length 20; Pred. No. 0.0083;

89.8%; 90.0%;

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|11 RENLRIALRY 20
1 REDLRIALRY 10
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8, 2000, 01:29:38 completed: February ne: 1750 sec Search comp Job time: 1

us-08-653-294-12.rpr

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

February 7, 2000, 11:54:23; Search time 117.7 Seconds (without alignments) 4.008 Million cell updates/sec Run on:

US-08-653-294-12 49 1 REDLRIALRY 10 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

142080 segs, 47169319 residues Searched:

142080 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

Database :

PIR_62:* 1: pir1: 2: pir2: 3: pir3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SHIMMARTES

SUMMARIES	Description	class I hi	MHC HLA-B38	class I	class I	class I	class I	class I histocompa	class	H	clas	н	н	class I histocompa				lymphocyte		MHC	MHC HLA-	class I hi	MHC clas	class I	class I hist	MHC clas	MHC class I histoc	HLA-AW24 pro	MHC class I	MHC class I histoc
SUM	Ω	138509	L 3	u)	180168	œ	I80169	180171	HLHU12	HLHUB8	B30345	JH0541	JH0539	JH0540	A45834	I84486	I62045	I84490	137521	A30345	I59633	S24434	137120	S07113	803537	D35997	877963	154416	I54493	HLHU32
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d	Query Match	. 6	σ.	δ.	86.8	9.	9.	σ.	6	6	6	φ.	σ.	6	φ.	6	6	6	9.	6	9.	6	φ.	δ.	σ,	σ.	6	6	6	7
	Score	44	44		44			44	44		44	44		44	44	44	44	44	44	44	44	44	44	44		44	44		44	43
	Result No.		7	٣	4	Ŋ	9	7	ω	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	58

MHC HLA-B27-HS - h HLA-B alpha-chain	MHC class I histoc MHC class I histoc	class I histocompa MHC class I histoc	MHC class I histoc	MHC HLA-844.2 Chai human lymphocyte a	MHC class I histoc MHC HLA-B27d - hum	class I histocompa indole-3-qlycerol-	MHC class I histoc hypothetical prote
2 I56116 2 I37516	L HLHUB2 2 C35997	2 S25415 2 A45850	168724	2 137485	2 I54442 2 I54289	2 JH0537 2 C75163	L HLMS1 2 H65082
338	362	362	362	362	362	365	298
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31 32	3 3 4	3 3 9 9	37	30 CC 70 CC	4 4	4 4 4 3	4 4 5 5

ALIGNMENTS

RESULT 1 188509 MHC class I histocompatibility antigen - human (fragment) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: 40 Sep-1996 #sequence_revision 06-Sep-1996 #text_change 23-Jul-1999 C;Ancession: 738509	Ricereb, N.; Choi, J.W.; Riu, K.Z.; Yang, S.Y. Tissue Antigens 44, 271-273, 1994 A;Title: HIA-B*5105, a newly identified B51 IEF variant. A;Reference number: I38509; WUID:95176331 A;Accession: I38509 A;Status: preliminary; translated from GB/EMBL/DDBJ	A:Molecule type: mRNA A:Residues: 1-273 <res. A:Gross references: EMBL:U06697; NID:9469544; PIDN:AAA92997.1; PID:9469545 C:Genetics: A:Gene:GDB:HLA-B A:Gross-references: GDB:120048; OMIM:142830 A:Map position: 6p21.3-6p21.3</res. 	C; Superfamily: class I histocompatibility antigen; immunoglobulin homology Query Match Best Local Similarity 90.0%; Pred. No. 0.12; Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	1 REDLRIALRY 10
I38509 MHC class I C;Species: B C;Date: 06-8	R.Cereb, N. Tissue Antic A.Title: HLA A.Reference A.Accession A.Status: pl	A, Molecule 1 A, Residues: A, Cross-refe C, Genetics: A, Gene: GDB A, Cross-refe	C; Superfami. Query Matches Matches	Oy 1 R1

Cispedies: Homo saplens (man)
Cispedies: Homo saplens (man)
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Cispedies: Homo saplens (man)
Cispedies: Homo saplens (man)
Cispedies: O7-Jun-1996 #sequence_revision O7-Jun-1996 #text_change 23-Jul-1999
Cispedies: O7-Jun-1996 #sequence_revision O7-Jun-1996 #text_change 23-Jul-1999
Cispedies: O.A.: Engler-Blum, G.; Gekeler, V.; Steiert, I.; Weiss, E.; Schmidt, H.
Immunogenetics 30, 200-207, 1989
A; Title: Genetic and serological heterogeneity of the supertypic HLA-B locus specific A; Accession: 154463; MUD:89379286
A; Accession: 154463
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Mesidues: 1-274 <RES
A; Cross-references: GB:M29864; NID:g187674; PIDN:AAA36222.1; PID:g187675
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology 154463 MHC HLA-B38 chain - human (fragment)

ö Gaps ö Query Match 89.8%; Score 44; DB 2; Length 274; Best Local Similarity 90.0%; Pred. No. 0.12; Matches 9; Conservative 1; Mismatches 0; Indels

Gaps

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Cispecies: Pan troglodytes (chimpanzee)
C;Species: Pan troglodytes (chimpanzee)
C;Species: 24 May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999
C;Accession: 180169
R;McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Wat Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A;Title: A uniquely high level of recombination at the HLA-B locus.
A;Reference number: 159308; MUID:94286544
A;Accession: 180169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              class I histocompatibility antigen - chimpanzee (fragment)
C;Species: Pan troglodytes (chimpanzee)
C;Species: 24-May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999
C;Accession: 180171
R;McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Wat Proc. Natl. Acad. Scl. U.S.A. 91, 5893-5897, 1994
A;Title: A uniquely high level of recombination at the HLA-B locus.
A;Reference number: 159308; MUID:94286544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1355 <RRES>
A; Cross-references: EMBL:U05580; NID:g454777; PIDN:AAA50183.1; PID:g454778
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
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A;Residues: 1.355 CRES.
A;Cross-references: EMBL:U05582; NID:g454781; PIDN:AAA50185.1; PID:g454782
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
A;Cross-references: EMBL:U05578; NID:g454773; PIDN:AAA50181.1; PID:g454774
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
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A;Molecule type: mRNA
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Pred. No. 0.16;
1; Mismatches
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Pred. No. 0.16;
1; Mismatches
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Pred. No. 0.16;
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90.0%;
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                                                                                                                                                                                                                                      Class I histocompatibility antigen - pygmy chimpanzee (fragment)
C; Species: Pan paniscus (pygmy chimpanzee, bonobo)
C; Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 23-Jul-1999
C; Accession : 159308
R; McAdam, S. N.; Boyson, J. E.; Liu, X.; Garber, T. L.; Hughes, A. L.; Bontrop, R. E.; Watkin Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A; Title: A uniquely high level of recombination at the HLA-B locus.
A; Reference number: 159308; MuID:94286544
A; Accession: 159308
A; Status: preliminary; translated from GB/EMBL/DDBJ
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C; Species: Pan troglodytes (chimpanzee)
C; Species: Pan troglodytes (chimpanzee)
C; Species: 24-May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999
C; Accession: 180068
R; McAdam, S. N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Watkin Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A; Title: A uniquely high level of recombination at the HLA-B locus.
A; Reference number: 159308; MUID:94286544
A; Accession: 180168
A; Status: preliminary; translated from GB/EMBL/DDBJ
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C;Species: Pan paniscus (pygmy chimparize, bonobo)
C;Cate: 24-May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999
C;Accession: 180167
R;Accession: 180167
R;Access
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A;Residues: 1-34 <RES.
A;Cross-references: EMBL:U05579; NID:g454775; PIDN:AAA50182.1; PID:g454776
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
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1; Mismatches
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91 RENLRIALRY 100
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91 RENLRIALRY 100
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A; Residues: 1-354 <RES>
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75 RENLRIALRY 8
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R:Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
J. Exp. Med. 174, 1491-1509, 1991
A:Title: Gorilla class I major histocompatibility complex alleles: comparison to huma A:Reference number: JH0534; MUID:92078860
A:Molecule type: DNA
A:Molecule type: DNA
A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 1-362 < LANA
A:Transmembrane protein
C:Genetics: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Reywords: transmembrane protein
F:11-206/Domain: alpha-1 < ALi2>
F:25-362/Product: class I histocompatibility antigen heavy chain, Gogo-B0103 *status
F:15-106/Domain: alpha-2 < ALi2>
F:20-285/Domain: alpha-3 < ALi3>
F:20-285/Domain: intracellular *status predicted <INT>
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A.Title: HLA-B51 and HLA-Bw52 differ by only two amino acids which are in the helical A. Reference number: A30345; MUID:89080265
A.Accession: B30345
A.Accession: B30345
A.Molecule type: DNA
A.Residues: 1-362 <HAY>
C.Superfamily: class I histocompatibility antigen; immunoglobulin homology
C.Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;220-285/Domain: immunoglobulin homology <HMM>
                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 29-Jan 1990 #sequence_revision 29-Jan-1990 #text_change 16-Feb-1997
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Species: Gorilla gorilla gorilla (lowland gorilla)
Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
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Pred. No. 0.16;
1; Mismatches
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A:Introns: 22/1; 112/1; 204/1; 296/1; 335/1; 346/1
A:Introns: 22/1; 112/1; 204/1; 296/1; 335/1; 346/1
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Superfamily: class I histocompatibility antigen; transmembrane protein; transplantatile; 1-21/Domain: signal sequence #status predicted <SIG>F:22-359/Product: class I histocompatibility antigen HLA alpha chain #status predicted <E72-304/Domain: extracellular #status predicted <EXT>F:22-304/Domain: alpha-1 <EXL>F:22-304/Domain: alpha-2 <EXL>F:212-303/Domain: immunoglobulin homology <IMM>F:217-822/Domain: immunoglobulin homology <IMM>F:217-822/Domain: immunoglobulin alpha-2 <EXL>F:217-822/Domain: immunoglobulin alpha-2 <EXL
                                                                                                                                                                                                                                                                                                                                                            PIDN:AAA36218.1; PID:9386873
the domain structure of this
R;Malissen, M.; Malissen, B.; Jordan, B.R.
Proc. Natl. Acad. Sci. U.S.A. 79, 893-897, 1982
A;Title: Exon/intron organization and complete nucleotide sequence of an HLA gene.
A;Reference number: A02189; MUID:82151002
A;Accession: A02189
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C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 05-Sep-1997
C;Accession: A33895
R;Ways, J.P.; Coppin, H.L.; Parham, P.
J. Biol. Cham. 260, 11934, 1985
J. Biol. Cham. 260, 11934, 11937, 1985
A;Title: The complete primary Structure of HLA-Bw58.
A;Reference number: A23895; WUID:86008247
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F:305-329/Domain: transmembrane #status predicted <TMM>
F:335-359/Domain: intracellular #status predicted <INT>
F:107/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:224-280/Disulfide bonds: #status predicted
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F;332-362/Domain: intracellular *status predicted <INT>
F;110/Binding site: carbohydrate (Asn) (covalent) *status predicted
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Pred. No. 0.16;
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A) Note: the authors translated the codon GCC for residue 349
C) Comment: This protein is a subtype of the HLA-B17 family.
                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:J00191; GB:V00526; NID:g187600; C;Comment: The seven exons correspond approximately to
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90.0%;
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| 96 RENLRIALRY 105
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Best Local Similarity
Matches 9; Conserv
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Matches 9; Conserv
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C;Species: Homo sapiens (man)
C;Date: 03-Uni-1993 #sequence_revision 03-Jun-1993 #text_change 23-Jul-1999
C;Date: 03-Uni-1993 #sequence_revision 03-Jun-1993 #text_change 23-Jul-1999
C;Accession: A45884
R;Hayashi, H.; Ooba, T.; Nakayama, S.; Sekimata, M.; Kano, K.; Takiguchi, M.
Immunoopenetics 32, 195-199, 1990
A;Tille: Allospecificities between HLA-Bw53 and HLA-B35 are generated by substitution A;Reference number: A45834; MUID:91033941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transmembrane glycoprotein - human
C;Species: Homo sapiens (man)
C;Date: 02-aug-1996 #sequence_revision 02-Aug-1996 #text_change 23-Jul-1999
C;Accession: 184486
R;Hildebrand, W.H.; Domena, J.D.; Shen, S.Y.; Lau, M.; Terasaki, P.I.; Bunce, M.; Mar
Tissue Antigens 43, 209-218, 1994
A;Title: HLA-B15: a widespread and diverse family of HLA-B alleles.
A;Reference number: 138421; MUID:94367483
                                                                                                                                                                                                                                                         A; Accession: A45834
A; Molecule type: DNA
A; Residues: 1-362 < CHAX>
A; Cross-references: GB:M58636; NID:g187756; PIDN:AAA36228.1; PID:g187757; GB:M33574
A; Note: this allele is designated B*5301
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GDB:120048; OMIM:142830
A;Cross-references: GDB:120048; OMIM:142830
A;Map position: 6p21.3-6p21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology C;Keywords: glycoprotein; heterodimer; transmembrane protein C;Keywords: glycoprotein; heterodimer; transmembrane protein F:124/Domain: signal sequence #status predicted <SIG>F;220-285/Domain: immunoglobulin homology <IMM'STAD-285/Domain: ammunoglobulin homology <IMM'STAD-285/Domain: carbohydrate (Asn) (covalent) #status predicted
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A;Molecule type: mRNA
A;Residues: 1-362 <RES>
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Pred. No. 0.16;
1; Mismatches
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Best Local Similarity 90.0
Matches 9; Conservative
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Matches 9; Conservative
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Job time: 24334 sec
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99 RENLRIALRY 108
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99 RENLRIALRY
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A; Residues: 1-362 < LAM>
A; Residues: 1-362 < LAM>
A; Cross-references: EMBL:X60255; NID:922865; PIDN:CAA42807.1; PID:922866
A: Experimental source: EBV-transformed B cell
C; Genetics: 25.1; 115/1; 207/1; 299/1; 338/1; 349/1
A: Introns: 25.1; 115/1; 207/1; 299/1; 338/1; 349/1
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
C; Reywords: transmembrane protein
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C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-362/Product: class.I histocompatibility antigen heavy chain, Gogo-B0102 #status pre
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R;Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
J. Exp. Med. 174, 1491-1509, 1991
A; Exp. Med. 174, 1491-1509, 1991
A;Title: Gorilla class I major histocompatibility complex alleles: comparison to human A; Afference number: JH0534; MUID:92078860
A;Accession: JH0540
                                                                        R;Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P. J. Exp. Med. 174, 1491–1509, 1991
A;Title: Gorilla class I major histocompatibility complex alleles: comparison to human A;Reference number: JH0534; MUID:92078860
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C.Species: Gorilla gorilla gorilla (lowland gorilla)
C.Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
    30-Jun-1992 #text_change 23-Jul-1999
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A:Experimental source: EBV-transformed B cell
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F;115-206/Domain: alpha-2 <AL2>
F;207-208/Domain: alpha-3 <AL3>
F;207-285/Domain: alpha-3 <AL3>
F;229-362/Domain: intracellular *status predicted <INT>
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F:207-298/Domain: alpha-3 <AL3>
F:220-285/Domain: immunoglobulin homology <IMM>
F:229-362/Domain: immunoglobulin *status predicted <INT>
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A; Residues: 1-362 <LAW>
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         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                              of hits satisfying chosen parameters:
                                                                   8, 2000, 00:59:52;
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1805_HUMAN
1816_HUMAN
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1A04_GORGO
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B-1 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
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01-JAN-1990 (Rel. 13, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-1 ALPHA CHAIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Nucleotide sequences of chimpanzee MHC class I alleles: evidence trans-species mode of evolution."; EMBO J. 7:2765-2774(1988).
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008136
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057554
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
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-1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAYER W.E., JONKER M., KLEIN D., IVANYI P., VAN SEVENTER KLEIN J.;
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PIR; S03537; S03537.
HSSP; P03989; 1HSA.
PROSITE; PS00290; IG_MHC; 1.
PFAM; PF00047; 1g; 1.
PFAM; PF00129; MHC_1; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
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DBS_HUMAN
1B19_HUMAN
HAD2_PSESP
Y089_METJA
HA10_MOUSE
HA13_MOUSE
HA1M_MOUSE
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DCDA_BACSU
RBL_BRYMA
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CYTOPLASMIC TAIL.
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SEQUENCE

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                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDILIE; 92078860.
LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
"Gorilla class I major histocompatibility complex alleles: comparison to human and chimpanatee class I.";
to human and chimpanatee class I.";
J. Exp. Med. 174:1491-1509(1991).
-i- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
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P30381.
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
cLASS. I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0103 ALPHA CHAIN PRECURSOR.
GORIlla gorilla gorilla (coviand gorilla).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                     01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0102 ALPHA CHAIN PRECURSOR.
GOTILLA GOTILLA GOTILLA (Lowland gorilla).
Eukaryota, Metazoa; Glordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrini; Hominidae; Gotilla.
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JR EMBL; X60693; CAA43101.1; -.
DR PRSP; P03899; 1BSA.
DR PROSTE; P8000290; IG_MHC; 1.
DR PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
MHC I; Transmembrane; Glycoprotein; Signal.
T C CLASS I HISTOCOMPATIBILITY ANTIGEN, GROGO-BOLD2 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
"TRACELLULAR ALPHA-2."
"TRACELLULAR ALPHA-3."
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Pred. No. 0.076;
1; Mismatches (
                                                       362 AA
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                                                       STANDARD;
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MICROGLOBULIN).
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362 AA;
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                                                       1B02_GORGO
P30380;
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1B03_GORGO
                                   1B02_GORGO
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"Gorilla class I major histocompatibility complex alleles: comparison
to human and chimpanzee class I.";
-1 EXP. Med. 174:1491-1509(1991)
-1 - FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
-1 - SUBNNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
                                                                                                                                                                                                                                                                                  01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last sequence update)
CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0101 ALPHA CHAIN PRECURSOR.
GOTILLA GOTILLA (LOWLAND GOTILLA).
EUKATYOTA: Metazoa; Chordata; Craniata; Metazoa; Chordata; Hominidae; Gotilla.
                                                                                           Gaps
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CLASS I HISTOCOMPATIBILITY ANTIGEN,
GOGO-BOlol ALPHA CHIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-3.
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                                                    Score 44; DB 1; Length 359;
Pred. No. 0.075;
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                                                                                       0; Indels
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5395FFC9 CRC32;
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                                                                                                                                                                                                                                                      362 AA.
                                                                                       1; Mismatches
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HSSP; P03989; JHSA.
PROSITE; PS00290; IG_MHC; 1.
PFAM; PF00147; Ig; 1.
PFAM; PF00129; MHC_L; 1.
MHC I; Transmembrane; Glycoprotein; S1
SIGNAL 124 BY SIMILA
40173 MW;
                                                  89.8%;
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                                   Ouery Match
Best Local Similarity 90.v.
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Best Local Similarity 90.0
Matches 9; Conservative
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362 AA;
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P30379;
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Length 362; 0; Indels

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Query Match
Best Local Similarity
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MEDLINE; 86042671.
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1B47_HUMAN
1D 1B47_HUMAN
AC P30487;
DT 01-APR-1993
DT 01-FEB-1996
DF HLA CLASS I
DE HLA CLASS I
DE PRECURSOR.
GN HLA-B OR HLA-
OC BUTANTYCEA;
CC EUTANTYCEA;
CC EU
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DISULFID
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                                                                        MEDLINE; 92078860.
LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
"Gorilla class I major histocompatibility complex alleles: comparison for himmon and chimpanzee class I.";
J. Exp. Med. 174:1491-1599(1991).
-:- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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SEEMANN G.H.A., REIN R.S., BROWN C.S., PLOEGH H.L.;
"Gene conversion-like mechanisms may generate polymorphism in human
class I genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
CLASS I HISTOCOMPATIBILITY ANTIGEN,
GOGO-BO103 ALPHA CLAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-3.
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01-MAR-1989 (Rel. 10, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2702 ALPHA CHAIN
PRECURSOR (B-27K) (B27.2).
HLA-B OR HLAB.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                            -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
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  Sutheria; Primates; Catarrhini; Hominidae; Gorilla
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1; Mismatches
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PIR; JH0341; JH0541.

PRSSITE; PS00290; IG_MHC; 1.

PFAM: PF00047; Ig; 1.

PFAM: PF00129; MHC_I; 1.

PFAM: PF00129; MHC_I; 1.
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SIMILARITY.
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90.0%;
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Best Local Similarity 90.0
Matches 9; Conservative
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362 AA;
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99 RENLRIALRY 108
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SEQUENCE FROM N.A.
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P10317;
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1B15_HUMAN
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                                                                                                                                                                                                               "Structural analysis of an HLA-B27 functional variant: identification of residues that contribute to the specificity of recognition by cytolytic T lymphocytes.";
Proc. Natl. Acad. U.S.A. 82:7394-7398(1985).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
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01-FBR-1996 (Rel. 33, Last sequence update)
01-FBR-1996 (Rel. 33, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-49(B-21) B*4901 ALPHA CHAIN
PRECURSOR.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 362;
SEQUENCE FROM N.A.
PARHAM P., ARNETI K.L., ADAMS E.J.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                              VEGA M.A., EZQUERRA A., ROJO S., APARICIO P., BRAGADO
LOPEZ DE CASTRO J.A.;
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EXTRACELLULAR ALPHA-2
EXTRACELLULAR ALPHA-3
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Pred. No. 0.076;
1; Mismatches
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MHC I; Transmembrane; Glycoprotein; Signal.
SIGNAL
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EMBL; X03667; CAA27301.1; JOINED.
EMBL; L38504; AAA69724.1; -.
PIS: B25092; HLHUBK.
HSSP; P03989; 1HSA.
MIM; 142830; -.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                          86-107 AND 171-181.
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90.0%;
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99 RENLRIALRY 108
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SIGNAL
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                                                      REVISION TO 78.
MEDINE: 93056229.
HILDEBRAND W.H., MADRIGAL J.A., BELICH M.P., ZEMMOUR J., WARD F.E.,
WILLIAMS R.C., PARHAM P.;
"Serologic cross-reactivities poorly reflect allelic relationships in
the HLA-B12 and HLA-B21 groups. Dominant epitopes of the alpha 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-51(B-5) B*5101 ALPHA CHAIN
PRECURSOR.
                                                                                                                                                                                                                                                                                                                                            HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-49(B-21) B*4901 ALPHA CHAIN. EXTRACELLULAR ALPHA-1.
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                                                                                                                                    -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS
THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
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HOMO sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 44; DB 1; Length 362;
Pred. No. 0.076;
1; Mismatches 0; Indels
                PARHAM P., LAWLOR D.A., LOMEN C.E., ENNIS P.D.; "Diversity and diversification of HLA-A,B,C alleles."; J. Immunol. 142:3937-3950(1989).
                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR ALPHA-2. EXTRACELLULAR ALPHA-3.
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BY SIMILARITY.
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; E996F82F CRC32;
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PROSITE; PS00290; IG_MHC; 1.
PFAM: PF00129; MHC_I: 1.
PFAM: PF00129; MHC_I: 1.
1 24
SIGNAL 12830011.
                                                                                                                          J. Immunol. 149:3563-3568(1992)
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90.0%;
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362 AA;
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Best Local Similarity
Matches 9; Conserv
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SEQUENCE FROM N.A. MEDLINE; 89235215.
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P18464;
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TRANSMEM
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MEDLINE; 90207291.
ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
"Rapid cloning of HAAA,B cDNA by using the polymerase chain
reaction: frequency and nature of errors produced in amplification.";
Proc. Natl. Acad. Sci. U.S.A. 87:2833-2837(1990);
                                                                                                                                 SEQUENCE FROM N.A.
MEDILIE; 89080265.
HATASHI H., ENNIS P.D., ARIGA H., SALTER R.D., PARHAM P., KANO K.,
TAKIGUCHI M.; ILLAWSZ differ by only two amino acids which are in the
"HLA-BSI and HLA-BASZ differ by only two amino acids which are in the
belical region of the alpha I domain.";
J. Immunol. 142:306-311(1989).
                                                                                                                                                                                                                                                                                                                                                                     POHLA H., KUON W., TABACZEWSKI P., DOERNER C., WEISS E.H.;
"Allelic variation in HLA-B and HLA-C sequences and the evolution of the HLA-B alleles."
Immunogenetics 29:297-307(1989).
-: FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
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EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
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4D846F30 CRC32;
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Pred. No. 0.076;
1; Mismatches
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PIR; A30548; A30548.

HSSP, P3049; 1A1M.

MIM; 142830; -.

PROSITE; PS00290; IG_MHC; 1.

PRAM; PF00047; 19; 1.

PFAM; PF00129; MHC_I:

MHC_I: Transmembrane; Glycoprotein; Signal.
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Best Local Similarity 90.0%;
Matches 9; Conservative
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115
207
309
333
110
125
362 AA;
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                                                                                                         SEQUENCE FROM N.A.

MEDLINE, 89080265.

HAYASHI H., ENNIS P.D., ARIGA H., SALTER R.D., PARHAM P., KANO K.,

TAKIGUCHI M.;

"HLA-BS1 and HLA-Bw52 differ by only two amino acids which are in the
helical region of the alpha 1 domain.";

J. Immunol. 142:306-311(1899).

-I- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO

THE IMMONE SYSTEM.

-I- SUBUNI: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-

MICROGLOBULIN).
CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-52(B-5) B*5201 ALPHA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-5218-5) B*5201 ALPHA CHAIN. EXTRACELLULAR ALPHA-1. EXTRACELLULAR ALPHA-2.
                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BY SIMILARITY.
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BY SIMILARITY.
; 38436FE8 CRC32;
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Last sequence update)
Last annotation update)
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PFAM; PF00047; 19; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
24 HT ALL SIGNAL.
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EMBL; M22793; AAA59645.1; JOINED.
EMBL; M22794; AAA59645.1; JOINED.
EMBL; M22795; AAA59645.1; JOINED.
EMBL; M22796; AAA59645.1; JOINED.
EMBL; M22796; AAA59645.1; JOINED.
EMBL; M22798; AAA59645.1; JOINED.
PIR; B305445; B30546.
PIR; B305445; B30548.
HSSP; P30491; IAIM.
MIN; 142830; ...
PROSITE; PS00290; IG_MHC; 1.
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362 AA;
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                             HLA-B OR HLAB.
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01-APR-1993 (
15-JUL-1998 (
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P30491;
              PRECURSOR
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DISULFID
SEQUENCE
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1B54_HUMAN
ID 1B54_H
AC P30491
DT 01-APR
DT 15-JUL
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                                                                                       01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
HA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-51(B-5) B*5104 ALPHA CHAIN
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EXTRACELLUIAR ALPHA-1.
EXTRACELLUIAR ALPHA-2.
CONNECTING PEPTIDE.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE: 92269955.
BELICH M.P., MADRIGAL J.A., HILDEBRAND W.H., ZEMMOUR J.,
MILLIAMS R.C., LUZ R., PETZL-ERLER M.L., PARHAM P.;
"Unusual HIA-B alleles in two tribes of Brazilian Indians.";
Nature 357:326-329(1992).
                                                                                                                                                                                                                                                                                                                                                            THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 362;
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Pred. No. 0.076;
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Last annotation update)
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HSSP; P30491; 1AlM.
MIM; 142830; -.
PROSITE; PS00290; IG_MHC; 1.
PFAM; PF00129; MHC_1; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
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SIMILARITY
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                                                                                                                                                                                         Homo sapiens (Human).
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01-APR-1993
                                                           1B52_HUMAN
P30489;
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P30490;
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                                                                                                                                                                                                MEDLINE; 90207291.

ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;

"Rapid cloning of HLA-A,B cDNA by using the polymerase chain
reaction: frequency and nature of errors produced in amplification.";

Proc. Natl. Acad. Sci. U.S.A. 87:2833-2837(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-57(B-17) B*5701 ALPHA CHAIN. EXTRACELLULAR ALPHA-1.
                                                                                                                                                                                                                                                                                                                          MEDLINE; 91067476.
ISAMAT M., GIRDLESTONE J., MILSTEIN C.;
Nucleotide sequence of an HA-BW57 gene.";
Nucleic Acids Res. 18:6702-6702(1990).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
HLA CLASS I HISTOCOMPAIDILITY ANTIGEN, B-57(B-17) B*5701 ALPHA
CHAIN PRECURSOR (BW57.1).
                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 0.076;
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PFAM; PF00129; MHC_1; 1.
MHC_1: Transmembrane; Glycoprotein; Signal.
1 24
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Best Local Similarity 90.0
Local 9; Conservative
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MIM; 142830; -.
PROSITE; PS00290; I
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362 AA;
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                         HLA-B OR HLAB
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1B61_HUMAN
ID 1B61_HUMAN
AC P30497;
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BW-53 B*5301 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                               "Bound water structure and polymorphic amino acids act together to allow the binding of different peptides to MHC class I HLA-B53."; Immunity 4:215-228(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                    -! - FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-53 B*5301 ALPHA CHAIN
                                                                                                                                                           HAYASHI H., OOBA T., NAKAYAMA S., SEKIMATA M., KANO K., TAKIGUCHI M.; "Allospecificities between HLA-Bw53 and HLA-B35 are generated by substitution of the residues associated with HLA-Bw4/Bw6 public
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                                                                                                                                                                                                                                                                                                                          SMITH K.J., REID S.W., HARLOS K., MCMICHAEL A.J., STUART D.I., BELL J.I., JONES E.Y.;
                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                         THE IMMUNE SYSTEM.

-!- SUBDRIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
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Pred. No. 0.076;
1; Mismatches 0; Indels
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PDB: IAIM: 08-APR-98.
PDB: IAIO: 08-APR-98.
MIM; 142830; -.
PROSITE; PS00290; IG_MHC; 1.
PRAM: PF00047; 19; 1.
PRAM: PF00147; 19; 1.
MHC I; Transmembrane; Glycoprotein; Signal; 3D-structure.
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90.0%;
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362
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362 AA;
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Best Local Similarity
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91033941
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                                     HLA-B OR HLAB.
                                                                                                                             SEQUENCE FROM
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Length 362; 0; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-58(B-17) B*5801 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                           INOUE T., OGAWA A.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN H PRECURSOR
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Eutheria; Primates; Catarrhin; Hominidae; Homo.
   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                   SEQUENCE FROM N.A.
MEDLINE; 86008247.
WAYS J.P., COPPIN H.L., PARHAM P.;
The complete primary structure of HLA-Bw58.";
J. Biol. Chem. 260:11924-11933(1985).
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Pred. No. 0.076;
1; Mismatches
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EMBL; AB008102; BAA22916.1; -.
PIR; A23895; HLHUB8.
HSSP; P30491; IAIM.
MIM; 142830; -.
PROSITE; PS00290; IG_MHC; 1.
PFAM; PF01047; 19; 1.
PFAM; PF01047; 19; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
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Best Local Similarity 90.0
Matches 9; Conservative
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HLA-H OR HLAH.
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99 RENLRIALRY 108
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P01893;
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HLAH_HUMAN
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01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-57(B-17) B*5702 ALPHA CHAIN
PRECURSOR (BW57.2).
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                                                                                                                                                                         SEQUENCE FROM N.A.
MADELINE, 395650B.
MADRIGAL J.A., BELICH M.P., HILDEBRAND W.H., BENJAMIN R.J.,
LITTLE A.-M., ZEMMOUR J., ENNIS P.D., WARD F.E., PETZL-ERLER M.L.,
MARTELL R.W., DU TOIT E.D., PARHAM P.,
"Distinctive HLA-A,B antigens of black populations formed by
interallelic conversion.",
                                                                                                                                                                                                                                                                                        J. IMMUND1. 149:3411-3415(1992).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
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P10319;
01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
15-UUL-1998 (Rel. 36, Last annotation update)
15-UL-1998 (Rel. 36, Last annotation update)
CHAIN PRECURSOR.
HLA-B OR HLAB.
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                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HLA CLASS I HISTOCOMPATIBILITY
B-57(b-17) B*5702 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89.8%; Score 44; DB 1; Length 362; 90.0%; Pred. No. 0.076; 1. Mismatches 0; Indels
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BY SIMILARITY.
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; 628C2156 CRC32;
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PIR; S16774; S16774.
HSSP: P30491; 1A1M.
MIM; 142830; -.
PROSITE; PS00290; IG_MHC; 1.
PFAM; PF00129; MHC_1; 1.
PFAM; PF00129; MHC_1; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
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362
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SIGNAL 1 24
CHAIN 25 363
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362 AA;
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99 RENLRIALRY 108
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Matches 9; Conserv
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RESULT 13 1B62_HUMAN

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Gaps

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Indels

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MICROGLOBULIN).
POLYMORPHISM: THE ONLY ALLELE OF A-23 KNOWN IS A*2301 WHICH IS
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                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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"Molecular definition of an elusive third HLA-A9 molecule: HLA-A9.3.";
Immunogenetics 35:41-45(1992).
-i- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                     MALISSEN M., MALISSEN B., JORDAN B.R.; "Exon/intron organization and complete nucleotide sequence of an HLA
                                                                                                                                                                                                                                                                                                                                                                    HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
ALPHA CHAIN H.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                       Proc. Natl. Acad. Sci. U.S.A. 79:893-897 (1982).
-i- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IRMUNE SYSTEM. COULD BE THE PRODUCT OF A PSEUDOGENE.
-i- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
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15-UUL-1999 (Rel. 38, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-23(A-9) ALPHA CHAIN
PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
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Pred. No. 0.076;
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BY SIMILARITY.
BY SIMILARITY.
'; 5E610F63 CRC32;
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PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
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PIR; A02189; HJH012.
HSSP: P01989; 1HSA.
MIM: 142800; -.
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90.08;
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Best Local Similarity 90.0
Matches 9; Conservative
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WEDLINE; 82151002.
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P30447;
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                                                                                                                                                                                                                                                                                                                         HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
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EXPRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
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Pred. No. 0.076;
1; Mismatches (
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90.08;
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HSSP; P01892; 1AQD.
MIM; 142800; -.
PROSITE; PS00290; IG_MHC;
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PFAM; PF00129; MHC_I; 1.
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99 RENLRIALRY 108
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia;
Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
CAO K., BUNDET L., ZHANG G., FERNANDEZ-VINA M.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF017320; AAB70286.2; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1998 (TrEMBLrel. 05, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
M1-MAY-1999 (TrEMBLrel. 10, Last annotation update)
HLA-B.
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046697;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
MHC CLASS I ANTIGEN HLA-H ORTHOLOG (FRAGMENT).
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Pred. No. 0.14;
1; Mismatches
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74 RENLRIALRY
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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sp_vertebrate:*
sp_unclassified:*
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sp_plant:*
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Maximum DB seq length: 1000000
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"An introdic mutation responsible for a low level of expression of an HIA-A*24 allele.";
Tissue Antigens 50:340-346(1997).
EMBL: 272423; CAB95633.1;
PFAM: PF00129; MHC_I: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHANDANATINGTONG D., SIRIKONG M., LONGTA K., SRINAK D., RUNGROUNG E., BEJCHANDRA S., JUJI T., TOKUNGA K.; Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.

EMBL: U90420; AAB50144.1; -. EMBL. UGA420; AAB50144.1; JOINED.

PEMBL: U90420; MAB50144.1; JOINED.
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CHANDANAYINGYONG D., SIRIKONG M., LONGTA K., SRINAK D., RUNGROUNG E.,
BEJCHANDRA S., BLASCZYK R., GROSSE-WILDE H.;
LAFORET M., FROELICH N., PARISSIADIS A., BAUSINGER H., PFEIFFER TONGIO M.M.;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-JAN-1998 (TIEMBLrel. 05, Last sequence update)
01-NOV-1998 (TIEMBLrel. 08, Last annotation update)
HLA-B. (FRAGMENT).
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I HLA-B (FRAGMENT).
                                                                                                                                                                                    Query Match 89.8%; Score 44; DB 7;
Best Local Similarity 90.0%; Pred. No. 0.23;
Matches 9; Conservative 1; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89.8%; Score 44; DB 7; 90.0%; Pred. No. 0.3; ative 1; Mismatches (
                                                                                                                  1 24 POTENTIAL.
138 138
138 AA; 15610 MW; B8417FAO CRC32;
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99 RENLRIALRY 108
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Best Local Similarity
Matches 9; Conserv
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1-JAN-1998 (TEMBLrel. 05, Last sequence update)
01-NOV-1999 (TEMBLrel. 12, Last annotation update)
MHC CLASS I HISTOCOMPATIBILITY ANTIGEN-B (HLA-B-27KSH) (FRAGMENT).
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 0.22;
                                                                                                                                                                                                    Length 90;
                                                                                                                                                                                                                               0; Indels
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                                            STRAIN-SHAWBA;
GRIMELEY C., MATHER K.A., OBER C.;
GRIMELEY G. (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: AF021212; AAC99794.1; -.
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PETERSDORF E.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
EMBL: U18659; AAB60357.1; -
MIM: 142830; -
        Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAY-1999 (TrEMBLrel. 10, Last annotation update)
HUMAN LEUKOCYTE ANTIGEN PRECURSOR (FRAGMENT).
                                                                                                                                                                                                  Score 44; DB 7;
Pred. No. 0.15;
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90 90
90 AA; 10689 MW; 5E5F2495 CRC32;
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90.0%;
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Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity
9; Conserv?
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27 RENLRIALRY 36
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                        Length 172;
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BLASC2XK R.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; X96473; CAA65327.1; -.
PFAM; PF00129; MHC_I; 1.
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CHANDANAYINGYONG D., SIRIKONG M., LONGTA K., SRINAK D.,
SIRIBOONRIT U., RUNGROUNG E., BEJCHANDRA S.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, U906612, AAB50151.1;
EMBL, U90611, AAB50151.1;
PFAM; PF00129; MHC_I; 1.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I HLA-B (FRAGMENT).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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172
19909 MW; CAAE5641 CRC32;
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172 172
172 AA; 20026 MW; 4D9A1043 CRC32;
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172 AA; 19942 MW; 1A73E47D CRC32;
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Pred. No. 0.3;
1; Mismatches
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90.0%;
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  PFAM; PF00129; MHC_I; 1.
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172 AA;
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Best Local Similarity
Matches 9; Conserv
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65 RENLRIALRY 74
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CHANDANAYINGYONG D., SIRIKONG M., LONGTA K., SRINAK D., RUNGROUNG E.,
BEJCHANDRAS S.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U90422; AAB50146.1;
EMBL; U90424; AAB50146.1;
PFAM; PF00129; MHC_L; 1.
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CHANDANAYINGYONG D., SIRIKONG M., LONGTA K., SRINAK D., RUNGROUNG E.,
BEJCHANDRA S., JUJI T., TOKUNAGA K.;
Submitted (FEB.1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U90419; AAB50143.1; ...
EMBL; U90418; AAB50143.1; JOINED.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                           Length 172;
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Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: U90423; AAB50145.1; -.
EMBL: U90422; AAB50145.1; JOINED.
PFAM: PF00129; MHC_I: 1.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I HLA-B (FRAGMENT).
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I HLA-B (FRAGMENT).
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Pred. No. 0.3;
1; Mismatches
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90.0%; Pred. No. 0.3;
live 1; Mismatches (
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90.0%;
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Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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SEQUENCE 172 AA;
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Homo sapiens (Human).
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TISSUE-BLOOD;
PETERSDORF E.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U28759; AAB60367.1; --
HSSP; P10318; 1R0G.
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                Q29694 PRELIMINARY; PRT; 175 AA. Q29694; Q1-NOV-1996 (TTEMBLrel. 01, Created) 01-NOV-1996 (TEMBLrel. 01, Last sequence update) MHC CLASS I HLA-B ANTIGEN (FRAGMENT).
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MHC CLASS I HLA-A (FRAGMENT).
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90.0%; Pred. No. 0.3;
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180 AA; 20811 MW; CECC3537 CRC32;
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Pred. No. 0.3;
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Matches 9; Conservative
Similarity 90.0
9; Conservative
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PFAM; PF00129; MHC_I; 1.
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                                                                              1 REDLRIALRY 10
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68 RENLRIALRY 77
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Best Local
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Q29694
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                               Score 44; DB 7; Length 172;
Pred. No. 0.3;
1; Mismatches 0; Indels
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CHANDANAXINGYONG D., SIRIKONG M., LONGTA K., SRINAK D.,
SIRIBDONRIT U., RUNGROUNG E., BEJCHANDRA S.;
Submitted (1921-1937) to the EMBL/GenBank/DDBJ databases.
EMBL, U90614; AAB50244.1;
EMBL, U90613; AAB50244.1;
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CHANDRAYINGYONG D., SIRIKONG M., LONGTA K., SRINAK D.,
SIRIBOONAYIUG', RUNGEROUNG E., BEJCHANDRA S.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U906616; AAB50245.1;
FEMBL; U906615, AAB50245.1;
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I HLA-B (FRAGMENT).
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01-JAN-1998 (TEMBLrel. 05, Created)
01-JAN-1998 (TEMBLrel. 05, Last sequence update)
01-JNOV-1998 (TEMBLrel. 08, Last annotation update)
MHC CLASS I HLA-B (FRAGMENT).
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172 172
172 AA; 20026 MW; 4D9A1043 CRC32;
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172
172 AA; 20052 MW; F6214671 CRC32;
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Best Local Similarity 90.0
Matches 9; Conservative
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68 RENLRIALRY 77
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01972
AC 019772
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                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89.8%; Score 44; DB 7; Length 180; 90.0%; Pred. No. 0.31; Live 1; Mismatches 0; Indels
                  0; Indels
                                                                                                                                                                                          019608 PRELIMINARY; PRT, 180 AA. 019608 (TEMBLEE). 05, Created) 01-JAN-1998 (TEMBLEE). 05, Last sequence update) 01-JAN-1999 (TEMBLEE). 12, Last annotation update) MHC CLASS I HLA-A (FRAGMENT).
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180 AA; 20811 MW; CECC3537 CRC32;
Best Local Similarity 90.0%; Pred. No. 0.31;
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Search completed: February 8, 2000, 13:17:39 Job time: 32488 sec

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AF030927 Homo sapiens MHC cl
AF030929 Homo sapiens MHC cl
U59699 Human MHC class I (HL
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1 (Dases I to 250)
Rojas-Munoz,A., Mendez,I. and Yunis,I.
Molecular evolution of HLA-B locus in a small population amerindian community: The Nukak-Maku
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submission
Submitted (07-07-1996) A. Rojas-Munoz, National Institute Of
Health, Immunogenetics, Avenida El Dorado, Carrera 50, Santafe De
Bogota / Zona 6, COLOMBIA
Location/Qualifiers
1. 250
/organism-"Homo sapiens"
/isolate-"Nancy-28"
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H.Sapiens HLA-B gene, exon 2, HB(a) allele.
Y08692
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H.Saplens HLA-B gene, exon 2, HB(b) allele.
Y08693
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/cell_type="white"
/lab_host="s.coli TG1"
/clone="cHBC2(A)"
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Rojas-Munoz, A.
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Locus HSHLABHBB
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gb_pr3:HS611HLA1
gb_pr3:HS639HLA1
gb_pr4:HSKM315S1
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Yo8692 H.Sapiens HLA-B gene, ex YO8694 H.Sapiens HLA-B gene, ex YO8694 H.Sapiens HLA-B gene, ex YO8694 H.Sapiens HLA-B gene, ex YO8694 H.Sapiens HLA-B gene, ex YO9613 Human cell line THAI DCH U90613 Human cell line THAI DCH U90412 Human cell line THAI DCH U90424 Human cell line THAI DCH U90424 Human cell line THAI DCH U90424 Human cell line THAI DCH U90424 Human cell line THAI DCH U90429 Human cell line THAI DCH U90418 Human cell line THAI DCH U90418 Human cell line THAI DCH U90418 Human Expension should be sequence of from patent I14591 Sequence 68 from patent I14592 Sequence 67 from patent I14592 Sequence 67 from patent I14593 Sequence 68 from patent I14593 Sequence 67 from patent I14593 Sequence 68 from patent I14593 Sequence 68 from patent I14593 Sequence 68 from patent I14593 Sequence 68 from patent I14593 Sequence 68 from patent I14593 Sequence 68 from patent I14593 Sequence 68 from patent I14593 Sequence 68 from patent I14593 Human HLA-A3 gene, alle U37114 Human HLA-A24 gene, alle U37112 Human HLA-A24 gene, alle U18987 Human HLA-A24 gene, alle U18987 Human HLA-A24 gene, alle U18987 Human HLA-A24 gene, alle U18987 Human HLA-A24 gene, alle U18987 Human HLA-A24 gene, alle U18987 Human HLA-A24 gene, alle U18987 Human HLA-A24 gene, alle U18987 Human HLA-A24 gene, alle U18987 Human HLA-A24 gene, alle U18987 Human HLA-A24 gene, alle U18987 Human HLA-A24 gene, alle U18987 Human HLA-A24 gene, alle U18987 Human HLA-A24 gene, alle U18987 Human HLA-A24 gene, alle U18987 Human HLA-A24 gene, alle U18987 Human HLA-A24 gene, alle U18987 Human HLA-A24 gene, alle U18987 Human HLA-A24 gene, alle U18987 Human HLA-A24 gene, alle U18987 Human HLA-A24 gene, alle U18987 Human HLA-A24 gene, alle U18987 Human HLA-A24 gene, alle U18987 Human HLA-A24 gene, alle U18987 Human HLA-A24 gene, alle U18987 Human HLA-A24 gene, alle U18987 Human HLA-A24 gene, alle U18987 Human HLA-A24 gene, alle U18987 Human HLA-A24 gene, alle U18987 Human HLA-A24 gene, alle U18987 Human HLA-A24 gene, alle U18987 Human HLA-A24 gene, alle 
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AF030925 Homo sapiens MHC
AF030911 Homo sapiens MHC
U52813 Human MHC
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-MODEL=frame+_p2n.model -DEV=x1p
-MODEL=frame+_p2n.model -DEV=x1p
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                                                                                  About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
    out_format
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  OM of: US-08-653-294-12 to: GenEmbl:*
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Query length: 10
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9b_pr2:HSHLABB1
9b_pr2:HSHLABB1
9b_pr2:HSHLABB1
9b_pr2:HSHLABJ1
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9b_pr2:HSHLABJ1
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gb_pr3:HS538HLA1
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                                                                      Rojas-Munoz, A., Mendez, I. and Yunis, I.
Molecular evolution of HLA-B locus in a small population amerindian community: The Nukak-Maku
(Unpublished)
(Dases 1 to 250)
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Eukaryota; Metazoa; Chordata; Homo.

1 (bases 1 to 250)
Rojas-Munoz, A., Mendez, I. and Yunis, I.
Rojas-Munoz, A., Mendez, I. and Yunis, I.
Molecular evolution of HLA-B locus in a small population amerindian community :The Nukak-Maku
                                                                                                                                                          Dajas murus, ...
Direct Submission
Submitted (07-OCT-1996) A. Rojas-Munoz, National Institute Of
Health, Immunogenetics, Avenida El Dorado, Carrera 50, Santafe De
Bogota / Zona 6, COLOMBIA
Location/Qualifiers
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            Homo sapiens
Eukaryota, Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 250)
                                                                                                                                                                                                                                                            /organism-"Homo sapiens"
/isolate="Tsabel-26"
/isolate="from amerindian community Nukak-Maku"
/db_xref="taxon:9606"
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H.Sapiens HLA-B gene, exon 2, HB(d) allele.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34
                                                                                                                                                                                                                                                                                                                                   /dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <i4. .>250
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/note="allel HB(b)"
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                                                                                                                                                                                                                                                                                                                           /chromosome="6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X08694.1 GI:1619289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 250)
Rojas-Munoz, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: HSHLABHBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-08-653-294-12 x HSHLABHBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51
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ACCESSION
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ORIGIN
SOURCE
ORGANISM
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AUTHORS
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
                                                                           AUTHORS
                                                         REFERENCE
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SOURCE
                                                                                                                                                                                                                                 FEATURES
                                                                                        TITLE
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Submitted (23-FEB-1997) Transfusion Medicine, Faculty of Medicine, Siriral Hospital, Mahidol University, Prannok Road, Bangkok 10700, Thailand
Submitted (07-ocr-1996) A. Rojas-Munoz, National Institute of Health, Immunogenetics, Avenida El Dorado, Carrera 50, Santafe De Bogota / Zona 6, COLOMBIA.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Munication Sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E (bases 1 to 250)
S (Chandanayingyong,D., Sirikong,M., Longta,K., Srinak,D., Rungroung,E., Bejchandra,S., Juji,T. and Tokunaga,K.

E (bases 1 to 250)
S (Chandanayingyong,D., Sirikong,M., Longta,K., Srinak,D., Rungroung,E., Bejchandra,S., Juji,T. and Tokunaga,K.)
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION Human cell line THAI DCH010 MHC class I HLA-B gene (allele ACCESSION FOLD), exon 2.
                                                                                                                                 /isolate="Norman-51"
/isolate="from amerindian community Nukak-Maku"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 10
Gaps: 0
Percent Identity: 90.000
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/cell_type="lymphoblastoid"
/cell_line="THAI DCH010"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 250
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/gene="HLA-B"
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U90420.1 GI:1905830
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